(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
31 October 2002 (31.10.2002)

PCT

(10) International Publication Number
WO 02/086443 A2

(51) International Patent Classification[7]: G01N

(21) International Application Number: PCT/US02/12476

(22) International Filing Date: 18 April 2002 (18.04.2002)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

60/284,770	18 April 2001 (18.04.2001)	US
60/290,492	10 May 2001 (10.05.2001)	US
60/339,245	9 November 2001 (09.11.2001)	US
60/350,666	13 November 2001 (13.11.2001)	US
60/334,370	29 November 2001 (29.11.2001)	US
60/372,246	12 April 2002 (12.04.2002)	US

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(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Declaration under Rule 4.17:
— *of inventorship (Rule 4.17(iv)) for US only*

Published:
— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 02/086443 A2

(54) Title: METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF LUNG CANCER

(57) Abstract: Described herein are methods and compositions that can be used for diagnosis and treatment of lung cancer and similar pathologies. Also described herein are methods that can be used to identify modulators of lung cancer and similar pathologies.

METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF LUNG CANCER

CROSS-REFERENCES TO RELATED APPLICATIONS

This application is related to USSN 60/284,770, filed April 18, 2001; USSN 60/290,492, filed May 10, 2001; USSN 60/334,370, filed November 29, 2001; USSN 60/339,245, filed November 9, 2001; USSN 60/350,666, filed November 13, 2001; and USSN 60/xxx,xxx, filed April 12, 2002 (Docket OMNI-002P); each of which is incorporated herein by reference in its entirety.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in lung cancer; and to the use of such expression profiles and compositions in diagnosis and therapy of lung cancer. The invention further relates to methods for identifying and using agents and/or targets that inhibit lung cancer or related conditions.

BACKGROUND OF THE INVENTION

Lung cancer is the second most commonly occurring cancer in the United States and is the leading cause of cancer-related death. It is estimated that there are over 160,000 new cases of lung cancer in the United States every year. Of those who are diagnosed with lung cancer, 86 percent will die within five years. Lung cancer is the most common visceral cancer in men and accounts for nearly one third of all cancer deaths in both men and women. In fact, lung cancer accounts for 7% of all deaths, due to any cause, in both men and women.

Smoking is the primary cause of lung cancer, with more than 80% of lung cancers resulting from smoking. About 400 to 500 separate gaseous substances are present in the smoke of a non-filter cigarette. The most noteworthy substances include nitrogen oxides, hydrogen cyanide, formaldehyde, benzene, and toluene. The particles present in cigarette smoke contain at least 3,500 individual compounds such as nicotine, tobacco alkaloids (nornicotine, anatabine, anabasine), polycyclic aromatic hydrocarbons (e.g., benzo(a)pyrene, B(a)P), naphthalenes, aromatic amines, phenols, and tobacco-specific nitrosamines.

Tobacco-specific nitrosamines are formed during tobacco curing and processing, and are suspected of causing lung cancer in humans. In rodent studies, regardless of the where or how it is applied, the tobacco-specific nitrosamine known as NNK produces lung adenomas and lung adenocarcinomas. The tobacco-specific nitrosamine known as NNAL also produces lung adenocarcinomas in rodents.

Many of the chemicals found in cigarette smoke also affect the nonsmoker inhaling "secondhand" or sidestream smoke. Indeed, the smoke inhaled by non-smokers has a chemical composition similar to the smoke inhaled by smokers, but, importantly, the concentrations of the carcinogenic tobacco-specific nitrosamines are present in higher concentrations in second hand smoke. For this and other reasons, "passive smoking" is an important cause of lung cancer, causing as many as 3,000 lung cancer deaths in nonsmokers each year.

In addition to smoking, other factors thought to be causes of lung cancer include on-the-job exposure to carcinogens such as asbestos and uranium, exposure to chemical hazards such as radon, polycyclic aromatic hydrocarbons, chromium, nickel, and inorganic arsenic, genetic factors, and diet.

Histological classification of various lung cancers define the types of cancer that begin in the lung. See, e.g., Travis, et al. (1999) Histological Typing of Lung and Pleural Tumours (International Histological Classification of Tumours, No 1. Four major cell types make up more than 88% of all primary lung neoplasms. These are: squamous or epidermoid carcinoma, small cell (also called oat cell) carcinoma, adenocarcinoma, and large cell (also called large cell anaplastic) carcinoma. The remainder include undifferentiated carcinomas, carcinoids, bronchial gland tumors, and other rarer types. The various cell types have different natural histories and responses to therapy, and, thus, a correct histologic diagnosis is the first step of effective treatment.

Small cell lung cancer (SCLC) accounts for 18-25% of all lung cancers, and occurs less frequently than non-small cell lung cancers, and generally spread to distant organs more rapidly than non-small cell lung cancer. In general, at the time of presentation small cell lung cancers have already spread beyond the beyond the bounds where surgery and curative intent can be undertaken. Hoever, if identified early enough, these cancers are often responsive to chemotherapy and thoracic radiation treatment.

Non-small cell lung cancers (NSCLC) are the more frequently occurring form of lung cancer. They comprise squamous cell carcinoma, adenocarcinoma, and large cell carcinoma

and account for more than 75% of all lung cancers. Non-small cell tumors that are localized at the time of presentation can sometimes be cured with surgery and/or radiotherapy, but usually are not identified until significant metastasis has occurred, which are typically not very responsive to surgical, chemotherapy, or radiation treatment..

The screening of asymptomatic persons at high risk for lung cancer has often proven ineffective. In general, only 5 to 15 percent of lung cancer patients have their disease detected while they are asymptomatic. Of course, early detection and treatment are critical factors in the fight against lung cancer. The average survival rate is 49% for those whose cancer is detected early, before the cancer has spread from the lung. Lung cancer often spreads outside of the lung, and it may have spread to the bones or brain by the time it is diagnosed. While the prognosis may be better for lung cancers that are detected early, because of the lack ofv effective curative treatments, early detection does not necessarily alter the total death rate from lung cancer.

Thus, methods for diagnosis and prognosis of lung cancer and effective treatment of lung cancer would be desirable. Accordingly, provided herein are methods that can be used in diagnosis and prognosis of lung cancer. Further provided are methods that can be used to screen candidate therapeutic agents for the ability to modulate, e.g., treat, lung cancer. Additionally, provided herein are molecular targets and compositions for therapeutic intervention in lung disease and other metastatic cancers.

SUMMARY OF THE INVENTION

The present invention provides nucleotide sequences of genes that are up- and down-regulated in lung cancer cells. Such genes are useful for diagnostic purposes, and also as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. The methods of detecting nucleic acids of the invention or their encoded proteins can be used for a number of purposes. Examples include early detection of lung cancers, monitoring and early detection of relapse following treatment of lung cancers, monitoring response to therapy of lung cancers, determining prognosis of lung cancers, directing therapy of lung cancers, selecting patients for postoperative chemotherapy or radiation therapy, selecting therapy, determining tumor prognosis, treatment, or response to treatment, and early detection of precancerous lesions of the lung. Examples of benign or precancerous lesions include: atelectasis, emphysema, brochitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis (HP), interstitial pulmonary fibrosis (IPF), asthma, and

bronchiectasis. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

In one aspect, the present invention provides a method of detecting a lung cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16. Alternatively, the sample may be contacted with a specific binding reagent, e.g., antibody.

In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-16. In another embodiment, the polynucleotide comprises a sequence as shown in Tables 1A-16.

In one embodiment, the biological sample is a tissue sample, or a body fluid. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label. In one embodiment, the polynucleotide is immobilized on a solid surface. In one embodiment, the patient is undergoing a therapeutic regimen to treat lung cancer. In another embodiment, the patient is suspected of having lung cancer. In one embodiment, the patient is a primate, e.g., a human.

In one embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy. Or the sample may be evaluated for protein, e.g., contacting the sample with an antibody.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated transcript to a level of the lung cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. Or the sample may be evalated for comparison of protein.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a

biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated antibody in the biological sample by contacting the biological sample with a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, wherein the polypeptide specifically binds to the lung cancer-associated antibody, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated antibody to a level of the lung cancer-associated antibody in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated polypeptide in the biological sample by contacting the biological sample with an antibody, wherein the antibody specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated polypeptide to a level of the lung cancer-associated polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1A-16. In one embodiment, an expression vector or cell comprises the isolated nucleic acid. In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16. In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical. In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting lung cancer in a a patient, the method comprising contacting a biological sample from the patient with an antibody or protein as described herein.

In another aspect, the present invention provides a method of detecting antibodies specific to a lung cancer gene in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprises a sequence from Tables 1A-16.

In another aspect, the present invention provides a method for identifying a compound that modulates a lung cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a lung cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16; and (ii) determining the functional effect of the compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect. In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant. In one embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation or another critical process of a lung cancer-associated cell to treat lung cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein. In one embodiment, the compound is an antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having lung cancer or a cell isolated therefrom; (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of lung cancer.

In one embodiment, the control is a mammal with lung cancer or a cell therefrom that has not been treated with the test compound. In another embodiment, the control is a normal cell or mammal, or a non-malignant lung disease.

In another aspect, the present invention provides a method for treating a mammal having lung cancer comprising administering a compound identified by the assay described herein.

In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having lung cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and treatment of lung disease or cancer, as well as methods for screening for compositions which modulate lung cancer. "Treatment, monitoring, detection or modulation of lung disease or cancer" includes treatment, monitoring, detection, or modulation of lung disease in those patients who have lung disease (whether malignant or non-malignant, e.g., emphysema, bronchitis, or fibrosis) as well as patients with lung cancers in which gene expression from a gene in Tables 1A-16 is increased or decreased, indicating that the subject is more likely to have disease. In particular,while these targets are identified primarily from lung cancer samples, these same targets are likely to be similarly found in analyses of other medical conditions. These other conditions may result from similar pathological processes which affect similar tissues, e.g., lung cancer, small cell lung carcinoma (oat cell carcinoma), non-small cell carcinomas (e.g., squamous cell carcinoma, adenocarcinoma, large cell lung carcinoma, carcinoid, granulomatous), fibrosis (idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), interstitial pneumonitis, nonspecific idiopathic pneumonitis (NSIP)), chronic obstructive pulmonary disease (COPD, e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, and esophageal cancer. See, e.g., the NCI webpage and USSN 60/347,349 and USSN 60/xxx,xxx (docket LFBR-001-1P, filed March 29, 2002), each of which is incorporated herein by reference. The treatment may be of lung cancer or related condition itself, or treatment of metastasis.

In particular, identification of markers selectively expressed on these cancers allows for use of that expression in diagnostic, prognostic, or therapeutic methods. As such, the invention defines various compositions, e.g., nucleic acids, polypeptides, antibodies, and small molecule agonists/antagonists, which will be useful to selectively identify those markers. For example, therapeutic methods may take the form of protein therapeutics which use the marker expression for selective localization or modulation of function (for those markers which have a causative disease effect), for vaccines, identification of binding partners, or antagonism, e.g., using antisense or RNAi. The markers may be useful for molecular characterization of subsets of lung diseases, which subsets may actually require

very different treatments. Moreover, the markers may also be important in related diseases to the specific cancers, e.g., which affect similar tissues in non-malignant diseases, or have similar mechanisms of induction/maintenance. Metastatic processes or characteristics may also be targeted. Diagnostic and prognostic uses are made available, e.g., to subset related but distinct diseases, or to determine treatment strategy. The detection methods may be based upon nucleic acid, e.g., PCR or hybridization techniques, or protein, e.g., ELISA, imaging, IHC, etc. The diagnosis may be qualitative or quantitative, and may detect increases or decreases in expression levels.

Tables 1A-16 provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in lung cancer samples. The tables also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster. In Table 1A, genes marked as "target 1" or "target 2" are particularly useful as therapeutic targets. Genes marked as "target 3" are particularly useful as diagnostic markers. Genes marked as "chron" are upregulated in chronically diseased lung (e.g., emphysema, bronchitis, fibrosis) relative to lung tumors and normal tissue. In certain analyses, the ratio for the "chron" category was determined using the 70th percentile of chronically diseases lung samples divided by the 90th percentile of normal lung samples. The ratio for the targets was determined using the 70th percentile of lung tumor samples divided by the 90th percentile of normal lung samples.

Definitions

The term "lung cancer protein" or "lung cancer polynucleotide" or "lung cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologs that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1A-16 and conservatively modified variants thereof; or (4)

have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "lung cancer polypeptide" and a "lung cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" lung cancer protein or nucleic acid refers to a lung cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains the elements normally contained in one or more naturally occurring, wild type lung cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translational processing or splicing, including alternative splicing.

"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a lung cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, archival materials, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or other mammal; or a bird; reptile; fish. Livestock and domestic animals are of interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues or materials, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the

same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using, e.g., a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site http://www.ncbi.nlm.nih.gov/BLAST/ or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions and/or insertions, substitutions, and naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer

Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology.

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) Proc. Nat'l. Acad. Sci. USA 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between

two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be negative large numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells *in vivo*, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least about 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant or component from the composition to be purified.

In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymier.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ-carboxyglutamate, and O-phosphoserine. Amino acid analogs refer to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain some basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refer to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that function similarly to another amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU each encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of

conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally similar molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions include for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton, Proteins (1984)).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts, et al. (1994) Molecular Biology of the Cell (3rd ed.) and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β-sheet and α-helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50 or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have at least one different linkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphophoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford University Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, in Sanghui and Cook, eds. Carbohydrate Modifications in Antisense Research, ASC Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary

strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, physiological, chemical, or other physical means. For example, useful labels include ^{32}P, fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The labels may be incorporated into the cancer nucleic acids, proteins, and antibodies. Many methods known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter, et al. (1962) Nature 144:945; David, et al. (1974) Biochemistry 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth., 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope tags, a toxin; activatable moieties, a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting "hard" e.g., beta radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method

using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, e.g., through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, preferably one that does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled, e.g., with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed *in vitro*, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed *in vitro* by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e., using the *in vivo* cellular machinery of the host cell rather than *in vitro* manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered

recombinant for the purposes of the invention. Similarly, a "recombinant protein" is a protein made using recombinant techniques, i.e., through the expression of a recombinant nucleic acid as depicted above.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is typically an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed in operable linkage to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule selectively to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to essentially no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Probes (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m, 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions are often: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32° C and 48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50° C to about 65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90° C - 95° C for 0.5 - 2 min., an annealing phase lasting 0.5 - 2 min., and an extension phase of about 72° C for 1 - 2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis, et al.(1990) PCR Protocols, A Guide to Methods and Applications.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This

occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous reference, e.g., Ausubel, et al. (ed.) Current Protocols in Molecular Biology Lippincott.

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a lung cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the lung cancer protein or nucleic acid, e.g., a physiological, enzymatic, functional, physical, or chemical effect, such as the ability to decrease lung cancer. It includes ligand binding activity; cell viability, cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein expression in cells undergoing metastasis, and other characteristics of lung cancer cells. "Functional effects" include *in vitro*, *in vivo*, and *ex vivo* activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a lung cancer protein sequence, e.g., physiological, functional, enzymatic, physical, or chemical effects. Such functional effects can be measured by many means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the lung cancer protein; measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation. Determination of the functional effect of a compound on lung cancer can also be performed using lung cancer assays known to those of skill in the art such as an *in vitro* assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein

expression in cells undergoing metastasis, and other characteristics of lung cancer cells. The functional effects can be evaluated by many means known to those skilled in the art, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for lung cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β-gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators", and "modulators" of lung cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using *in vitro* and *in vivo* assays of lung cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of lung cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may seem to inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate lung cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of lung cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules and the like. Such assays for inhibitors and activators include, e.g., expressing the lung cancer protein *in vitro*, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of lung cancer can also be identified by incubating lung cancer cells with the test compound and determining increases or decreases in the expression of 1 or more lung cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50 or more lung cancer proteins, such as lung cancer proteins encoded by the sequences set out in Tables 1A-16.

Samples or assays comprising lung cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a lung cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more

preferably 200-500% (i.e., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics *in vitro* or *in vivo*, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., Freshney (1994) Culture of Animal Cells a Manual of Basic Technique pp. 231-241 (3rd ed.).

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells, or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy (see, Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (3rd ed.)).

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul, Fundamental Immunology.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible

for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain joined to V_H-C_H1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see Paul (ed. 1999) Fundamental Immunology (4th ed.). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized *de novo* either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized *de novo* using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty, et al. (1990) Nature 348:552-554).

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many technique known in the art can be used (see, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. (1985), pp. 77-96 in Monoclonal Antibodies and Cancer Therapy; Coligan (1991 and supplements) Current Protocols in Immunology; Harlow and Lane (1988) Antibodies, A Laboratory Manual; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.)). Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens (see, e.g., McCafferty, et al. (1990) Nature 348:552-554; Marks, et al. (1992) Biotechnology 10:779-783).

A "chimeric antibody" is an antibody molecule in which, e.g, (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the

variable region, or a portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

Identification of lung cancer-associated sequences

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different lung cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of lung cancer (chronic disease, adenocarcinoma, etc.)

The identification of sequences that are differentially expressed in lung cancer versus non-lung cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate lung cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, a treatment step may induce other markers which may be used as targets to destroy tumor cells. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Malignant diseasemay be compared to non-malignant conditions. Metastatic tissue can also be analyzed to determine the stage of lung cancer in the tissue, or origin of primary tumor, e.g., metastasis from a remote primary site. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the lung cancer expression profile. This may be done by making biochips comprising sets of the important lung cancer genes, which can then be used in these screens. PCR methods may be applied with selected primer pairs, and analysis may be of RNA or of genomic sequences. These methods can also be done on the protein basis; that is, protein expression levels of the lung cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the lung cancer

nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the lung cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs or as protein or DNA vaccines.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in lung cancer relative to normal tissues and/or non-malignant lung disease, or in different types of lung disease, herein termed "lung cancer sequences." As outlined below, lung cancer sequences include those that are up-regulated (i.e., expressed at a higher level) in lung cancer, as well as those that are down-regulated (i.e., expressed at a lower level). In a preferred embodiment, the lung cancer sequences are from humans; however, as will be appreciated by those in the art, lung cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other lung cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (dogs, cats, etc.). Lung cancer sequences from other organisms may be obtained using the techniques outlined below.

Lung cancer sequences can include both nucleic acid and amino acid sequences. As will be appreciated by those in the art and is more fully outlined below, lung cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the lung cancer sequences can be generated.

A lung cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the lung cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, e.g., using homology programs or hybridization conditions.

For identifying lung cancer-associated sequences, the lung cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, cancer and non-malignant conditions, non-malignant conditions and normal tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing lung cancer samples with metastatic cancer samples from other cancers, such as, breast, other gastrointestinal cancers, prostate, ovarian,

etc. Samples of, non metastatic disease tissue and tissue undergoing metastasis are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix, Santa Clara, CA. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal lung, but also including, and not limited to colon, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the lung cancer screen that are expressed in significant amounts in other tissues (e.g., essential organs) are removed from the profile, although in some embodiments, this is not necessary (e.g., where organs may be dispensible at a later stage of life). That is, when screening for drugs, it is usually preferable that the target expression be disease specific, to minimize possible side effects on other organs.

In a preferred embodiment, lung cancer sequences are those that are up-regulated in lung cancer; that is, the expression of these genes is higher in cancerous tissue than in normal lung or other tissue. "Up-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater. Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. Unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, DA, et al (1998) Nucleic Acids Research 26:1-7 and http://www.ncbi.nlm.nih.gov/. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, such as FGENESH (Salamov and Solovyev (2000) Genome Res. 10:516-522). In other situations, sequences have been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, lung cancer sequences are those that are down-regulated in the lung cancer; that is, the expression of these genes is lower in cancerous tissue

or normal lung or other tissue. "Down-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater, or, when the ratio is presented as a number less than one, that the ratio is less than one, preferably 0.5 or less, more preferably 0.25 or less.

Informatics

The ability to identify genes that are over or under expressed in lung cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with lung cancer. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA (June 11-12, 1998)). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample representing lung cancer, i.e., the identification of lung cancer-associated sequences described herein, provide an abundance of information, which can be correlated with

pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

See also Mount, et al. (2001) Bioinformatics; Durbin, et al. (eds., 1999) Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids (; Baxevanis and Oeullette (eds., 1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins); Rashidi and Buehler (1999) Bioinformatics: Basic Applications in Biological Science and Medicine; Setubal, et al. (eds 1997) Introduction to Computational Molecular Biology; Misener and Krawetz (eds, 2000) Bioinformatics: Methods and Protocols; Higgins and Taylor (eds., 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical

Approach; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the Internet; Han and Kamber (2000) Data Mining: Concepts and Techniques (2000); and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for lung cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may

be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC,

MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

Characteristics of lung cancer-associated proteins

Lung cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In one embodiment, the lung cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes (see, e.g., Alberts (ed. 1994) Molecular Biology of the Cell (3d ed.). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2

domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden (see, e.g., Bateman, et al (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420; Bateman, et al. (1999) Nuc. Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-322).

In another embodiment, the lung cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels, pumps, and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the

localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site http://psort.nibb.ac.jp/).

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, hormones, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they may mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains may also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Lung cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for extracellular immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins *in situ* or in histological analysis. Alternatively, antibodies can also label intracellular proteins, in which case analytical samples are typically permeablized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful lung markers of disease.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the lung cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit

signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, sax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Lung cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.

Use of lung cancer nucleic acids

As described above, lung cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the lung cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

The lung cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1A-16, can be fragments of larger genes, i.e., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the lung cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, et al., *supra*. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, http://www.ncbi.nlm.nih.gov/UniGene/).

Once a lung cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire lung cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant lung cancer nucleic acid can be further-used as a probe to identify and isolate

other lung cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant lung cancer nucleic acids and proteins.

The lung cancer nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the lung cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, RNAi, vaccine, and/or antisense applications. Alternatively, the lung cancer nucleic acids that include coding regions of lung cancer proteins can be put into expression vectors for the expression of lung cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to lung cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the lung cancer nucleic acids, i.e., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under appropriate reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally complements of ORFs or whole genes are not used. In some embodiments, nucleic acids of lengths up to hundreds of bases can be used.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a

particular target. The probes can be overlapping (i.e., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is typically meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to a biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. Often the substrate may contain discrete individual sites appropriate for ndivitual partitioning and identification. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in US application entitled Reusable Low Fluorescent Plastic Biochip, U.S.

Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized, and then attached to the surface of the solid support. Either the 5' or 3' terminus may be attached to the solid support, or attachment may be via linkage to an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized *in situ*, using known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of lung cancer-associated sequences. These assays are typically performed in conjunction with

reverse transcription. In such assays, a lung cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of lung cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols, A Guide to Methods and Applications.

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560, Landegren, et al. (1988) Science 241:1077, and Barringer, et al. (1990) Gene 89:117), transcription amplification (Kwoh, et al. (1989) Proc. Natl. Acad. Sci. USA 86:1173), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Nat. Acad. Sci. USA 87:1874), dot PCR, and linker adapter PCR, etc.

Expression of lung cancer proteins from nucleic acids

In a preferred embodiment, lung cancer nucleic acids, e.g., encoding lung cancer proteins, are used to make a variety of expression vectors to express lung cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known to those of skill in the art (see, e.g., Ausubel, *supra*, and Fernandez and Hoeffler (eds 1999) Gene Expression Systems) and are used to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the lung cancer protein. The term "control sequences" refers to DNA

sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the lung cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences may be either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector often contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating

vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art (e.g., Fernandez and Hoeffler, *supra*).

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The lung cancer proteins of the present invention are usually produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a lung cancer protein, under the appropriate conditions to induce or cause expression of the lung cancer protein. Conditions appropriate for lung cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaebacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the lung cancer proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral and adenoviral systems. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez and Hoeffler, *supra*). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived form SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, lung cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the lung cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez and Hoeffler, *supra*). The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, lung cancer proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, lung cancer protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*,

Kluyveromyces fragilis and *K. lactis*, *Pichia guillerimondii,* and *P. pastoris,* *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The lung cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the lung cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the lung cancer protein may be made as a fusion protein to increase expression for affinity purification purposes, or for other reasons. For example, when the lung cancer protein is a lung cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In a preferred embodiment, the lung cancer protein is purified or isolated after expression. Lung cancer proteins may be isolated or purified in a variety of appropriate ways. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the lung cancer protein may be purified using a standard anti-lung cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes (1982) Protein Purification. The degree of purification necessary will vary depending on the use of the lung cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the lung cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, therapeutic entities, for production of antibodies, as transcription or translation inhibitors, etc.

Variants of lung cancer proteins

In one embodiment, the lung cancer proteins are derivative or variant lung cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative lung cancer peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at a particular residue within the lung cancer peptide.

Also included within one embodiment of lung cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three

classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the lung cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant lung cancer protein fragments having up to about 100-150 residues may be prepared by *in vitro* synthesis. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the lung cancer protein amino acid sequence. The variants typically exhibit a similar qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed lung cancer variants screened for the optimal combination of desired activity. Techniques exist for making substitution mutations at predetermined sites in DNA having a known sequence, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of mutants is often done using assays of lung cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be occasionally tolerated. Deletions generally range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. Larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of a lung cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution chart provided in the definition section.

Variants typically exhibit essentially the same qualitative biological activity and will elicit the same immune response as a naturally-occurring analog, although variants also are selected to modify the characteristics of lung cancer proteins as needed. Alternatively, the

variant may be designed or reorganized such that a biological activity of the lung cancer protein is altered. For example, glycosylation sites may be added, altered, or removed.

Covalent modifications of lung cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a lung cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a lung cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking lung cancer polypeptides to a water-insoluble support matrix or surface for use in a method for purifying anti-lung cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimidate.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serinyl, threonyl or tyrosyl residues, methylation of the γ-amino groups of lysine, arginine, and histidine side chains (Creighton (1983) Proteins: Structure and Molecular Properties, pp. 79-86), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the lung cancer polypeptide encompassed by this invention is an altered native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended herein to mean adding to or deleting one or more carbohydrate moieties of a native sequence lung cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express lung cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to lung cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence lung cancer polypeptide (for O-linked glycosylation sites). The lung cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the lung cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the lung cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330, and in Aplin and Wriston (1981) CRC Crit. Rev. Biochem., pp. 259-306.

Removal of carbohydrate moieties present on the lung cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al. (1987) Arch. Biochem. Biophys., 259:52 and by Edge, et al. (1981) Anal. Biochem., 118:131. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura, et al. (1987) Meth. Enzymol., 138:350.

Another type of covalent modification of lung cancer comprises linking the lung cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192, or 4,179,337.

Lung cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a lung cancer polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a lung cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the lung cancer polypeptide. The presence of such epitope-tagged forms of a lung cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the lung cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a lung cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known and examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies

thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3(6):547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:6393-6397).

Also included are other lung cancer proteins of the lung cancer family, and lung cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related lung cancer proteins from primates or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include unique areas of the lung cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. PCR reaction conditions are well known in the art (e.g., Innis, PCR Protocols, *supra*).

Antibodies to lung cancer proteins

In a preferred embodiment, when a lung cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the lung cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller lung cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are well known (e.g., Coligan, *supra*; and Harlow and Lane, *supra*). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 1A-16 or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal

being immunized. Immunogenic proteins include, e.g., keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Adjuvants include, e.g., Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of the tables, or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding (1986) Monoclonal Antibodies: Principles and Practice, pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovin, or primate origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are typically monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of the tables or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to lung cancer protein are capable of reducing or eliminating a biological function of a lung cancer protein, in a naked form or conjugated to an effector moiety. That is, the addition of anti-lung cancer protein antibodies (either polyclonal or preferably monoclonal) to lung cancer tissue (or cells containing lung cancer) may reduce or eliminate the lung cancer. Generally, at least a 25% decrease in activity, growth, size or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the lung cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Medarex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of a human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. A humanized antibody optimally also will typically comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones, et al. (1986) <u>Nature</u> 321:522-525; Riechmann, et al. (1988) <u>Nature</u> 332:323-329; and Presta (1992) <u>Curr. Op. Struct. Biol.</u> 2:593-596). Humanization can be performed following the method of Winter and co-workers (Jones, et al. (1986) <u>Nature</u> 321:522-525; Riechmann, et al. (1988) <u>Nature</u> 332:323-327; Verhoeyen, et al. (1988) <u>Science</u> 239:1534-1536), by substituting rodent CDRs or CDR sequences for corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by corresponding sequence from a non-human species.

Human-like antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom and Winter (1991) J. Mol. Biol. 227:381; Marks, et al. (1991) J. Mol. Biol. 222:581). The techniques of Cole, et al. and Boerner, et al. are also available for the preparation of human monoclonal antibodies (Cole, et al. (1985) Monoclonal Antibodies and Cancer Therapy, p. 77 and Boerner, et al. (1991) J. Immunol. 147(1):86-95). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in nearly all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Fishwild, et al. (1996) Nature Biotechnology 14:845-51; Neuberger (1996) Nature Biotechnology 14:826; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

By immunotherapy is meant treatment of lung cancer with an antibody raised against a lung cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the lung cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, may bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted lung cancer protein.

In another preferred embodiment, the lung cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment may bind the extracellular domain of the lung cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The

antibody may cause down-regulation of the transmembrane lung cancer protein. The antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the lung cancer protein. The antibody may be an antagonist of the lung cancer protein or may prevent activation of a transmembrane lung cancer protein, or may induce or suppress a particular cellular pathway. In some embodiments, when the antibody prevents the binding of other molecules to the lung cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF-α, TNF-β, IL-1, INF-γ, and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody may belong to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, lung cancer may be treated by administering to a patient antibodies directed against the transmembrane lung cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be various molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of a lung cancer protein. In another aspect the therapeutic moiety may modulate an activity of molecules associated with or in close proximity to a lung cancer protein. The therapeutic moiety may inhibit enzymatic or signaling activity such as protease or collagenase activity associated with lung cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to lung cancer tissue or cells results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with lung cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, saporin, auristatin, and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against lung cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane lung cancer proteins not only serves to increase the local concentration of therapeutic moiety in the lung cancer

afflicted area, but also serves to reduce deleterious side effects that may be associated with the untargeted therapeutic moiety.

In another preferred embodiment, the lung cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein or other entity which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the lung cancer protein can be targeted within a cell, i.e., the nucleus, an antibody theretomay contain a signal for that target localization, i.e., a nuclear localization signal.

The lung cancer antibodies of the invention specifically bind to lung cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μM, preferably at least about 0.1 μM or better, and most preferably, 0.01 μM or better. Selectivity of binding to the specific target and not to related other sequences is also important.

Detection of lung cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the lung cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing lung cancer), in lung cancer tissue (and in some cases, for varying severities of lung cancer that relate to prognosis, as outlined below), or in non-malignant disease are evaluated to provide expression profiles. A gene expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g.,

normal versus lung cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; i.e., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart (1996) Nature Biotechnology 14:1675-1680, hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e., upregulation or downregulation) is typically at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the RNA or DNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the lung cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to lung cancer genes, e.g., those identified as being important in a lung cancer or disease phenotype, can be evaluated in a lung cancer diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes.

The lung cancer nucleic acid probes may be attached to biochips as outlined herein for the detection and quantification of lung cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity. Multiple protein expression monitoring can be performed as well. Similarly, these assays may be performed on an individual basis as well.

In a preferred embodiment nucleic acids encoding the lung cancer protein are detected. Although DNA or RNA encoding the lung cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a lung cancer protein is detected.

Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed *in situ*. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxygenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a lung cancer protein is detected by binding the digoxygenin with an anti-digoxygenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, lung cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as markers of lung cancer, e.g., for prognostic or diagnostic purposes. Detection of these proteins in putative lung cancer tissue allows for detection, prognosis, or diagnosis of lung cancer or similar disease, and perhaps for selection of therapeutic strategy. In one embodiment, antibodies are used to detect lung cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the lung cancer protein is detected, e.g., by immunoblotting with antibodies raised against the lung cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the lung cancer protein find use in *in situ* imaging techniques, e.g., in histology (e.g., Asai (ed. 1993) Methods in Cell Biology:

Antibodies in Cell Biology, volume 37. In this method cells are contacted with from one to many antibodies to the lung cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label, e.g., multicolor fluorescence or confocal imaging. In another method the primary antibody to the lung cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of lung cancer proteins. Many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing lung cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of lung cancer proteins. Antibodies can be used to detect a lung cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous lung cancer protein or vaccine.

In a preferred embodiment, *in situ* hybridization of labeled lung cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including lung cancer tissue and/or normal tissue, are made. *In situ* hybridization (see, e.g., Ausubel, *supra*) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to lung cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple

genes may be useful in various combinations. As above, lung cancer probes may be attached to biochips for the detection and quantification of lung cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

In a preferred embodiment, the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, et al. (1998) Science 279:84-8; Heid (1996) Genome Res. 6:986-94.

In a preferred embodiment, the lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified lung cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the lung cancer phenotype or an identified physiological function of a lung cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, *supra.*

Having identified differentially expressed genes herein, a variety of assays may be performed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene with altered regulation in lung cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the lung cancer protein. "Modulation" thus includes an increase or a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing lung cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in lung cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in lung

cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the lung cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene or protein expression monitoring of a number of entities, i.e., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the lung cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of lung cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more lung cancer-associated sequences, e.g., a polynucleotide sequence set out in the tables. Generally, in a preferred embodiment, a test compound is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate lung cancer, modulate lung cancer proteins, bind to a lung cancer protein, or interfere with the binding of a lung cancer protein and an antibody, substrate, or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the lung cancer phenotype or the expression of a lung cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles of nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a lung cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induces a lung cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

In one aspect, a modulator will neutralize the effect of a lung cancer protein. By "neutralize" is meant that activity of a protein and the consequent effect on the cell is inhibited or blocked.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a lung cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks (Gallop, et al. (1994) J. Med. Chem. 37(9):1233-1251).

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature, 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Nat. Acad. Sci. USA 90:6909-6913), vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et

al. (1992) J. Amer. Chem. Soc. 114:9217-9218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661), oligocarbamates (Cho, et al. (1993) Science 261:1303), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14(3):309-314, and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, Baum (1993) C&EN, Jan 18, page 33; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual synthetic operations performed by a chemist. The above devices, with appropriate modification, are suitable for use with the present invention. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect modulation of lung cancer gene transcription, polypeptide expression, and polypeptide activity.

High throughput assays for evaluating the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins,

U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (i.e., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate procedures, including sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that the nucleic acid or peptide consists of essentially random sequences of nucleotides and amino acids, respectively. Since these random peptides (or nucleic acids, discussed below) are often chemically synthesized, they may incorporate a nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. In a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc.

Modulators of lung cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. Digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After a candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence is analyzed. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an *in vitro* transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

Nucleic acid assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos.

5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allow formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the lung cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state,

screens are performed to identify agents that bind and/or modulate the biological activity of the gene product, or evaluate genetic polymorphisms.

Genes can be screened for those that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress a lung cancer expression pattern leading to a normal expression pattern, or to modulate a single lung cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated lung cancer tissue reveals genes that are not expressed in normal tissue or lung cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for lung cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated lung cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of lung cancer cells, that have an associated lung cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once a test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., lung cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress a lung cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on lung cancer activity. By defining such a signature for the lung cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

Measure of lung cancer polypeptide activity, or of lung cancer or the lung cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the metastatic polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of lung cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian lung cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed *in vitro*. For example, a lung cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the lung cancer polypeptide levels are determined *in vitro* by measuring the level of protein or mRNA. The level of protein is typically measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the lung cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNAse protection, dot blotting, are preferred. The level of protein or mRNA is typically detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using a lung cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β-gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed

genes are sometimes referred to herein as "lung cancer proteins." The lung cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the lung cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a lung cancer protein and a candidate compound, and determining the binding of the compound to the lung cancer protein. Preferred embodiments utilize the human lung cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative lung cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the lung cancer protein or the candidate agent is non-diffusably bound to an insoluble support, preferably having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is typically not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition, and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation

sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the lung cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the lung cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled *in vitro* protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the lung cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the lung cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor may be a binding moiety known to bind to the target molecule (i.e., a lung cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between 4 and 40° C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically

between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by a test compound. Displacement of the competitor is an indication that the test compound is binding to the lung cancer protein and thus is capable of binding to, and potentially modulating, the activity of the lung cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the lung cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the lung cancer protein.

In a preferred embodiment, the methods comprise differential screening to identity agents that are capable of modulating the activity of the lung cancer proteins. In one embodiment, the methods comprise combining a lung cancer protein and a competitor in a first sample. A second sample comprises a test compound, a lung cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the lung cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the lung cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native lung cancer protein, but cannot bind to modified lung cancer proteins. The structure of the lung cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a lung cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results.

Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a lung cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising lung cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a lung cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate lung cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the lung cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting lung cancer cell division is provided. The method comprises administration of a lung cancer inhibitor. In another embodiment, a method of inhibiting lung cancer is provided. The method may comprise administration of a lung cancer inhibitor. In a further embodiment, methods of treating cells or individuals with lung cancer are provided, e.g., comprising administration of a lung cancer inhibitor.

In one embodiment, a lung cancer inhibitor is an antibody as discussed above. In another embodiment, the lung cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, viability, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of lung cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described in Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (3rd ed.), herein incorporated by reference. See also, the methods section of Garkavtsev, et al. (1996), *supra*, herein incorporated by reference.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (^{3}H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (1994), *supra*. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (^{3}H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a lung cancer-associated sequence and are grown for 24 hours at saturation density in

non-limiting medium conditions. The percentage of cells labeling with (^{3}H)-thymidine is determined autoradiographically. See, Freshney (1994), *supra*.

Growth factor or serum dependence

Transformed cells typically have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) J. Natl. Cancer Insti. 37:167-175; Eagle, et al. (1970) J. Exp. Med. 131:836-879); Freshney, *supra*. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g., Gullino, "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) Biological Responses in Cancer, pp. 178-184). Similarly, Tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) "Angiogenesis and Cancer" in Sem Cancer Biol.).

Various techniques which measure the release of these factors are described in Freshney (1994), *supra*. Also, see, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino, "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) Biological Responses in Cancer, pp. 178-184; Freshney Anticancer Res. 5:111-130 (1985).

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate lung cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), *supra*, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by prelabeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), *supra*.

Tumor growth in vivo

Effects of lung cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the lung cancer gene is disrupted or in which a lung cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous lung cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous lung cancer gene with a mutated version of the lung cancer gene, or by mutating the endogenous lung cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi, et al. (1989) Science 244:1288). Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual, Cold Spring Harbor Laboratory and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach, , IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) J. Natl. Cancer Inst. 52:921), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) Br. J. Cancer 38:263; Selby, et al. (1980) Br. J. Cancer 41:52) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a lung cancer-associated sequences are injected subcutaneously. After a suitable length of time,

preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

Polynucleotide modulators of lung cancer

Antisense and RNAi Polynucleotides

In certain embodiments, the activity of a lung cancer-associated protein is downregulated, or entirely inhibited, by the use of antisense or an inhibitory polynucleotide, i.e., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a lung cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the lung cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized *in vitro*. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for lung cancer molecules. A preferred antisense molecule is for a lung cancer sequence in the tables, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein

is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659 and van der Krol, et al. (1988) BioTechniques 6:958).

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) Sciencexpress (21March2002); Sharp (1999) Genes Dev. 13:139-141; and Cathew (2001) Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

Ribozymes

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of lung cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25: 289-317 for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparing are well known to those of skill in the art (see, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-45; Leavitt, et al. (1995) Proc. Natl. Acad. Sci. USA 92:699-703; Leavitt, et al. (19994) Human Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126).

Polynucleotide modulators of lung cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of lung cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by

formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating lung cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-lung cancer antibody that reduces or eliminates the biological activity of an endogenous lung cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a lung cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the lung cancer sequence is down-regulated in lung cancer, such state may be reversed by increasing the amount of lung cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous lung cancer gene or administering a gene encoding the lung cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, e.g., when the lung cancer sequence is up-regulated in lung cancer, the activity of the endogenous lung cancer gene is decreased, e.g., by the administration of a lung cancer antisense or RNAi nucleic acid.

In one embodiment, the lung cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to lung cancer proteins. Similarly, the lung cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify lung cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a lung cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The lung cancer antibodies may be coupled to standard affinity chromatography columns and used to purify lung cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the lung cancer protein.

Methods of identifying variant lung cancer-associated sequences

Without being bound by theory, expression of various lung cancer sequences is correlated with lung cancer. Accordingly, disorders based on mutant or variant lung cancer genes may be determined. In one embodiment, the invention provides methods for

identifying cells containing variant lung cancer genes, e.g., determining all or part of the sequence of at least one endogenous lung cancer genes in a cell. In a preferred embodiment, the invention provides methods of identifying the lung cancer genotype of an individual, e.g., determining all or part of the sequence of at least one lung cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced lung cancer gene to a known lung cancer gene, i.e., a wild-type gene.

The sequence of all or part of the lung cancer gene can then be compared to the sequence of a known lung cancer gene to determine if any differences exist. This can be done using known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the lung cancer gene of the patient and the known lung cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the lung cancer genes are used as probes to determine the number of copies of the lung cancer gene in the genome.

In another preferred embodiment, the lung cancer genes are used as probes to determine the chromosomal localization of the lung cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the lung cancer gene locus.

Administration of pharmaceutical and vaccine compositions

In one embodiment, a therapeutically effective dose of a lung cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques (e.g., Ansel, et al. (1992) Pharmaceutical Dosage Forms and Drug Delivery; Lieberman, Pharmaceutical Dosage Forms (vols. 1-3), Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding; and Pickar (1999) Dosage Calculations). Adjustments for lung cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration,

drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the lung cancer proteins and modulators thereof of the present invention can be done in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the lung cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a lung cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose,

lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that lung cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise a lung cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., Remington's Pharmaceutical Science (15th ed., 1980) and Hardman, et al. (eds. 1996) Goodman and Gilman: The Pharmacologial Basis of Therapeutics).

Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent to those skilled in the art, e.g., Remington's Pharmaceutical Science and Goodman and Gilman, The Pharmacologial Basis of Therapeutics, *supra*.

The compositions containing modulators of lung cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present lung cancer protein-modulating compounds can be administered alone or in combination with additional lung cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in the tables, such as antisense or RNAi polynucleotides or ribozymes, will be introduced into cells, *in vitro* or *in vivo*. The present invention provides methods, reagents, vectors, and cells useful for expression of lung cancer-associated polypeptides and nucleic acids using *in vitro* (cell-free), *ex vivo*, or *in vivo* (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors and other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (see, e.g.,

Berger and Kimmel, Guide to Molecular Cloning Techniques, Methods in Enzymology volume 152 (Berger), Ausubel, et al. (eds. 1999) Current Protocols (supplemented through 1999), and Sambrook, et al. (1989) Molecular Cloning - A Laboratory Manual (2nd ed., Vol. 1-3).

In a preferred embodiment, lung cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, lung cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the lung cancer coding regions) can be administered in a gene therapy application. These lung cancer genes can include antisense or inhibitory applications, e.g., as inhibitory RNA or gene therapy (e.g., for incorporation into the genome) or as antisense compositions.

Lung cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses.. Such vaccine compositions can include, e.g., lipidated peptides (see, e.g.,Vitiello, et al. (1995) J. Clin. Invest. 95:341), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in immune stimulating complexes (ISCOMS) (see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin Exp Immunol. 113:235-243), multiple antigen peptide systems (MAPs) (see, e.g., Tam (1988) Proc. Natl. Acad. Sci. U.S.A. 85:5409-5413; Tam (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p. 379 In: Kaufmann (ed. 1996) Concepts in vaccine development; Chakrabarti, et al. (1986) Nature 320:535; Hu, et al. (1986) Nature 320:537; Kieny, et al. (1986) AIDS Bio/Technology 4:790; Top, et al. (1971) J. Infect. Dis. 124:148; Chanda, et al. (1990) Virology 175:535), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25; Eldridge, et al. (1993) Sem. Hematol. 30:16; Falo, et al. (1995) Nature Med. 7:649), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369; Gupta, et al. (1993) Vaccine 11:293), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585; Rock (1996) Immunol. Today 17:131), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745; Robinson, et al. (1993) Vaccine 11:957; Shiver, et al., p. 423 In: Kaufmann (ed. 1996) Concepts in vaccine development; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923 and Eldridge, et al. (1993) Sem. Hematol. 30:16). Toxin-targeted

delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bortadella pertussis* or *Mycobacterium tuberculosis* derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff, et. al. (1990) Science 247:1465 as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivicaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode lung cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors useful for therapeutic administration or immunization e.g., adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the

like, will be apparent to those skilled in the art from the description herein (see, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85).

Methods for the use of genes as DNA vaccines are well known, and include placing a lung cancer gene or portion of a lung cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a lung cancer patient. The lung cancer gene used for DNA vaccines can encode full-length lung cancer proteins, but more preferably encodes portions of the lung cancer proteins including peptides derived from the lung cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a lung cancer gene. For example, lung cancer-associated genes or sequence encoding subfragments of a lung cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the lung cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment lung cancer genes find use in generating animal models of lung cancer. When the lung cancer gene identified is repressed or diminished in metastatic tissue, gene therapy technology, e.g., wherein antisense or inhibitory RNA directed to the lung cancer gene will also diminish or repress expression of the gene. Animal models of lung cancer find use in screening for modulators of a lung cancer-associated sequence or modulators of lung cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the lung cancer protein. When desired, tissue-specific expression or knockout of the lung cancer protein may be necessary.

It is also possible that the lung cancer protein is overexpressed in lung cancer. As such, transgenic animals can be generated that overexpress the lung cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene.

Animals generated by such methods will find use as animal models of lung cancer and are additionally useful in screening for modulators to treat lung cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In diagnostic and research applications such kits may include at least one of the following: assay reagents, buffers, lung cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, RNAi, dominant negative lung cancer polypeptides or polynucleotides, small molecule inhibitors of lung cancer-associated sequences, etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing instructions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. A medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of lung cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a lung cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing lung cancer-associated activity. Optionally, the kit contains biologically active lung cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes typically will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

EXAMPLES

Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

Tables 1A and 1B were previously filed on April 18, 2001 in USSN 60/284,770 (18501-001500US) and on November 29, 2001 in USSN 60/334,370 (18501-001520US)

Table 1A

Pkey	ExAccn	UnigeneID	Unigene Title	70% chron/90% NL	70% SQAD/90% NL
100134	D13264	Hs.49	macrophage scavenger receptor 1	1.61	0.74
100780	HG3731-HT4001		""Immunoglobulin Heavy Chain, Vdjrc Reg	2.68	3.28
100971	J02874	Hs.83213	fatty acid binding protein 4; adipocyte	1.96	0.14
101088	L05568	Hs.553	solute carrier family 6 (neurotransmitte	0.79	0.07
101102	L07594	Hs.79059	transforming growth factor; beta recepto	2.55	1
101168	L15388	Hs.211569	G protein-coupled receptor kinase 5	0.88	0.27
101277	L38486	Hs.118223	microfibrillar-associated protein 4	0.89	0.26
101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	0.59	0.29
101336	L49169	Hs.75678	FBJ murine osteosarcoma viral oncogene h	1.15	0.41
101345	L76380	Hs.152175	calcitonin receptor-like	0.81	0.31
101678	M62505	Hs.2161	complement component 5 receptor 1 (C5a l	1.31	0.77
101764	M80563	Hs.81256	S100 calcium-binding protein A4 (calcium	1.44	0.82
101771	M81750	Hs.153837	myeloid cell nuclear differentiation ant	0.96	0.45
101842	M93221	Hs.75182	mannose receptor; C type 1	1.27	0.37
102283	U31384	Hs.83381	guanine nucleotide binding protein 11	1.04	0.3
102363	U39447	Hs.198241	amine oxidase; copper containing 3 (vasc	0.96	0.26
102507	U52154	Hs.193044	potassium inwardly-rectifying channel; s	2.81	3.45
102698	U75272	Hs.1867	progastricsin (pepsinogen C)	0.95	0.23
103025	X54131	Hs.123641	protein tyrosine phosphatase; receptor t	1.62	0.21
103280	X79981	Hs.76206	cadherin 5; VE-cadherin (vascular epithe	0.9	0.41
103496	Y09267	Hs.132821	flavin containing monooxygenase 2	1.27	0.49
103541	Z11697	Hs.79197	CD83 antigen (activated B lymphocytes; i	1.86	1
103554	Z18951	Hs.74034	caveolin 1; caveolae protein; 22kD	1.27	0.47
104212	AB002298	Hs.173035	KIAA0300 protein	1.17	0.16
104691	AA011176	Hs.37744	ESTs	1.08	0.35
104825	AA035613	Hs.141883	ESTs	0.75	0.27
104857	AA043219	Hs.19058	ESTs	2.6	3.3
104865	AA045136	Hs.22575	ESTs	1.23	0.49
104989	AA102098	Hs.118615	ESTs	0.63	0.32
105729	AA292694	Hs.3807	ESTs; Weakly similar to PHOSPHOLEMMAN PR	0.86	0.34
105847	AA398606	Hs.32241	ESTs	1.32	0.4
105894	AA400979	Hs.25691	calcitonin receptor-like receptor activi	0.78	0.28
106490	AA451861	Hs.115537	ESTs; Weakly similar to dipeptidase prec	1.2	0.47
106536	AA453997	Hs.23804	ESTs	0.82	0.15
106605	AA457718	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	0.99	0.07
106667	AA461086	Hs.16578	ESTs	1.17	0.4
106773	AA478109	Hs.188833	ESTs	1.46	0.43
106797	AA478962	Hs.169943	ESTs	1.18	0.32
106844	AA485055	Hs.158213	sperm associated antigen 6	0.98	0.51
106870	AA487576	Hs.26530	serum deprivation response (phosphatidyl	1.05	0.14
106954	AA496980	Hs.204038	ESTs	1.25	0.33
107054	AA600150	Hs.14366	ESTs	1.11	0.4
107292	T30407	Hs.4789	ESTs; Weakly similar to oxidative-stress	1.07	2.58
107994	AA036811	Hs.165030	ESTs	0.7	0.21
107997	AA037388	Hs.82223	Human DNA sequence from clone 141H5 on c	1.02	0.48
108041	AA041552	Hs.61957	ESTs	1.44	0.51
108087	AA045709	Hs.40545	ESTs	1.98	1
108382	AA074885	Hs.67726	macrophage receptor with collagenous str	1.52	0.72
108435	AA078787	Hs.194101	ESTs	2.53	1.53
108480	AA081093	Hs.68055	ESTs	1.56	0.48
109252	AA194830	Hs.85944	ESTs	2.69	3.18
109550	F01534	Hs.26981	ESTs	1.19	0.65
109613	F03031	Hs.27519	ESTs	1.01	0.29
109837	H00656	Hs.29792	ESTs	0.81	0.15
109893	H04768	Hs.30484	ESTs	1.44	0.32
109984	H09594	Hs.10299	ESTs	0.62	0.14
110099	H16568	Hs.23748	ESTs	1.01	0.28
110837	N30796	Hs.17424	ESTs; Weakly similar to semaphorin F [H.	1.1	0.22
111247	N69825	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	1.26	0.26
111341	N80935	Hs.22483	ESTs	1.57	0.52
111510	R07856	Hs.16355	ESTs	3.96	1
111737	R25410	Hs.9218	ESTs	0.97	0.24
113195	T57112		""yc20g11.s1 Stratagene lung (#937210)	1.22	0.35
113238	T62979	Hs.189813	ESTs	2.27	0.45
113540	T90496	Hs.16757	ESTs	1.06	0.22
113552	T90889	Hs.16026	ESTs	1.16	0.42
113606	T93093	Hs.17125	ESTs	1.48	0.7
113695	T96965	Hs.17948	ESTs	1.54	0.28
113946	W84753	Hs.37896	ESTs	1.79	0.72
114251	Z39898	Hs.21948	ESTs	1.95	0.25
114359	Z41589	Hs.153483	ESTs; Moderately similar to H1 chloride	1.42	0.13
115230	AA278300	Hs.182980	ESTs	2.62	0.42
115279	AA279760	Hs.63671	ESTs	1.79	0.91
115566	AA398083	Hs.43977	ESTs	0.86	0.2
115965	AA446661	Hs.173233	ESTs	0.79	0.04
116166	AA461556	Hs.202949	KIAA1102 protein	2.29	0.68
116279	AA486073	Hs.57362	ESTs	2.27	0.78
117023	H88157	Hs.41105	ESTs	1.36	0.16

117209	H99959	Hs.42768	ESTs	1.46	0.48
118901	N90719	Hs.94445	ESTs	1.51	1
118981	N93839	Hs.39288	ESTs	1.34	0.48
119073	R32894	Hs.45514	v-ets avian erythroblastosis virus E26 o	1.14	0.27
119221	R98105		""yr30g11.s1 Soares fetal liver spleen	1.32	0.53
119824	W74536	Hs.184	advanced glycosylation end product-speci	1	0.19
119861	W80715		ESTs; Moderately similar to !!!! ALU SUB	1.83	0.45
120041	W92775	Hs.59368	ESTs	1.23	0.55
120132	Z38839	Hs.125019	ESTs; Highly similar to KIAA0886 protein	0.91	0.37
120467	AA251579	Hs.187628	ESTs	1.87	1.91
121314	AA402799	Hs.182538	ESTs	1.3	0.31
121643	AA417078	Hs.193767	ESTs	2.31	0.68
121690	AA418074	Hs.110286	ESTs	1.47	0.51
122633	AA454080	Hs.34853	inhibitor of DNA binding 4; dominant neg	1.31	0.63
123978	C20653	Hs.170278	ESTs	1.52	0.32
124214	H58608	Hs.151323	ESTs	0.93	0.35
124357	N22401		""yw37g07.s1 Morton Fetal Cochlea Homo	1.29	1
124438	N40188	Hs.102550	ESTs	1.36	0.7
125167	W45560	Hs.102541	ESTs	1.46	0.69
125174	W51835	Hs.231082	EST	3.07	3.76
125422	AA903229	Hs.153717	ESTs	1.34	0.3
125561	AI417667	Hs.22978	ESTs	1.89	0.63
125831	D60988		""HUM145B09B Clontech human fetal brain	0.94	0.36
127002	R35380	Hs.24979	ESTs	3.02	4.06
127307	AA369367	Hs.126712	ESTs; Weakly similar to pIL2 hypothetica	1.01	0.69
127609	AA622559	Hs.150318	ESTs	1.21	0.32
127959	AI302471	Hs.124292	ESTs	2.5	1
128458	D52193	Hs.56340	ESTs	1.13	0.33
128624	AA479209	Hs.102647	ESTs	1.45	0.58
128789	AA486567	Hs.105695	ESTs	1.1	0.34
128798	AF014958	Hs.105938	chemokine (C-C motif) receptor-like 2	1.16	0.55
128952	R51076	Hs.107361	ESTs; Highly similar to Rap2 interacting	2.04	2.4
129057	X62466	Hs.214742	CDW52 antigen (CAMPATH-1 antigen)	1.77	0.73
129210	AA401654	Hs.202949	KIAA1102 protein	1.11	0.36
129240	W24360	Hs.237868	interleukin 7 receptor	0.91	0.41
129402	T63781		""yc21g01.s1 Stratagene lung (#937210)	1.36	0.43
129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1	0.67	0.08
129593	AA487015	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	1.3	0.42
129626	AA447410	Hs.11712	ESTs; Weakly similar to !!!! ALU SUBFAMI	1.28	0.46
129699	AA458578	Hs.12017	KIAA0439 protein; homolog of yeast ubiqu	1.58	1
129898	N48595	Hs.13256	ESTs	1.13	0.53
129958	L20591	Hs.1378	annexin A3	0.81	0.31
130273	U59914	Hs.153863	MAD (mothers against decapentaplegic; Dr	0.59	0.22
130655	N92934	Hs.17409	cysteine-rich protein 1 (intestinal)	1.44	0.76
130657	T94452	Hs.201591	ESTs	0.96	0.42
131061	N64328	Hs.22567	ESTs; Moderately similar to HYPOTHETICAL	1.51	0.45
131066	F09006	Hs.22588	ESTs	0.97	0.37
131263	R38334	Hs.24950	regulator of G-protein signalling 5	2.34	2.82
131589	U52100	Hs.29191	epithelial membrane protein 2	1.2	0.62
131686	AA157428	Hs.30687	Grb2-associated binder 2	0.95	0.38
131751	H18335	Hs.31562	ESTs	1.47	0.52
132430	T23630	Hs.258675	EST	1.86	2.09
132476	N67192	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	1.73	0.58
132836	F09557	Hs.57929	slit (Drosophila) homolog 3	0.91	0.29
133120	X64559	Hs.65424	tetranectin (plasminogen-binding protein	0.82	0.2
133488	D45370	Hs.74120	adipose specific 2	1.29	0.48
133565	H57056	Hs.204831	ESTs	2.25	0.57
133651	U97105	Hs.173381	dihydropyrimidinase-like 2	1.65	0.62
133835	AA059489	Hs.76640	ESTs; Highly similar to RGC-32 [R.norveg	1.16	0.34
133978	W73859	Hs.78061	transcription factor 21	0.79	0.27
133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec	0.99	0.28
134299	AA487558	Hs.8135	ESTs	1.02	0.46
134300	U81984	Hs.166082	endothelial PAS domain protein 1	0.86	0.42
134323	AA028976	Hs.8175	Homo sapiens mRNA; cDNA DKFZp564M0763 (f	1.19	0.27
134343	D50683	Hs.82028	transforming growth factor; beta recepto	1.21	0.67
134417	D87969	Hs.82921	solute carrier family 35 (CMP-sialic aci	1.28	1
134561	U76421	Hs.85302	adenosine deaminase; RNA-specific; B1 (h	2.12	0.55
134624	W67147	Hs.8700	deleted in liver cancer 1	2.35	2.74
134696	H88354	Hs.8861	ESTs	1.35	0.33
134749	L10955	Hs.89485	carbonic anhydrase IV	0.89	0.2
134786	L06139	Hs.89640	TEK tyrosine kinase; endothelial (venous	0.48	0.21
134869	T35288	Hs.90421	ESTs; Moderately similar to !!!! ALU SUB	2.14	2.64
135346	M21056	Hs.992	phospholipase A2; group IB (pancreas)	0.63	0.13
100113	D00591	Hs.84746	Chromosome condensation 1	1	2.15
100147	D13666	Hs.136348	Homo sapiens mRNA for osteoblast specifi	0.5	2
100280	D42085	Hs.155314	KIAA0095 gene product	1.02	1.39
100335	D63391	Hs.6793	platelet-activating factor acetylhydrola	1	5.58
100360	D78335	Hs.75939	Uridine monophosphate kinase	0.91	2.04
100372	D79997	Hs.184339	KIAA0175 gene product	0.75	2.03
100486	HG1112-HT1112		TIGR: ras-like protein TC4	1.09	1.93
100559	HG2197-HT2267		"collagen, type VII, alpha 1"	0.97	3.6
100576	HG2290-HT2386		"calcitonin/alpha-CGRP, alt. transcript	1	1
100668	HG2981-HT3938		"TIGR: CD44 (epican, alt. transcript 12	0.85	1.9
100906	HG4716-HT5158		Guanosine 5'-Monophosphate Synthase	1.18	2.29
100930	HG721-HT4827		"TIGR: placental protein 14, endometrial	1	1.45

100960	J00124	Hs.117729	keratin 14 (epidermolysis bullosa simple	0.84	2.6
101031	J05070	Hs.151738	"Matrix metalloproteinase 9 (gelatinase	0.77	1.52
101111	L08424	Hs.1619	Achaete-scute complex (Drosophila) homol	1	1
101124	L10343	Hs.112341	"Protease inhibitor 3, skin-derived (SKA	0.62	2.67
101175	L18920	Hs.36980	"Melanoma antigen, family A, 2"	1	1
101204	L24203	Hs.82237	Ataxia-telangiectasia group D-associated	0.74	4.1
101431	M19888	Hs.1076	Small proline-rich protein 1B (cornifin)	0.85	2.51
101448	M21389	Hs.195850	keratin 5 (epidermolysis bullosa simplex	0.61	8.83
101511	M27826	Hs.267319	Endogenous retroviral protease	1.03	1.13
101526	M29540	Hs.220529	Carcinoembryonic antigen-related cell ad	1.07	4.61
101548	M31328	Hs.71642	"Guanine nucleotide binding protein (G p	0.97	1.13
101625	M57293		"Human parathyroid hormone-related pepti	1	1
101649	M60047	Hs.1690	Heparin-binding growth factor binding pr	1	2.7
101724	M69225	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	1	8.98
101748	M76482	Hs.1925	Desmoglein 3 (pemphigus vulgaris antigen	1	2.78
101759	M80244	Hs.184601	"Solute carrier family 7 (cationic amino	1.07	2.45
101804	M86699	Hs.169840	TTK protein kinase	1	1
101806	M86757	Hs.112408	S100 calcium-binding protein A7 (psorias	0.74	1.76
101809	M86849		"Homo sapiens connexin 26 (GJB2) mRNA, c	1	7
101845	M93426	Hs.78867	"Protein tyrosine phosphatase, receptor-	1	1
101851	M94250	Hs.82045	Midkine (neurite growth-promoting factor	1.13	2.6
102083	U10323	Hs.75117	"Interleukin enhancer binding factor 2,	1.03	1.61
102154	U17760	Hs.75517	"Laminin, beta 3 (nicein (125kD), kalini	0.94	3.62
102193	U20758	Hs.313	secreted phosphoprotein 1 (osteopontin;	0.34	4.59
102305	U33286	Hs.90073	chromosome segregation 1 (yeast homolog)	1.45	2.97
102348	U37519	Hs.87539	Aldehyde dehydrogenase 8	0.52	2.25
102581	U61145	Hs.77256	Enhancer of zeste (Drosophila) homolog 2	0.91	2.46
102610	U65011	Hs.30743	Preferentially expressed antigen in mela	1	3.88
102623	U66083	Hs.37110	"Melanoma antigen, family A, 9 (MAGE-9)"	1	1
102669	U71207	Hs.29279	Eyes absent (Drosophila) homolog 2	1	1
102696	U74612	Hs.239	Forkhead box M1	1.06	2.77
102829	U91618	Hs.80962	Neurotensin	1	1
102888	X04741	Hs.76118	Ubiquitin carboxyl-terminal esterase L1	1.13	2.59
102913	X07696	Hs.80342	keratin 15	0.7	4.72
102915	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin	1.15	3.35
102963	X15943	Hs.37058	"Calcitonin/calcitonin-related polypepti	1	1
103021	X53587	Hs.85266	"Integrin, beta 4"	1.38	2.34
103036	X54925	Hs.83169	Matrix metalloprotease 1 (interstitial c	1	14.93
103058	X57348	Hs.184510	Stratifin	1.25	4.17
103060	X57766	Hs.155324	matrix metalloproteinase 11 (stromelysin	1	1.72
103119	X63629	Hs.2877	"Cadherin 3, P-cadherin (placental)"	1.16	7.38
103206	X72755	Hs.77367	monokine induced by gamma interferon	0.71	1.48
103242	X76342	Hs.389	"Alcohol dehydrogenase 7 (class IV), mu	1	1
103312	X82693	Hs.3185	"Lymphocyte antigen 6 complex, locus D;	0.92	1.28
103478	Y07755	Hs.38991	S100 calcium-binding protein A2	1.05	5.81
103558	Z19574	Hs.2785	keratin 17	0.65	6.68
103576	Z26317	Hs.2631	Desmoglein 2	0.79	1.73
103587	Z29083	Hs.82128	5T4 Oncofetal antigen	1	3.93
103594	Z31560	Hs.816	"SRY (sex determining region Y)-box 2, p	0.71	7.23
103768	AA089997		"ESTs, Highly similar to integral membra	0.99	1.8
104158	AA454908	Hs.8127	KIAA0144 gene product	0.96	1.29
104558	R56678	Hs.88959	Human DNA sequence from clone 967N21 on	1.23	7.23
104689	AA010665		ESTs	0.96	2.11
104733	AA019498	Hs.23071	ESTs	1.18	1.88
104906	AA055809	Hs.26802	Protein kinase domains containing protei	1.11	3.15
104978	AA088458	Hs.19322	ESTs; Weakly similar to !!!! ALU SUBFAMI	1.64	2.89
105012	AA116036	Hs.9329	"Homo sapiens mRNA for fls353, complete	1.19	3.91
105175	AA186804	Hs.25740	ESTs; Weakly similar to unknown [S.cerev	0.9	4.63
105263	AA227926	Hs.6682	ESTs	0.95	2.87
105298	AA233459	Hs.26369	ESTs	1	1.13
105312	AA233854	Hs.23348	S-phase kinase-associated protein 2 (p45	1.32	3.01
105719	AA291644	Hs.36793	Hypothetical protein FLJ23188	1.28	2.31
105743	AA293300	Hs.9598	ESTs	1	1
106012	AA411621	Hs.8895	ESTs; same as BFH6?	0.94	2.04
106231	AA429571	Hs.38002	KIAA1355 protein	1.04	1.5
106540	AA454607	Hs.38114	Hypothetical protein FLJ11100	1.26	2.26
106575	AA456039	Hs.105421	ESTs	1	2
106632	AA459897	Hs.11950	GPI-anchored metastasis-associated prote	0.87	1.32
106727	AA465342	Hs.34045	Hypothetical protein FLJ20764	0.87	1.59
106906	AA490237	Hs.222024	Transcription factor BMAL2 (cycle-like f	0.61	1.6
107059	AA608545	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	0.48	2.67
107104	AA609786	Hs.15243	Nucleolar protein 1 (120kD)	1.01	1.44
107151	AA621169	Hs.8687	ESTs; procollagen I-N proteinase	0.97	2.89
107284	S74039	Hs.291904	Accessory proteins BAP31/BAP29	1.15	3.65
107901	AA026418	Hs.91539	ESTs	0.72	3.44
107922	AA028028	Hs.61460	Ig superfamily receptor LNIR precursor	1	2.48
107932	AA029317	Hs.18878	Hypothetical protein FLJ21620	1	1
108695	AA121315	Hs.70823	KIAA1077 protein	0.91	3.53
108857	AA133250	Hs.62180	ESTs	1	1
108860	AA133334	Hs.129911	ESTs	0.73	7.3
108990	AA152296	Hs.72045	ESTs	1	1
109166	AA179845	Hs.73625	"RAB6 interacting, kinesin-like (rabkine	1	4.55
109424	AA227919	Hs.85962	Hyaluronan synthase 3	1	1.28
109665	F05012	Hs.27027	Hypothetical protein DKFZp762H1311	1.42	2
109970	H09281	Hs.13234	ESTs	1.13	2.16

110015	H10998	Hs.7164	A disintegrin and metalloproteinase doma	0.84	1.95
110156	H18957	Hs.4213	ESTs	0.94	1.41
110561	H59617	Hs.5199	HSPC150 protein similar to ubiquitin-con	0.91	3.18
111223	N68921	Hs.34806	ESTs; Weakly similar to neogenin [H.sapi	0.91	3.13
111345	N89820	Hs.14559	Hypothetical protein FLJ10540	1	1.25
111876	R38239	Hs.293246	"ESTs, Weakly similar to putative p150 [	0.83	1.27
111902	R39191	Hs.109445	KIAA1020 protein	0.91	0.91
112244	R51309	Hs.70823	KIAA1077 protein	0.77	3.01
112973	T17271		"cDNA FLJ13308 fis, clone OVARC1001436,	1	1
112989	T23482	Hs.89981	"Diacylglycerol kinase, zeta (104kD)"	0.55	1.03
113047	T25867	Hs.7549	ESTs	0.87	2
113095	T40920	Hs.126733	ESTs	1	1
113531	T90345	Hs.16740	Hypothetical protein FLJ11036	0.42	1.44
113970	W86748	Hs.8109	ESTs	1.17	1.73
114346	Z41450	Hs.130489	"ATPase, aminophospholipid transporter-l	0.86	0.82
114407	AA010188	Hs.103305	ESTs	0.8	1.88
114471	AA028074	Hs.104613	RP42 homolog	1.06	1.34
114509	AA043551	Hs.101799	KIAA1350 protein	1.82	2.32
115060	AA253214	Hs.198249	"Gap junction protein, beta 5 (connexin	0.79	1.49
115091	AA255900	Hs.184523	KIAA0965 protein	0.72	1.92
115123	AA256642	Hs.236894	"ESTs, High sim to LRP1_hu low density l	0.59	1.97
115291	AA279943	Hs.122579	ESTs	1	1.25
115506	AA292537	Hs.45207	Hypothetical protein KIAA1335	1.15	1.48
115522	AA331393	Hs.47378	ESTs	0.5	3.29
115536	AA347193	Hs.62180	ESTs	1	1
115697	AA411502	Hs.63325	Homo sapiens type II membrane serine pro	1	6.53
115909	AA436666	Hs.59761	ESTs	1	6.98
115978	AA447522	Hs.69517	Differentially expressed in Fanconi anem	1	2.31
116028	AA452112	Hs.42644	thioredoxin-like	0.99	1.68
116107	AA456968	Hs.92030	ESTs	1.14	1.8
116134	AA460246	Hs.50441	CGI-04 protein	1.11	1.86
116157	AA461063	Hs.44298	Hypothetical protein	0.99	1.9
116158	AA461187	Hs.61762	Hypoxia-inducible protein 2	0.44	0.86
116335	AA495830	Hs.87013	"Homo sapiens cDNA FLJ10238 fis, clone H	0.62	3.89
116483	C14092	Hs.76118	Ubiquitin carboxyl-terminal esterase L1	1.04	2.36
117320	N23239	Hs.211092	LUNX protein; PLUNC(palate lung & nasal	0.51	0.64
117557	N33920	Hs.44532	Diubiquitin	1.11	2.63
117693	N40939	Hs.112110	PTD007 protein	0.98	1.79
117881	N50073	Hs.260622	Butyrate-induced transcript 1	1	1.43
118368	N64339	Hs.48956	ESTs	0.67	2.86
118566	N68558	Hs.42824	Hypothetical protein FLJ10718	1.21	0.83
118695	N71781	Hs.50081	KIAA1199 see CVA7.doc	0.88	1.63
119780	W72967	Hs.191381	ESTs; Weakly similar to hypothetical pro	1	1
119845	W79920	Hs.58561	G protein-coupled receptor 87	1	1
120102	W95428	Hs.132927	"ESTs, Moderately similar to p53 regulat	1	1
120104	W95477	Hs.180479	ESTs	0.69	3.07
120486	AA253400	Hs.137569	Tumor protein 63 kDa with strong homolog	1.08	12.05
120859	AA350158	Hs.1619	Achaete-scute complex (Drosophila) homol	1	1
120880	AA360240	Hs.97019	EST	1	1
120948	AA397822	Hs.104650	Hypothetical protein FLJ10292	1.04	2.15
120983	AA398209	Hs.97587	EST	1	1
121362	AA405500	Hs.97932	Chondromodulin I precursor	1	1
121369	AA405657	Hs.128791	CGI-09 protein	1	1.8
121791	AA423978	Hs.293317	"ESTs, Weakly similar to JM27 [H.sapiens	1	1
123005	AA479726	Hs.105577	ESTs	1	1
123044	AA481549	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	0.95	1.88
123160	AA488687	Hs.284235	ESTs	1.59	4.98
123479	AA599469	Hs.135056	clone RP5-850E9 on chromosome 20	1.19	1.64
123571	AA608956	Hs.112619	"ESTs, Weakly similar to PQ0109 Purkinje	1.03	1.14
123829	AA620697	Hs.112208	XAGE-1 protein	1.39	2.2
124006	D60302	Hs.108977	ESTs	1	4.85
124059	F13673	Hs.99769	ESTs	1.49	8.62
124960	T15386	Hs.194766	Seizure related gene 6 (mouse)-like	0.76	0.77
125218	W73561	Hs.110024	NADH:ubiquinone oxidoreductase MLRQ subu	1.33	1.77
125453	R06041	Hs.18048	"Melanoma antigen, family A, 10"	0.8	1.42
125759	AA425587	Hs.82226	Glycoprotein (transmembrane) nmb	1.52	2.26
125972	AA434562	Hs.35406	"ESTs, Highly similar to unnamed protein	1.05	2.48
125994	H55782	Hs.270799	EST	1	1.95
126395	N70192	Hs.278956	Hypothetical protein FLJ12929	1	1.35
126645	AI167942	Hs.61635	STEAP1 (Homo sapiens BAC clone RG041D11	1	2.23
127221	AI354332	Hs.72365	ESTs	0.73	3.27
127479	AA513722	Hs.179729	collagen; type X; alpha 1 (Schmid metaph	0.51	1.94
128192	AI204246		KIAA1085 protein	1.8	3.16
128610	L38608	Hs.10247	activated leucocyte cell adhesion molecu	0.89	0.97
128777	U46006	Hs.10526	Cysteine and glycine-rich protein 2	1	1
128924	AA234962	Hs.26557	Plakophilin 3	1.3	2.97
129041	H58873	Hs.169902	"Solute carrier family 2 (facilitated gl	0.84	2.04
129099	H50398	Hs.108660	"ATP-binding cassette, sub-family C (CFT	0.87	1.04
129404	AA172056	Hs.111128	ESTs	1	1
129466	L42583		"Genbank Homo sapiens keratin 6 isoform	0.72	12.67
129605	S72493	Hs.115947	Keratin 16 (focal non-epidermolytic palm	0.92	1.5
129628	U26727	Hs.1174	"Cyclin-dependent kinase inhibitor 2A (m	0.85	1.93
130023	X13461	Hs.239600	Calmodulin-like 3	0.84	1.22
130080	X14850	Hs.147097	"H2A histone family, member X"	0.98	1.96
130385	AA126474	Hs.155223	stanniocalcin 2	1	1

130410	V01514	Hs.155421	Alpha-fetoprotein	0.63	0.63
130441	U35835	Hs.301387	"Human DNA-PK mRNA, partial cds"	1.15	3.65
130482	L32866	Hs.1578	Baculoviral IAP repeat-containing 5 (sur	1	1.88
130553	AA430032	Hs.252587	Pituitary tumor-transforming 1	0.92	1.96
130577	M35410	Hs.162	Insulin-like growth factor binding prote	1.17	4.7
130627	L23808	Hs.1695	Matrix metalloproteinase 12 (macrophage	0.69	4.05
130800	AA223386	Hs.19574	ESTs; Weakly similar to katanin p80 subu	1.13	2.41
130939	AA598689	Hs.21400	ESTs	0.8	0.89
131046	X02530	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN PRECURS	0.8	1.15
131244	D38076	Hs.24763	RAN binding protein 1	1.13	1.85
131877	J04088	Hs.156346	Topoisomerase (DNA) II alpha (170kD)	1	1
131927	AA461549	Hs.34780	"Doublecortex; lissencephaly, X-linked (	0.81	0.62
131965	W90146	Hs.35962	ESTs	0.74	3.27
131978	D80008	Hs.36232	KIAA0186 gene product	1	1
132354	L05187	Hs.211913	Small proline-rich protein 1A	0.69	1.43
132543	AA417152	Hs.5101	ESTs; Highly similar to protein regulati	0.79	4.27
132632	N59764	Hs.5398	guanine-monophosphate synthetase	1	1.08
132653	U31201	Hs.54451	"laminin gamma2 chain gene (LAMC2), exon	1	1
132659	Z75190	Hs.54481	"Low density lipoprotein receptor-relate	0.89	0.89
132710	W93726	Hs.55279	"Serine (or cysteine) proteinase inhibit	0.64	4.41
132758	W52432	Hs.56105	"ESTs, Weakly similar to WDNM RAT WDNM1	1.55	2.08
132767	L05188	Hs.231622	Small proline-rich protein 2B	0.83	1.66
132816	M74542	Hs.575	Aldehyde dehydrogenase 3	0.55	0.55
132990	AA458761	Hs.18387	transcription factor AP-2 alpha (activat	1	3.53
133070	U69611	Hs.64311	"A disintegrin and metalloproteinase dom	1.16	2
133282	U52960	Hs.286145	"SRB7 (suppressor of RNA polymerase B, y	1	2.7
133317	AA215299	Hs.70830	U6 snRNA-associated Sm-like protein LSm7	0.95	1.42
133370	AA156897	Hs.72157	Homo sapiens mRNA; cDNA DKFZp564I1922	1.12	2.55
133391	X57579	Hs.727	H.sapiens activin beta-A subunit (exon 2	1.65	1.76
133832	H03387	Hs.241305	estrogen-responsive B box protein (EBBP)	1.02	1.39
134032	Z81326	Hs.78589	"Serine (or cysteine) proteinase inhibit	1	1
134168	AA398908	Hs.181634	"Homo sapiens cDNA: FLJ23602 fis, clone	0.95	1.53
134218	AA227480	Hs.80205	Pim-2 oncogene	1.36	2.48
134405	R67275	Hs.82772	"""collagen, type XI, alpha 1"""	0.76	2.86
134453	X70683	Hs.83484	SRY (sex determining region Y)-box 4	1.89	3.78
134470	X54942	Hs.83758	CDC28 protein kinase 2	1.82	4.11
134645	U87459	Hs.167379	"Cancer/testis antigen (NY-ESO-1, CTAG1,	0.82	0.83
134781	M17183	Hs.89626	Parathyroid hormone-like hormone	1	1
135002	U19147	Hs.272484	G antigen 6	1	1
100040	M97935		AFFX control: STAT1	0.92	1.25
101201	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin;	2.92	8.5
101664	M60752	Hs.121017	H2A histone family; member A	1	1
102025	U03911	Hs.78934	mutS (E. coli) homolog 2 (colon cancer;	0.8	1.61
102031	U04898	Hs.2156	RAR-related orphan receptor A	1	1
102221	U24576		LIM domain only 4	1	1
102270	U30255	Hs.75888	phosphogluconate dehydrogenase	1.08	1.43
102339	U37022	Hs.95577	cyclin-dependent kinase 4	0.88	1.32
102391	U41668	Hs.77494	deoxyguanosine kinase	1.07	1.58
103000	X51956	Hs.146580	enolase 2; (gamma; neuronal)	0.91	1.49
103395	X94754	Hs.119503	methionine-tRNA synthetase	0.89	1.32
105638	AA281599	Hs.20418	Homo sapiens mRNA for for histone H2B; c	0.91	1.25
105726	AA292328	Hs.9754	activating transcription factor 5	0.94	1.48
114841	AA234722	Hs.55408	ESTs; Moderately similar to CALCIUM-DEPE	0.78	1.56
115206	AA262491	Hs.186572	ESTs	1	1
115906	AA436616	Hs.82302	ESTs	0.74	2.52
119132	R49046	Hs.107911	ATP-binding cassette; sub-family B (MDR/	1.1	1.51
124163	H30539	Hs.189838	ESTs	1	1
126487	AA482505	Hs.184601	solute carrier family 7 (cationic amino	1.01	1.46
127141	AA307960	Hs.75478	KIAA0956 protein	0.85	1.4
128034	AA905754	Hs.75103	tyrosine 3-monooxygenase/tryptophan 5-mo	1	1.18
128609	AA234365	Hs.102456	survival of motor neuron protein interac	1	1.5
128895	R37753	Hs.106985	ESTs	1.7	2
130199	Z48579	Hs.172028	a disintegrin and metalloprotease domain	1	1
130524	U89995	Hs.159234	forkhead box E1	1	1
133000	U24152	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	1	1
133658	M25756	Hs.75426	secretogranin II (chromogranin C)	1	1
135047	AA460466	Hs.93597	ESTs	1	1
100053	M27830		AFFX control: 28S ribosomal RNA	0.88	1.53
100114	D00596	Hs.82962	thymidylate synthetase	0.68	1.86
100128	D11094	Hs.61153	proteasome (prosome; macropain) 26S subu	1.29	2.03
100154	D14657	Hs.81892	KIAA0101 gene product	0.71	4.26
100161	D14694	Hs.77329	phosphatidylserine synthase 1	1.02	1.56
100168	D14874	Hs.394	adrenomedullin	0.46	1.17
100187	D17793	Hs.78183	aldo-keto reductase family 1; member C3	1	1
100188	D21063	Hs.57101	minichromosome maintenance deficient (S.	0.97	1.4
100217	D26600	Hs.89545	proteasome (prosome; macropain) subunit;	1.13	1.9
100220	D28364		"""Human mRNA for annexin II, 5'UTR (seq	1.11	1.53
100287	D43950	Hs.1600	chaperonin containing TCP1; subunit 5 (e	1.13	2.09
100297	D49489	Hs.182429	protein disulfide isomerase-related prot	0.92	1.78
100330	D55716	Hs.77152	minichromosome maintenance deficient (S.	1.07	1.61
100355	D78129		"""Homo sapiens mRNA for squalene epoxid	0.96	1.87
100364	D78586	Hs.154868	carbamoyl-phosphate synthetase 2; aspart	1.49	2.46
100368	D79987	Hs.153479	extra spindle poles; S. cerevisiae; homo	0.59	1.32
100398	D84557	Hs.155462	minichromosome maintenance deficient (mi	1.08	1.9
100438	D87448	Hs.91417	topoisomerase (DNA) II binding protein	1	2.15

100455	D87953	Hs.75789	N-myc downstream regulated	0.91	1.48
100491	HG1153-HT1153		Nucleoside Diphosphate Kinase Nm23-H2s	0.99	1.41
100518	HG174-HT174		Desmoplakin I	1.28	3.17
100528	HG1828-HT1857		"""Nexin, Glia-Derived"""	0.68	1.9
100661	HG2874-HT3018		Ribosomal Protein L39 Homolog	1.1	5.44
100667	HG2981-HT3127		"""Epican, Alt. Splice 11"""	0.8	1.97
100830	HG4074-HT4344		Rad2	1.01	2.12
101061	K03515	Hs.944	glucose phosphate isomerase	0.91	1.79
101131	L10838	Hs.167460	splicing factor; arginine/serine-rich 3	1.23	1.87
101162	L14595	Hs.174203	solute carrier family 1 (glutamate/neutr	1.35	2.73
101181	L19686	Hs.73798	macrophage migration inhibitory factor (	1.03	1.78
101183	L19779	Hs.795	H2A histone family; member O	0.57	1.3
101216	L25876	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	0.7	2.2
101228	L27706	Hs.82916	chaperonin containing TCP1; subunit 6A (	0.99	1.99
101233	L29008	Hs.878	sorbitol dehydrogenase	0.82	2.11
101247	L33801	Hs.78802	glycogen synthase kinase 3 beta	1.2	1.91
101332	L47276		"""Homo sapiens (cell line HL-6) alpha t	0.69	2.78
101342	L76191	Hs.182018	interleukin-1 receptor-associated kinase	1.04	1.84
101396	M15796	Hs.78996	proliferating cell nuclear antigen	0.95	3.55
101423	M18391	Hs.89839	EphA1	1	1.5
101445	M21259	Hs.1066	small nuclear ribonucleoprotein polypept	1.21	1.96
101505	M27396	Hs.75692	asparagine synthetase	0.93	1.6
101525	M29536	Hs.12163	eukaryotic translation initiation factor	1.19	1.93
101535	M30448	Hs.251669	casein kinase 2; beta polypeptide	0.96	1.42
101607	M38690	Hs.1244	CD9 antigen (p24)	1.11	1.25
101624	M55998		"""Human alpha-1 collagen type I gene, 3	1.17	1.98
101758	M77836	Hs.79217	pyrroline-5-carboxylate reductase 1	1.77	3.45
101839	M93036	Hs.692	membrane component; chromosomal 4; surfa	0.71	1.45
101853	M94362	Hs.76084	lamin B2	0.84	1.19
101977	S83364		"""putative Rab5-interacting protein (cl	0.89	1.9
101992	U01038	Hs.77597	polo (Drosophia)-like kinase	0.66	1.46
102009	U02680	Hs.82643	protein tyrosine kinase 9	1.23	3.35
102012	U03057	Hs.118400	singed (Drosophila)-like (sea urchin fas	0.85	1.88
102039	U05861	Hs.201967	aldo-keto reductase family 1; member C1	0.93	2.32
102123	U14518	Hs.1594	centromere protein A (17kD)	1	4.28
102130	U15009	Hs.1575	small nuclear ribonucleoprotein D3 polyp	0.89	1.42
102148	U16954	Hs.75823	ALL1-fused gene from chromosome 1q	0.8	2.95
102210	U23028	Hs.2437	eukaryotic translation initiation factor	1.01	1.34
102220	U24389	Hs.65436	lysyl oxidase-like 1	1.15	2.34
102260	U28386	Hs.159557	karyopherin alpha 2 (RAG cohort 1; impor	1.14	2.69
102330	U35451	Hs.77254	chromobox homolog 1 (Drosophila HP1 beta	1.05	1.7
102423	U44754	Hs.179312	small nuclear RNA activating complex; po	1.14	2.99
102455	U48705	Hs.75562	discoidin domain receptor family; member	1.05	2.01
102499	U51478	Hs.76941	ATPase; Na+/K+ transporting; beta 3 poly	1.27	1.92
102522	U53347	Hs.183556	solute carrier family 1 (neutral amino a	0.84	1.31
102590	U62136		"""Homo sapiens enterocyte differentiati	1.11	1.6
102676	U72514	Hs.12045	putative protein	1.04	2.17
102687	U73379	Hs.93002	ubiquitin carrier protein E2-C	0.86	2.28
102704	U76638	Hs.54089	BRCA1 associated RING domain 1	1.12	1.63
102781	U83843		"""Human HIV-1 Nef interacting protein (	0.9	1.39
102784	U85658	Hs.61796	transcription factor AP-2 gamma (activat	0.98	2.16
102827	U91327	Hs.6456	chaperonin containing TCP1; subunit 2 (b	0.96	1.62
102935	X13482	Hs.80506	small nuclear ribonucleoprotein polypept	1.21	4.2
102972	X16662	Hs.87268	annexin A8	1.25	2.32
102983	X17620	Hs.118638	non-metastatic cells 1; protein (NM23A)	1.03	1.83
103023	X53793	Hs.117950	multifunctional polypeptide similar to S	1.58	5.44
103038	X54941	Hs.77550	CDC28 protein kinase 1	1.32	3.79
103075	X59543	Hs.2934	ribonucleotide reductase M1 polypeptide	1.11	2.58
103168	X68314	Hs.2704	glutathione peroxidase 2 (gastrointestin	0.75	3.05
103185	X69910	Hs.74368	transmembrane protein (63kD); endoplasmi	1.01	1.97
103212	X73874	Hs.2393	phosphorylase kinase; alpha 1 (muscle)	0.95	1.72
103223	X74801	Hs.1708	chaperonin containing TCP1; subunit 3 (g	0.97	1.77
103260	X78416	Hs.3155	casein; alpha	1	1
103262	X78565	Hs.204133	hexabrachion (tenascin C; cytotactin)	1.23	3.09
103330	X85373	Hs.77496	small nuclear ribonucleoprotein polypept	1.12	2.25
103364	X90872	Hs.75854	SULT1C sulfotransferase	2.85	4.62
103375	X91868	Hs.54416	sine oculis homeobox (Drosophila) homolo	1	2.48
103391	X94453	Hs.114366	pyrroline-5-carboxylate synthetase (glut	1	1.53
103404	X95586	Hs.78596	proteasome (prosome; macropain) subunit;	0.92	1.53
103437	X98260	Hs.82254	M-phase phosphoprotein 11	0.92	1.54
103448	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	0.55	0.96
103605	Z35402	Hs.194657	cadherin 1; E-cadherin (epithelial)	1.32	2.51
103646	Z68228	Hs.2340	junction plakoglobin	0.88	1.28
103658	Z74615	Hs.172928	collagen; type I; alpha 1	1.06	2.98
103774	AA092898	Hs.92918	ESTs; Weakly similar to R07G3.8 [C.elega	1.88	4.66
104261	AF008442	Hs.5409	RNA polymerase I subunit	0.87	2.17
104276	C02193	Hs.85222	ESTs; Weakly similar to R27090_2 [H.sapi	1.4	2.49
104289	C16281	Hs.75478	KIAA0956 protein	1.15	1.68
104434	L02870	Hs.1640	collagen; type VII; alpha 1 (epidermolys	1.04	1.49
104453	M19169	Hs.123114	cystatin SN	0.38	0.76
104611	R98280	Hs.125845	ribulose-5-phosphate-3-epimerase	1.08	2.25
104758	AA024661	Hs.7010	ESTs; Weakly similar to ACYL-COA DEHYDRO	1.14	1.65
105114	AA156532	Hs.11801	adenosine A2b receptor pseudogene	0.91	1.38
105132	AA159501	Hs.247280	HBV associated factor	1.08	1.7
105174	AA186613	Hs.34744	ESTs	0.95	2.05

105280	AA232215	Hs.14600	ESTs	1	1.4
105344	AA235303	Hs.8645	ESTs	0.72	2.02
105516	AA257971	Hs.21214	ESTs	1.35	3.56
105621	AA280865	Hs.6375	Homo sapiens mRNA; cDNA DKFZp564K0222 (f	1.23	1.82
105698	AA287393	Hs.15202	ESTs; Weakly similar to oligodendrocyte-	0.98	1.28
105705	AA290767	Hs.101282	Homo sapiens mRNA; cDNA DKFZp434B102 (fr	0.92	1.32
105724	AA292098	Hs.22934	ESTs; Weakly similar to ZINC FINGER PROT	0.99	1.41
105782	AA350215	Hs.21580	ESTs	1	1
105799	AA372018	Hs.24743	ESTs	1.08	1.78
105807	AA393803	Hs.16869	ESTs; Moderately similar to COLLAGEN ALP	0.95	1.34
105891	AA400768	Hs.26662	ESTs; Weakly similar to tumor necrosis f	0.87	2.25
105936	AA404338		ESTs	1.14	1.46
106069	AA417741	Hs.29899	ESTs; Weakly similar to ZINC FINGER PROT	1	1
106103	AA421104	Hs.12094	ESTs	1.04	1.44
106140	AA424524	Hs.14912	KIAA0286 protein	1.23	2.11
106149	AA424881	Hs.256301	ESTs	0.83	1.48
106154	AA425304	Hs.6994	ESTs	0.77	2.05
106182	AA426609	Hs.10862	ESTs	0.74	2.23
106220	AA428582	Hs.32196	ESTs; Moderately similar to metargidin p	0.97	1.99
106228	AA429290	Hs.17719	ESTs	0.99	1.54
106318	AA436570	Hs.9605	pre-mRNA cleavage factor Im (25kD)	0.95	2.09
106341	AA441798	Hs.5243	ESTs; Moderately similar to pIL2 hypothe	0.98	2.66
106432	AA448850	Hs.17138	ESTs	0.95	1.93
106474	AA450212	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (fr	1	1
106483	AA451676	Hs.30299	IGF-II mRNA-binding protein 2	1.4	2.29
106599	AA457235	Hs.12842	ESTs; Moderately similar to non-function	1	1.82
106611	AA458904	Hs.26267	ESTs; Weakly similar to torsinA [H.sapie	1.49	2.78
106654	AA460449	Hs.3784	ESTs; Highly similar to phosphoserine am	1	1.4
107076	AA609145	Hs.21143	ESTs; Weakly similar to fos39554_1 [H.sa	1.11	1.49
107115	AA610108	Hs.27693	ESTs; Highly similar to CGI-124 protein	1	1.03
107129	AA620553	Hs.4756	flap structure-specific endonuclease 1	1.13	3.63
107159	AA621340	Hs.10600	ESTs; Weakly similar to ORF YKR081c [S.c	1.05	2.09
107444	W28391	Hs.5181	proliferation-associated 2G4; 38kD	1.18	1.9
107481	W58247	Hs.27437	Homo sapiens kinesin superfamily motor K	0.99	2.74
107516	X56597	Hs.99853	fibrillarin	0.94	1.77
107529	Y12065	Hs.5092	nucleolar protein (KKE/D repeat)	1.05	2.29
107531	Y13936	Hs.17883	protein phosphatase 1G (formerly 2C); ma	1.06	1.62
107801	AA019433	Hs.173100	ESTs	1.03	1.4
107957	AA031948	Hs.57548	ESTs	0.95	1.46
108565	AA085342	Hs.1526	ATPase; Ca++ transporting; cardiac muscl	0.59	1.35
108780	AA128561	Hs.117938	collagen; type XVII; alpha 1	1	7.63
108828	AA131584	Hs.71435	DKFZP564O0463 protein	1.33	2.56
109060	AA160879	Hs.241551	chloride channel; calcium activated; fam	0.67	1.42
109112	AA169379	Hs.72865	ESTs	1.03	2.31
109344	AA213696	Hs.86559	poly(A)-binding protein-like 1	0.97	1.55
109412	AA227145	Hs.209473	ESTs; Weakly similar to REGULATOR OF MIT	0.76	1.87
110780	N23174	Hs.22891	solute carrier family 7 (cationic amino	0.9	0.95
110958	N50550	Hs.24587	signal transduction protein (SH3 contain	1.17	2.26
111018	N54067	Hs.3628	mitogen-activated protein kinase kinase	1.21	1.85
111337	N79612	Hs.16607	ESTs; Highly similar to Myosin heavy cha	1	1.45
112305	R54822	Hs.26244	ESTs	1	1
112401	R61279	Hs.237536	ESTs; Weakly similar to F25B5.3 [C.elega	1.24	1.64
112853	T02843	Hs.4351	EST	1.56	1.96
112869	T03313	Hs.4747	dyskeratosis congenita 1; dyskerin	1.03	1.57
112992	T23513	Hs.7147	ESTs	1	1
113048	T25895	Hs.184008	ESTs; Weakly similar to RNA-binding prot	1.37	2.26
113063	T32438	Hs.5027	ESTs	1	1
113179	T55182	Hs.152571	ESTs; Highly similar to IGF-II mRNA-bind	1.33	2.7
113573	T91166	Hs.15990	ESTs	0.76	1.47
113811	W44928	Hs.4878	ESTs	0.79	1.51
114086	Z38266	Hs.12770	Homo sapiens PAC clone DJ0777O23 from 7p	0.9	1.34
114587	AA070827	Hs.180320	ESTs; Weakly similar to GOLGI 4-TRANSMEM	1.02	1.76
114846	AA234929	Hs.44343	ESTs	1.32	2.36
114964	AA243873	Hs.82184	ring finger protein 3	1.1	1.84
115047	AA252627	Hs.22554	homeo box B5	1.01	2.36
115166	AA258409	Hs.198907	myelin protein zero-like 1	1.05	2.31
115167	AA258421	Hs.43728	hypothetical protein	1.62	2.52
115239	AA278650	Hs.73291	ESTs; Weakly similar to similar to the b	0.7	2.57
115278	AA279757	Hs.67466	ESTs; Weakly similar to BACN32G11.d [D.m	1.14	2.12
115652	AA405098	Hs.38178	ESTs	0.82	4.67
115875	AA433943	Hs.43946	ESTs; Weakly similar to Weak similarity	1.2	1.98
116004	AA449122	Hs.76086	ESTs; Highly similar to small zinc finge	0.96	1.31
116121	AA459254	Hs.48855	ESTs	0.97	1.55
116129	AA459956	Hs.49163	ESTs; Highly similar to putative ribonuc	1.08	2.73
116190	AA464963	Hs.67776	ESTs	0.8	1.57
116312	AA490494	Hs.65403	ESTs	1.37	2.65
116732	F13779	Hs.165909	ESTs	0.92	1.8
117602	N35020	Hs.44685	ESTs; Weakly similar to GOLIATH PROTEIN	1.15	1.84
117950	N51394	Hs.75478	KIAA0956 protein	1.04	2.36
117992	N52000	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586B0222 (f	0.62	1.29
118785	N75386	Hs.111867	GLI-Kruppel family member GLI2	1	1
119717	W69134	Hs.57987	ESTs	1	1.4
119814	W74069	Hs.58350	ESTs	0.78	1.77
120128	Z38499	Hs.91448	MKP-1 like protein tyrosine phosphatase	0.86	1.46
120242	Z98443	Hs.86366	ESTs	0.83	2.01

120483	AA252994	Hs.1578	apoptosis inhibitor 4 (survivin)	0.74	1.64
121054	AA398604	Hs.97387	ESTs	1.05	1.93
121326	AA404246	Hs.97031	ESTs; Weakly similar to Similar to phyto	0.98	1.3
121376	AA405699	Hs.166232	ESTs; Moderately similar to SODIUM- AND	0.91	1.83
121457	AA411448	Hs.208985	ESTs	0.91	1.59
121780	AA422086	Hs.124660	ESTs	0.46	0.55
121781	AA422150	Hs.98370	cytochrome P540 family member predicted	1.07	1.54
121844	AA425732	Hs.98485	gap junction protein; beta 2; 26kD (conn	0.94	1.4
122059	AA431737	Hs.98749	EST	1.93	2.33
122338	AA443311	Hs.98998	ESTs	1	1
122354	AA443772	Hs.186692	ESTs	0.88	1.39
122591	AA453265	Hs.99311	ESTs; Weakly similar to MRJ [H.sapiens]	2.28	2.93
122790	AA460156	Hs.99556	ESTs	0.88	1.3
123398	AA521265	Hs.105514	ESTs	1	1.93
123518	AA608531	Hs.170313	ESTs	1	1
123673	AA609471	Hs.112712	ESTs	1	1.15
124000	D57317	Hs.74861	activated RNA polymerase II transcriptio	0.74	1.12
124367	N24006	Hs.99348	distal-less homeo box 5	0.67	1.1
124447	N48000	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (fr	1.19	1.7
125756	W25498	Hs.81634	ATP synthase; H+ transporting; mitochond	0.93	1.59
125769	AI382972	Hs.82128	5T4 oncofetal trophoblast glycoprotein	1.65	6.76
125852	H09290	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	0.72	2.26
125924	AA526849	Hs.82109	syndecan 1	1.22	2.25
126037	M85772	Hs.6066	KIAA1112 protein	1.36	1.63
126214	N29455	Hs.74316	desmoplakin (DPI; DPII)	1.93	3.55
126414	N78770	Hs.223439	ESTs	1.21	1.66
126737	AA488132	Hs.62741	ESTs	1	1
126743	AA179253	Hs.172182	poly(A)-binding protein; cytoplasmic 1	1.3	2.16
126926	AA179546	Hs.832	ESTs; Highly similar to INTEGRIN BETA-8	2.53	2.8
127432	AA501734	Hs.170311	heterogeneous nuclear ribonucleoprotein	1.57	2.12
128218	H02682	Hs.99189	ESTs; Moderately similar to recombinatio	1.24	2.09
128527	M31523	Hs.101047	transcription factor 3 (E2A immunoglobul	1.08	1.78
128568	X60673	Hs.247568	adenylate kinase 3	1.23	3.48
128584	M11433	Hs.101850	retinol-binding protein 1; cellular	0.87	2.42
128628	C14037	Hs.251978	EST	1.22	1.9
128691	W27939	Hs.103834	ESTs	1.1	1.73
128714	V00599	Hs.179661	Homo sapiens clone 24703 beta-tubulin mR	0.92	1.17
128733	AA328993	Hs.104558	ESTs	1.34	1.94
128781	X85372	Hs.105465	small nuclear ribonucleoprotein polypept	0.9	1.34
129052	AA496297	Hs.182740	ribosomal protein S11	2.59	3.19
129095	L12350	Hs.108623	thrombospondin 2	1.04	3.2
129241	AA435665	Hs.109706	ESTs; Moderately similar to HN1 [M.muscu	0.95	1.61
129665	M88458	Hs.118778	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	1.28	2.63
129703	AA401348	Hs.179999	ESTs	0.97	1.63
129720	AA476582	Hs.12152	ESTs; Moderately similar to SIGNAL RECOG	1.09	1.79
129850	N20593	Hs.56845	GDP dissociation inhibitor 2	0.74	1.68
129896	AA043021	Hs.13225	UDP-Gal:betaGlcNAc beta 1;4- galactosylt	1.43	4.19
130069	AA055896	Hs.146428	collagen; type V; alpha 1	1.17	1.98
130405	H88359	Hs.155396	nuclear factor (erythroid-derived 2)-lik	1.26	1.79
130541	X05608	Hs.211584	neurofilament; light polypeptide (68kD)	1	1
130599	M91670	Hs.174070	ubiquitin carrier protein	1.07	1.66
130867	J04093	Hs.2056	UDP glycosyltransferase 1	1	4.8
131009	AA063596	Hs.22142	ESTs; Weakly similar to NADH-CYTOCHROME	0.93	1.05
131028	U20240	Hs.2227	CCAAT/enhancer binding protein (C/EBP);	1	1.23
131083	U66661	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.1	1.8
131091	T35341	Hs.22880	ESTs; Highly similar to dipeptidyl pepti	1.28	1.98
131144	C14412	Hs.23528	ESTs; Highly similar to HSPC038 protein	1.43	2.06
131148	C00038	Hs.23579	ESTs	0.88	3.38
131164	Y00503	Hs.182265	keratin 19	1.19	2.77
131185	M25753	Hs.23960	cyclin B1	0.86	3.84
131219	C00476	Hs.24395	small inducible cytokine subfamily B (Cy	0.66	2.96
131454	AA455896	Hs.2699	glypican 1	0.99	1.54
131687	L11066	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	1	1.18
131689	AA599653	Hs.30696	transcription factor-like 5 (basic helix	1	1.95
131692	D50914	Hs.30736	KIAA0124 protein	1.55	2.39
131786	AA135554	Hs.32125	ESTs	1	1.33
131843	AA195893	Hs.184062	ESTs; Moderately similar to putative Rab	0.83	1.63
131860	U02082	Hs.334	Oncogene TIM	1.08	2.2
131884	H90124	Hs.3463	ribosomal protein S23	1.23	1.24
131903	AA481723	Hs.3436	deleted in oral cancer (mouse; homolog)	0.91	1.18
131945	M87339	Hs.35120	replication factor C (activator 1) 4 (37	1	2.8
131958	AA093998	Hs.3566	ESTs; Highly similar to phosphorylation	0.87	1.36
131964	W42508	Hs.3593	ESTs	1	1.25
132001	J00277	Hs.37003	v-Ha-ras Harvey rat sarcoma viral oncoge	1.12	1.43
132040	AA146843	Hs.172894	BH3 interacting domain death agonist	1	1.55
132065	D82226	Hs.211594	proteasome (prosome; macropain) 26S subu	0.89	1.27
132109	AA599801	Hs.40098	ESTs	1	1.05
132112	AA150661	Hs.40154	jumonji (mouse) homolog	0.99	1.44
132123	AA447123	Hs.250705	ESTs	1.06	2.46
132162	H89551	Hs.41241	ESTs	1.08	2.46
132180	AA405569	Hs.418	fibroblast activation protein; alpha; se	1.02	4.56
132309	AA460917	Hs.2780	jun D proto-oncogene	1.16	1.8
132371	AA235448	Hs.46677	ESTs	0.8	1.26
132618	AA253330	Hs.5344	adaptor-related protein complex 1; gamma	0.5	1.49
132736	U68019	Hs.211578	MAD (mothers against decapentaplegic; Dr	1.21	1.81

132771	AA488432	Hs.56407	phosphoserine phosphatase	1	1.3
132833	U78525	Hs.57783	eukaryotic translation initiation factor	0.91	1.43
132922	T23641	Hs.6066	KIAA1112 protein	1.16	1.53
132959	AA028103	Hs.61472	ESTs; Weakly similar to unknown [S.cerev	1.02	1.88
132994	AA505133	Hs.7594	solute carrier family 2 (facilitated glu	0.72	2.97
133005	C21400	Hs.103329	KIAA0970 protein	0.88	1.34
133065	X62535	Hs.172690	diacylglycerol kinase; alpha (80kD)	0.93	1.23
133083	N70633	Hs.6456	chaperonin containing TCP1; subunit 2 (b	1.14	1.76
133086	L17131	Hs.139800	high-mobility group (nonhistone chromoso	0.97	1.43
133134	T89703	Hs.65648	RNA binding motif protein 8	1.1	1.8
133195	AA350744	Hs.181409	KIAA1007 protein	2.29	2.69
133313	AA249427	Hs.70704	ESTs	1.07	1.68
133331	T62039	Hs.158675	ribosomal protein L14	0.85	1.18
133438	D13370	Hs.73722	APEX nuclease (multifunctional DNA repai	0.91	1.45
133445	T99303	Hs.73797	guanine nucleotide binding protein (G pr	0.94	1.68
133483	X52426	Hs.74070	keratin 13	0.85	1.14
133492	L40397	Hs.74137	transmembrane trafficking protein	1.1	1.69
133504	W95070	Hs.74316	desmoplakin (DPI; DPII)	0.7	6.21
133517	X52947	Hs.74471	gap junction protein; alpha 1; 43kD (con	0.95	1.3
133540	D78151	Hs.74619	proteasome (prosome; macropain) 26S subu	0.91	1.25
133594	L07758	Hs.172589	nuclear phosphoprotein similar to S. cer	0.84	1.29
133627	U09587	Hs.75280	glycyl-tRNA synthetase	1.09	1.99
133671	T25747	Hs.75471	zinc finger protein 146	1.02	1.5
133859	U86782	Hs.178761	26S proteasome-associated pad1 homolog	1.11	3.33
133865	F09315	Hs.170290	discs; large (Drosophila) homolog 5	1.84	6.7
133913	W84712	Hs.7753	calumenin	1.15	1.86
133963	L34587	Hs.184693	transcription elongation factor B (SIII)	1.3	1.91
133982	U47621	Hs.207251	nucleolar autoantigen (55kD) similar to	1.3	1.99
134100	L07540	Hs.171075	replication factor C (activator 1) 5 (36	0.72	1.65
134110	U41060	Hs.79136	LIV-1 protein; estrogen regulated	1.04	1.62
134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	1	1.55
134161	U97188	Hs.79440	IGF-II mRNA-binding protein 3	0.82	1.95
134193	F09570	Hs.7980	ESTs	0.98	1.48
134367	X54199	Hs.82285	phosphoribosylglycinamide formyltransfer	1	2.8
134402	U25165	Hs.82712	fragile X mental retardation; autosomal	1.26	2
134457	D86963	Hs.174044	dishevelled 3 (homologous to Drosophila	1	1.47
134469	X17567	Hs.83753	small nuclear ribonucleoprotein polypept	0.94	1.57
134498	M63180	Hs.84131	threonyl-tRNA synthetase	1.2	2.64
134501	W84870	Hs.211568	eukaryotic translation initiation factor	0.84	1.36
134507	M63488	Hs.84318	replication protein A1 (70kD)	1.7	2.93
134548	U41515	Hs.85215	Deleted in split-hand/split-foot 1 regio	1.46	2.73
134599	X99226	Hs.86297	Fanconi anemia; complementation group A	1.36	2.22
134692	R73567	Hs.8850	a disintegrin and metalloproteinase doma	0.77	1.64
134693	N70361	Hs.8854	ESTs	1.09	1.82
134806	Z49099	Hs.89718	spermine synthase	0.98	1.35
134821	Z34974	Hs.198382	plakophilin 1 (ectodermal dysplasia/skin	0.99	1.4
134864	Y08999	Hs.90370	actin related protein 2/3 complex; subun	0.95	1.42
134914	U29615	Hs.91093	chitinase 1 (chitotriosidase)	1.16	1.29
134953	L10678	Hs.91747	profilin 2	0.95	1.76
134993	AA282343	Hs.9242	purine-rich element binding protein B	0.98	1.73
135051	C15324	Hs.93668	ESTs	1.35	2.11
135158	U51711		Human desmocollin-2 mRNA; 3' UTR	0.86	1.16

Table 1B shows the accession numbers for those pkeys in Table 1A lacking unigeneID's. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the Accession column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT	Accessions
100661	23182_1	BE623001 L05096 AA383604 AW966416 N53295 AA460213 AW571519 AA603655
100667	26401_3	L05424 X56794 S66400 X55150 W60071 AW351820 X55938 M83326 BE005289 BE070059 M83324 BE005248 BE069717 BE181648 BE069700 AW606203 BE069721 AW382138 AW803776 BE463954 BE005334 BE005274 T27386 AA932714 AA972695 AW377728 AI632506 T29066 AI783934 AW377727 BE163715 AL047291 AA279047 AA523003 BE008048 BE440141 W23614 BE090519 BE092193 N29181 N20358 N44153 BE546944 T69231 AW377441 AA907406 H50799 AW051416 AI420712 BE620922 AI279161 AA992549 W47198 BE005241 AI342696 H50700 AI969974 AI863855 AA374490 AW130675 AI950633 AA146687 H99482 X55150 BE005414 BE005339 N28294 AI673068 AI887890 AW804171 AI675961 AW804172 AA778841 AL048050 AI127757 AI095568 AW204965 AW468978 W31898 AI052595 AI278771 BE464018 AI081503 AI824196 AA513211 AA411062 AW084376 N48752 AA703209 N35580 AW059918 AA054563 AI280942 T27619 BE621435 N66010 AW589527 AI160414 AA283090 AA962536 H82726 W52115 W45432 W60433 AA577548 AA146714 BE150994 AA054615 AW796025 AW382768 BE565671 C00444 AA054555
100668	26401_3	L05424 X56794 S66400 X55150 W60071 AW351820 X55938 M83326 BE005289 BE070059 M83324 BE005248 BE069717 BE181648 BE069700 AW606203 BE069721 AW382138 AW803776 BE463954 BE005334 BE005274 T27386 AA932714 AA972695 AW377728 AI632506 T29066 AI783934 AW377727 BE163715 AL047291 AA279047 AA523003 BE008048 BE440141 W23614 BE090519 BE092193 N29181 N20358 N44153 BE546944 T69231 AW377441 AA907406 H50799 AW051416 AI420712 BE620922 AI279161 AA992549 W47198 BE005241 AI342696 H50700 AI969974 AI863855 AA374490 AW130675 AI950633 AA146687 H99482 X55150 BE005414 BE005339 N28294 AI673068 AI887890 AW804171 AI675961 AW804172 AA778841 AL048050 AI127757 AI095568 AW204965 AW468978 W31898 AI052595 AI278771 BE464018 AI081503 AI824196 AA513211 AA411062 AW084376 N48752 AA703209 N35580 AW059918 AA054563 AI280942 T27619 BE621435 N66010 AW589527 AI160414 AA283090 AA962536 H82726 W52115 W45432 W60433 AA577548 AA146714 BE150994 AA054615 AW796025 AW382768 BE565671 C00444 AA054555
101332	25130_1	J04088 NM_001067 AF071747 AJ011741 N85424 AL042407 AA218572 BE296748 BE083981 AL040877 AW499918 AW675045 H17813 BE081283 AA670403 AW504327 BE094229 AA104024 AI471482 AI970337 AA737616 AI827444 AW003286 AI742333 AI344044 AI765634

		AI948838 AW235336 AW172827 AA095289 BE046383 AI734240 W16699 AI660329 AI289433 AA933778 AW469242 AA468838 AA806983 AA625873 W78031 BE206307 AA550803 AI743147 AI990075 AA948274 AA129533 AI635399 AA605313 AI624669 AW594319 AI221834 AI337434 AA307706 BE550282 AI760467 AI630636 AI221521 AW674314 AW078889 AI933732 AI686969 AI186928 AW074595 AI127486 AL079644 AI910815 H17814 AA310903 AW137854 T19279 AA026682 AA306035 AW383390 AW383389 AW383422 AW383427 AW383395 H09977 AA306247 AA352501 AW403639 F05421 AA224473 AA305321 H93904 AA089612 AW391543 AW402915 AW173382 AW402701 AW403113 R94438 N73126 H93466 AA090928 AA095051 T29025 AW951071 L47277 L47276 AI375913 BE384156 W24652 AA746288 AA568223 BE090591 H93033 N57027 AA504348 AA327653 AW959913 N53767 AA843715 AI453437 AW263710 AI076594 AA583483 AW873194 AW575166 AI128799 AI803319 AL042776 AW074313 AI887722 AI032284 AA447521 AI123885 N29334 AI354911 AW090687 AA236763 AA435535 AA236910 AA047124 AA236734 AW514610 H93467 AA962007 AI446783 AA127259 AI613495 AI686720 AI587374 AA936731 AA702453 AI859757 AA216786 AI251819 AI469227 AA806022 AI092324 N71868 AA968782 AA236919 AA809450 AA227220 AA765284 AI192007 AA768810 AA805794 AA729280 AA806238 AW768817 N71879 AI050686 AA505822 AA668974 AI688160 BE045915 AW466315 AA731314 AA649568 AA834316 AW591901 AW063876 AW294770 AI300266 AI336094 AI560380 AA721755 H09978 D20305 D29155 AW821790 BE150864 F01675 AI457474 AW466316 AA550969 AA630788
100780	458_127	BE561958 BE561728 BE397612 BE514391 BE269037 BE514207 BE562381 BE514256 BE514403 BE514250 BE397832 BE269598 BE559865 BE396881 BE560031 BE514199 BE560037 BE560454
100830	4002_1	AC004770 W05005 AA356068 AA094281 H29358 T56781 AW875313 L37374 BE312466 BE311755 BE207106 BE293320 BE018115 AW239090 BE548830 AW247547 AA776062 BE397382 AA486713 T10111 T09340 AW498981 BE547280 AA356003 AW581520 AW875331 AA580720 AW875336 BE276873 BE408229 AW188148 BE255166 BE253761 AW793727 AW373141 AW581548 AA471223 AA305950 BE263976 AA626820 BE257409 AW360962 AA090655 C00312 BE312741 BE407213 AA209352 AW298199 AW248553 AW297794 AW731722 BE300586 AW731972 AW615446 BE301599 AW615520 AA486714 AW440257 AA196516 AA564630 AA618079 AW192592 AW474985 AA604580 AI627461 AA765440 AI680394 AL135548 AI683224 AI581126 AW245096 AW194154 H29274 N70363 AA629758 AA580602 AA862006 AI863841 AI097667 AI928583 AI358774 BE243487 AA620553 AA653297 AA292690 T10110 Z38906 AA908544 AA340930 AI185438 T03328 T28844 AI687010 AI864965 AI872575 BE388740 T56780 AW373138 BE258717 AA699671
100906	4312_1	AU076916 BE298110 AW239395 AW672700 NM_003875 U10860 AW651755 BE297958 C03806 AI795876 AA644165 T36030 AW392852 AA446421 AW881866 AI469428 BE548103 T96204 R94457 N78225 AI564549 AW004984 AW780423 AW675448 AW087890 AA971454 AA305698 AA879433 AA535069 AI394371 AA928053 AI378367 N59764 AI364000 AI431285 T81090 AW674657 AW674987 AA897396 AW673412 BE063175 AW674408 AI202011 R00723 AI753769 AI460161 AW079585 AW275744 AI873729 D25791 BE537646 T81139 R00722
100930	16865_1	J04129 NM_002571 AA293088 AA477016 AA404631 T28299 AA476904 AA433965 AA430486 AA495907 AI151391 AA291495 AA402723 W25651 AA706816 AI826712 AW296294 AA293479 AI276581 AW044154 AI080180 AI417985 AI274168 AI474212 AA495908 AA635664 AI092114 AI804952 AA479874 AI597661 AI420511 AA479738 AA421417 AA421247 AA436220 AL047797 M34046 N42277 AA228076 W02698 AI420297 AA434011 AI369971 AA479731 AI865541 AI418020 AA421246 AA452764 AL048051
102221	3861_1	NM_006769 U24576 AW161961 AW160473 AW160465 AW160472 AW161069 AI824831 AW162635 AI990356 AW162477 AW162571 AI520836 AW162352 AW162351 AW162752 AI962216 AI537346 AA853902 H17667 BE045346 BE559802 BE255391 AA985217 AA235051 AI129757 AW366451 T34489 D56106 D56351 AI936579 AW023219 AW889335 AW889120 AW889232 AW889175 BE093702 AW889349 AA147546 AI952998 AA912579 AI143356 AW902211 R64717 AW157236 AI815242 D45274 AW263991 AA442920 AA129965 AL035713 AI923255 AI949082 AI142826 AI684160 AI701987 AI678954 AI827349 BE463635 AW628092 AW302281 AA493203 BE348856 BE536419 AW193969 AW673561 AW592609 AI224044 H43943 AA091912 R49632 R48353 AI568409 R48256 AI198046 H27986 H43899 AI678759 AI680310 AI624220 H17052 AA156410 N56062 AI699430 AA664529 T09406 T10459 AA627506 AI379584 N83831 N88633 AW022651 AA971281 AA248036 AI039197 AI914689 AA973825 AL047305 AA129966 AI798369 AW264348 AI445879 AI658759 N67924 AI933507 AI216121 AI333174 T10972 AI375028 AI186756 AI273778 AA610487 AI797946 AA853903 AA903939 AI338587 AI278494 AW627595 AA904019
101809	32963_1	M86849 AA315280 NM_004004 AA315269 BE142653 AA461400 AW802042 BE152893 AW383155 AA490688 AW117930 AW384563 AW384544 AW384566 AW378307 AW378323 AW839085 AA257102 AW378317 AW276060 AW271245 AW378298 AW384497 AI598114 AW264544 AI018136 AW021810 AA961504 AW086214 AW771489 AW192483 AI290266 AW192488 AW384490 AW007451 AW890895 AA554460 AA613715 AW020066 AI783695 AI589498 AI917637 AW264471 AW384491 AI816732 AW368530 AW368521 AW368463 AA461087 AI341438 AI970613 AI040737 AI418400 AA947181 AA962716 AI280695 AW769275 AW023591 AI160977 AA055400 N71882 AA490466 AW243772 AW316636 AI076554 AW511702 N69323 H88912 AA257017 AI952506 H88913 AI912481 AA600714 BE465701 N64149 C00523 N64240 AA677120
102590	15932_1	R61573 BE005029 X98091 AA297307 BE537267 BE566138 BE566139 F11561 BE564795 BE568776 AW064005 BE566479 BE380035 BE567012 BE568634 BE566568 AA298060 BE566043 BE568813 BE568618 AA283070 BE565414 BE566738 BE568585 BE565667 BE566116 BE566433 U62136 AF049140 BE567057 BE567297 BE567403 BE564316 BE567400 BE568854 BE566588 AA448772 AA071363 AW732642 BE564996 AA297763 AA278550 AA421083 AA298184 AA091007 AA984577 AA205916 N28759 AL031291 C15757 C15761 H02728 BE566410 AA129335 AA419499 N87741 BE379689 BE004824 BE379611 D25874 AA148454 AA323654 AW950311 AA448795 AW749423 AA773386 AA773843 AW020327 BE348580 BE504258 BE549990 BE220200 AI673334 AI202679 AA975515 D61421 AI168688 AA102843 AW246621 AI276203 AI074054 AI633824 AI962927 AI148926 N50969 AI308911 AA410994 AW373025 AA148455 H02620 AA688293 AI246318 N22220 AI917777 AI050943 AI097286 AA663794 AW368662 AW627826 AW078734 AI253060 AA749154 AA832236 AI192358 AW024676 AA448676 AA764891 BE439467 AA661534 AA258061 AI090546 AA995157 AI051011 AA584421 AI026032 AW591338 AW589563 AA776914 AW024684 AA421002 F09219 BE464500 AI383595 AA954244 AA601583 AA737304 AA195549 AA805778 AI055876 AA164942 AW013961 AI672608 AW514211 D59441 AW582574 AA160935 BE566501 BE564612 BE565353 BE568195 BE565447 BE568302 BE566097 BE565470 BE564249 AL036217 AW749424 BE567494 AA102842 AA314761 AV661237 C14211 AA651866 AW798997 AA470605
101977	29073_1	AF112213 AL050318 T24804 AW248136 BE386341 BE263177 W16677 BE250224 BE563669 BE267405 BE546577 AV651354 AV651292 AI346903 AI539128 AI189171 S83364 AW073849 AI816760 AW073309 AI422690 AA296692 AI860301 AI805446 N77735 AI340328 BE092530 AW028742 BE088442 AA657742 AA742438 AW170086 AI038920 AI432379 N36073 AI936194 AA868655 AA983612 AI077505 BE080433 AI375014 AI126547 AI348244 AI346077 AI748952 N26915 AI753574 AI093341 AI278762 BE092517 N74204 H06158 T58149 AI129303 N58366 AA524456 BE122661 AA542925 AI246120 AI735203 AA706829 AA877544 AI082289 AA926687 N92840 AW249798 AA934763 AW998363 AI128632 N25202 AI240209 AW118892 N80744 R35655 AI342321 AI340141 AW878792 AI857321 H09610 W04601 AW006650 AA126006 AA553675 AI052791 AW059835 AI041906 AA814658 AW002059 AA729483 AI609301 AA994633 AA903651 AI459183 T95072 AW088630 AA126112 AI800091 AI561215 H17502 AW475072 AI819003 AI683272 AI262701 AW793140 T81787 R99586 AI275160 AI310420 AI698929 AA159174 AI827968 F30305 F30309 AA806662 AI091923 AW878722 AA583430 AW571913 AI674584 AA292533 AI079471 AA642325 AA719050 AW793172 AA305476 AW103745 T23459 N79525 AI784438 AA534551 AW193751 AI074360 BE281214 T32229 W25066 W01205 T63086 AW795348 AI361287 AW795353 AW795349 AA594759 AI400295 D11489 AI370689 AA482356 AA485295 W40151 AA564661 AW300745 AI346938 AI374975 AI423782 AW193899 AA612604 AI183409 AA996156 AW366963 AW366977 AI284860 AA846503 AI985064 AA844576 AA737921 AA873274 BE241546 BE241540 AA484058 AW468970 AA127876 AA159120 AW001568 AW795213 AW795258 AW795330 BE250589 BE387572 AA910895 AA161217 BE250380 W31500 T95167 AI719306 AI359224
102781	20812_1	BE258778 BE281230 BE410044 T33723 AW672694 AW410439 NM_006429 AF026292 T35505 BE542333 T08940 AU076737 AW247471 BE393215 AW328640 BE542408 T32170 BE302544 T31955 BE206898 BE275738 T32570 BE386426 BE298746 BE389937 BE293991 BE315289 BE389578 R34739 R15312 BE279365 BE277756 AL036019 T33725 BE277779 BE302962 AL047294 BE276505 T09070 T33673 BE312580 AW387774 BE257175 AW674367 BE253331 BE270344 BE299831 BE273576 T32062 AI751831 BE618381 AA304899 BE252268 U46364 BE256790 BE207199 BE256209 BE251941 BE250791 BE313955 BE269806 BE543623 BE279212 BE252289 T31699 BE262220 T31669 AA315781 AA192212 N84547 BE292737 BE259631 AA232179 AI133144 T31292 AA315945 BE407301 BE251184 BE409006 AI880158 AI904003 AI904114 AW651768 AW651763 R58247 BE271897 U83843 C05298 BE261609 BE255973 AA351650 N84631 BE263637 AW452910 AA328465 AA324549 AW579525 BE252296 BE257551 AL048332 BE208630 AA359336 AW327897 AA151742 AA305816 BE076862 BE076796 BE263161 AA323785 AA676588 AA626565 AA078917 W87657 R09002 R94021 AA312032 BE276665 AA295608 AW407162 AA329374 AW877912 N27885 AA369256 AA360968 BE250476 N85427 BE265569 AI278639 AI816576 AI691037 AW328583 AI567949 AI983455 AI927732 AI811297 AI571508 AW073674 BE296039 BE467326 AI828796 AI816578 AW511604 AI921213 AW152427 AI795787 AI801618 AW168866 AI628144 AI890339 AW173690 AW511540 BE535620 AA383014 BE301164 AI866596 AW514909 AA658050 AW575243 AA074631 AI093488 AW575408 AW675443 AW615636 AW732207 AW377638 AA321784 AA641629 AA633105 AA527640 AW129146 AW615672 BE394607 AA483902 AW475032 BE378532

		AA872808 AI469388 AW105268 BE047301 AW591843 AW410066 AW517153 AI950495 AA746641 AI914878 AA873185 AI696911 AA548625 AA911505 AA148762 AW674535 AI587329 BE328328 AW270348 AA158225 AW117705 AW474997 AW519193 AA614757 AW664383 AI082647 AW590973 AI476711 AA192213 N88741 BE464552 AW072679 AI453708 AA152166 AA805924 AI581078 AI125768 AW173484 AI961980 BE300766 AI199698 AI636792 AW247333 AW272861 AA078818 AA150012 AA551232 AA678821 AW873869 AW768266 AI660315 AA319210 AA814551 AA157994 AA318886 AI582962 AW089224 AI356098 AI343694 AW072598 N21054 AI301249 AA742924 H17917 AW328584 AW248898 AI751830 AA907816 R08898 AW087989 AI828300 AA148596 AI269577 T33426 AA213571 AI973201 AA666279 R49612 AI573183 AW799762 AW410068 AW769666 AI962097 AI475204 D57490 AW517531 BE245270 AW470008 T33427 AW005731 AI795795 T23753 AW272981 T15747 AA552875 T23644 AW361289 AI758558 BE207435 AA876958 T03361 AA883569 F37533 AA582321 AW082524 R42212 AA973847 T18900 AA086202 AI559867 AI302418 AA948667 AA745670 T08939 T33724 T33722 BE621568 D57489 D25906 BE621151 F16510 C05966 T35127 AA630427 AI933481 AA309426 AI918440 BE561854 BE618866 BE394675 BE296173 AW951687 BE383739 BE616141 BE312730 BE535351 AW080575 BE313330 BE616664 AI354390 AA847315 BE544509 BE515212 BE297833 BE278808 BE544844 AW090178 AI890664 BE546708 AW189943 BE274412 BE382399 BE266392 BE254949 BE280696 BE383237 BE261756 BE257721 BE312683 BE275476 BE514880 BE545314 BE313587 BE384537 BE386691 BE264813 AW592575 AI336332 AI278641 AI795791 BE222662 AW249316 AA314361 AL036012 AW402923 BE266845 AA075945 AA314436 BE384640 AW731769 AW957077 AA552234 AA573560 AW367038 AA313399 AI983873 BE410159 BE263803 BE514339 BE409073 BE281296 BE543396 BE395387 BE088360 BE546946 BE546570 BE390626 AA074638 AA301821 AW845230 AW582379 AI949222 AW029572 AA515843 AW272394 BE250234
119221	102947_1	C14322 W74050 AI074232 AA595624 BE048955 AI148417 AI583145 AI473460 AI801688 AW573593 AI950741 AI628140 AW467921 R98105 AI149258 AI247584 AI078378 AI139850 AA489411 W24744 R98104 AI033826 AA699589 AI033120 N55544 W88984 AW970771 AA703362 AA099138 AA706792 AA046150 H98981 AI916674 AA953018 AI972749 AI921343 AA909044 AA094751 AI203124 AA582143 AI446654 AW235415 R70377 AA099236 F20703 AA524436 R69484
125831	1522905_1	H04043 D60988 D60337
128192	45743_3	AI204246 AI204250 AI194050
113195	178688_1	H83265 T63524 AA304359 AW960551 AI672874 AI749427 AA227777 AW027055 AA971834 T49644 T54122 AI983239 AI808233 T91264 T96544 AI350945 AI709114 R72382 T48788 R48726 AW385418 AI095484 T49645 AA928653 AA570082 AW007545 T57178 AA516413 AA913118 T57112 AA564433 AA774503 AA367671 T59757
119861	238266_1	W78816 AI720806 AI633854 AI632086 AI668663 N70894 AW571809 AI383592 AI201348 W80715 N91880 AW963101 AA339011
112973	4868_1	AB033023 BE391906 BE275965 BE277872 BE003882 AA313774 BE019159 BE298024 BE299727 BE300011 BE390277 BE394764 N87550 BE409419 BE408652 BE408197 AL119332 AA622427 AI816265 AA610118 T07318 AA019839 AA634430 BE205794 BE049461 AI042322 AI652711 AI917645 AA630045 AW191969 AI817882 T17271 AI803663 AI095533 H46019 AW592438 AI624836 AI675552 D51149 AW132058 AA639614 AI925762 AW088153 T17455 AA018640 AW751475 BE300241 AI816255 BE391981 AW408671 AA353910 AW875446 AW875703 AW875926 AW875645 AW875647 AW938037 AL138042 AW892619 BE243018 AW995454 BE246381 BE009082 BE278921 AW967842 AA262454 H30121
129402	47367_1	W72062 AF088057 W76255 AI827219 AI631461 AW449295 AI354957 AI913803 T62772 AI222040 T62921 T63781
105936	260931_1	AI678765 H12175 R14664 AI914049 AA995383 H08009 H19418 AW953728 AI358021 AA587361 AI269377 AA369905 AW957113 H27693 AI300474 H73776 W74397 AA579604 AI131018 W72331 AI719085 AA568348 AI859045 AI814819 AI888714 BE467470 AW131268 H19419 H27694 AI342165 AI914155 AA534872 BE018176 R60206 H11647 R45641 AI860466 BE301656 AI125453 AI498120 AA593735 AA879110 AI016404 T35018 AA588397 AW449767 AA470365 BE501139 AA588354 AI337500 AW078532 Z41279 AI125449 AA935725 AA404338
129466	2094_50	L42583 NM_005554 L42601 BE183076 AI541221 BE140567 L42610 V01516 J00269 AW275792 AW383052 AW380143 AI541102 BE612846 AI541344 AW238368 BE613405 BE615705 BE615530 BE615301 AW379823 AW794706 AA194806 AA194992 AW384024 AW384000 AA641239 AI246504 AI540333 AW238681 AA640939 AI540863 AI608860 AW862564 AW366725 AW368983 AW366870 AA596020 AW794721 AW794511 AI591181 BE182523 AW794644 AW794620 AI935234 AI608903 AI608623 AW797060 AW084935 BE182517 BE182319 AI890082 AW238346 AW797012 BE182522 AW794838 AI608794 AW304289 AA147193 AA595995 AW381128 AW366720 AA583718 AI828416 BE122864 AW368343 AA431080 AW082039 AW380976 AA587144 AA443636 AW872937 AW794448 AW378382 AW085761 AW794718 AW263895 AA583587 AA583991 AA583994 AA586886 AA586880 AW368365 AI814460 AA586991 AI282829 AW378406 AA586721 AI609242 AA431973 AA232959 AI831095 AW263854 AW378391 AW378415 AW378381 AA036990 AW238395 AI285446 BE208219 BE049526 AA583605 AA583918 AW366711 AI285580 AW082642 AI285712 AA582875 AW591216 AW368719 AW378408 BE122835 AA582976 BE350422 AA418328 AI541454 AI565930 AA583700 AA150575 AW238427 AI287474 AA912658 AA584223 AW238528 C17918 AW136169 AA159847 AI923797 AI609009 BE182479 AI915198 AW378114 AA147179 AA584239 AA150532 AW168862 AW085999 AW082480 AA659742 AW079703 AI872793 AA583981 AI824571 BE182316 BE182507 AA233331 AI824572 AI540586 D29492 BE182931 AA036948 BE551821 D29401 AW378365 C00141 D29181 D29567 AW103359 W95238 AI991663 AA587298 BE184608 AA099833 W95121 W95150 D29584 AI934111 D29456 D29533 AW265380 D29290 AW238463 AA121041 D29204 AA595925 D29441 AW081840 AA587018 D29323 AA582891 BE182433 BE182437 BE158295 BE182434
100220	45374_1	AW015534 AA314369 AA290715 BE568683 AW629494 D28364 AW995678
100355	12538_1	AI907114 AA580734 AL041945 AA101515 AA121344 D78130 NM_003129 AA341650 T84166 AF098865 AA130976 BE089553 H05719 F13446 T66122 AW175590 F05344 AI114790 R12900 AA194871 AA132298 D78129 AA132213 AW948930 AW948919 AA263053 AW946593 AW948840 AA278558 R50895 N26940 N40818 AW021255 AA054851 AA663379 AW948795 AW948893 AA400356 AW948911 N85024 W78844 AI341546 AI760182 AA286783 BE617763 BE617263 AW263690 BE049454 BE617928 AW515038 AW950584 AA601009 AI079194 AA147204 AW083163 AA130981 AI218369 AA604784 AI806257 AI559556 AA232318 AA258065 AI471982 AA687949 AI143944 N30172 AA400196 AI769049 AI084342 AI221380 AA948469 AI802469 H05720 AA113270 AA158138 AA076231 AI521024 AI810962 AI133616 AA805106 AA101516 R40052 R50778 R43280 T65036 AW131924 AA114251 AA152331 F09650 AA580614 AA558927 C75491 Z38352 AA954595 C75606 W80742
100491	34803_1	D56165 M36981 X58965 NM_002512 BE379177 AA314836 BE256445 BE252016 AW248343 AI720933 AW085701 BE386050 BE619742 BE277805 AA147951 AA603113 BE253293 AI246588 AI183405 AI954174 AI126891 AI829101 AI123832 AW129670 AA471268 AW170242 AW873079 AA148011 AI608620 AA482961 AI003658 H43261 AA657978 AI735072 R83138 AA722002 AA626271 AW273877 BE464626 AA071483 AA429973 AA494342 AA620436 AA775597 AA775601 AA826847 AI192585 AA826359 AA411159 AI193419 AI204013 AA705323 AA716255 AI784611 AI081144 AI128227 AA828464 AI148911 AI493446 AI626084 AI189180 AI721196 AI190618 AA284987 AI128543 AA632064 AI333073 AI278470 AA131688 AI491768 AA937581 AA630065 AA834257 AW249841 AA583742 AI309756 AA961676 AI760860 AA557818 AA954238 H43655 AI302564 AA127545 AI609219 H20426 AI042292 AI056466 AA581836 W47002 AA422057 AA937673 F29757 AA829208 AW327462 AA372098 W02144 AA036805 AA487365 AA961037 AI139946 AA487250 AA737118 AI952504 AI242293 AA650552 AI708401 AI633133 AA630848 AA654317 F24128 AI434165 W46252 AW043879 AI033763 F37228 AA687809 N49087 AA876981 AA506947 AI914572 AI833284 F22253 AA026222 R50166 AI219267 N27095 AA496512 AI784222 AI289904 AA513146 AA528547 AA418700 F36721 AI880700 AI601170 AI862851 AI708633 AA524499 AA642220 AA496628 AI718709 W80579 AI720547 F20718 AA649943 AA588229 N40503 H46029 BE262669 BE391069 BE537538 AI510751 AI906968 AI318611 H46099 AI472604 T60667 AA373087 W32479 AA514034 BE619183 AA134672 AA127544 H26942 BE536689 AW327461 AA422139 AW262357 AW327348 F33510 AI630382 AW827126 F27133 AI335189 AW517599 W80471 AA885814 N89681 BE393173 AA617760 AA584268 AA460537 AA446261 H20425 N64040 AW276801 AA316367 AA071232 BE545409 AA308292 BE274447 AA380861 AA340038 AA341806 AA865579 AI018634 AI766314 AI919302 AA872367 AA991404 AI906961 AA888375 BE621012 AA505388 AA935192 AA290828 R50220 H50814 H44721 AW951723 AA514796 AA418708 AW673377 AA379622 AA977995 AA708224 AA708216 AI318249 AI318233 AA411160 AA026221 AA316774 AA486908 AI500094 AA096362 AW583742 BE536422 BE618653 R70203 AA131732 AA345048 BE562720 T28342
100518	13165_1	NM_004415 AL031058 M77830 BE149760 AW752599 AW848723 AW376697 AW376817 AW376699 AW848371 AW376782 AW848789 AW361413 AW849074 AW997139 AW799304 AW799309 BE077020 BE077017 BE185187 AW997196 BE156621 BE179915 BE006561 BE143155 AW890985 BE002107 AW103521 AA857316 AW383133 BE011378 AW170253 BE185750 AW886475 BE160433 J05211 BE082576 BE082584 BE004047 AW607238 AW377700 AW377699 BE082526 BE082505 BE082507 BE082514 AW178000 AW177933 AI905935 AW747877 AW748114 BE148516 AW265328 AW847678 AW847688 AW365151 AW365148 AW365153 AW365156 AW365175 AW365157 AW365154 AW068840 BE005272 AW365145 BE001925 BE182166 BE144243 BE001923 AI951766 AI434518 BE184920 BE184933 AI284090 BE184941 AW804674 BE184924 C04715 W39488 AW995615 BE184948 BE159646 AW606653 AA099891 AA131128 AA337270 AA340777 AW384371 AA852212 R58704 AW366566 AW364859 AA025851 AA025852 AA455100 AA719958 AW352220 AW996245 BE165351 BE073467 AA377127 AW890264 AW609750 AW391912 AW849690 T87267 AW853812 AA852213 W74149 BE009090 AA056401 H91011 AW368529 AW390272 C18467

		AW674920 N57176 AA026480 AW576767 H93284 AA026863 AW177787 AA026654 AW177786 BE092134 BE092137 BE092136 AW177784 AI022862 BE091653 AW376811 AW848592 AA040018 BE185331 BE182164 AA368564 AW951576 T29918 AA131077 W95048 W25458 AW205789 H90899 N29754 W32490 R20904 BE167181 BE167165 N84767 H27408 H30146 AI190590 C03378 AI554403 AI205263 AA128470 AI392926 AF139065 AW370813 AW370827 AW798417 AW798780 AW798883 AW798569 R33557 AA149190 C03029 AW177783 AA088866 AW370829 AA247685 BE002273 AI760816 AI439101 AW879451 AI700963 AA451923 AI340326 AI590975 T48793 AI568096 AI142882 AA039975 AI470146 AA946936 BE067737 BE067786 W19287 AA644381 AA702424 AI417612 AI306554 AI686869 AI568892 AW190555 AI571075 AI220573 AA056527 AI471874 AI304772 AW517828 AI915596 AI627383 AI270345 AW021347 AW166807 AW105614 AI346078 AA552300 W95070 AI494069 AI911702 AA149191 AA026864 AI830049 AI887258 AW780435 AI910434 AI819984 AI858282 AI078449 AI025932 AI860584 AI635878 AA026047 AA703232 D12062 AW192085 AA658154 AW514597 AW591892 T87181 AA782066 AW243815 AW150038 AW268383 AW004633 AI927207 AA782109 AW473233 AI804485 AW169216 AI572669 AA602182 AW015480 AW771865 AI270027 AA961816 AA283207 AI076962 AI498487 AI348053 AI783914 H44405 AW799118 AA128330 AA515500 AA918281 W02156 AI905927 AA022701 W38382 R20795 T77861 AW860878
100528	45979_1	BE386801 AU077299 AA143755 BE302747 AA853375 U30162 BE274163 BE277479 BE408180 BE274874 C15000 AA047476 N27099 AI359165 AI638794 AI151283 AI863925 AW444977 AI207392 AA931263 AA443112 R40138 AW068538 AA351008 AA676972 R62503 AA916492 AW001865 H42334 H38280 AA121497 AA114137 AI750938 M17783 AA383786 BE274462 AI753182 C05975 AA347404 AW069298 AI754351 AI754044 AA188808 AA186879 AA565243 AL040655 AA456177 AI750722 AA045756 AA213580 C16936 AW578747 AW753731 H41632 N44761 R58560 R61260 AA039902 N59721 AW992543 R68380 AA149686 T29017 H03739 BE383822 BE387105 BE408251 BE410425 H41560 AA247591 BE389677 AI752233 AI566195 AA868004 AI424523 AW753720 AA852159 BE386803
100559	2260_1	NM_000094 L02870 D13694 S51236 M96984 AW946290 M65158 AI285422 D29523 AL119886 AW630655 L06862 AI884355 AW168737 T29085 AW797005 AW801340 AI355504 AW079048 AW801337 AI690455 AI972063 AW268565 W68588 AA587326 AA883498 AI033523 AW510356 AW591998 H98463 AL043852 AI150055 AI566239 AI624803 AA844717 H40670 AA922334 AI864424 AW615094 AW451233 AI302203 F31221 AI872170 W68589 AA904478 AI917631 AW014208 AW450759 AA847625 AI284033 AA848176 AA598507
100576	9986_1	X00356 NM_001741 M26095 X03662 M12667 X02330 X02330 AA716058 AW296074 X04861 AI695720 AA719597
124357	genbank_N22401	N22401
101624	entrez_M55998	M55998
101625	entrez_M57293	M57293
135158	57963_1	AL037551 AI804716 AW439811 AI569470 AA075299 AI738572 AI270388 AI816783 AW263026 AI633951 AI655285 AI990572 AI950425 AW241533 AA916883 AA576693 AA160156 AA613783 AW078884 AI888282 AI275241 AI133467 AA164921

Tables 2A-8C were previously filed on November 9, 2001 in USSN 60/339,245 (18501-004100US)

Table 2A shows 504 genes down-regulated in lung tumors relative to normal lung and chronically diseased lung. Chronically diseased lung samples represent chronic non-malignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: 90th percentile of AI for normal lung samples divided by the 80th percentile of AI for adenocarcinoma and squamous cell carcinoma lung tumor samples.
R2: median of AI for normal lung samples divided by 90th percentile of AI for adenocarcinoma and squamous cell carcinoma lung tumor samples.
R3: median of AI for normal lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of AI for adenocarcinoma and squamous cell carcinoma lung tumor samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples.
R4: average of AI for normal lung samples divided by average AI for squamous cell carcinoma and adenocarcinoma lung tumors.
R5: median of AI for normal lung samples divided by the 90th percentile of AI for adenocarcinomas.
R6: median of AI for normal lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of AI for adenocarcinomas minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples.
R7: average of AI for normal lung samples divided by the 90th percentile of AI for squamous cell carcinomas.
R8: median of AI for normal lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of AI for squamous cell carcinomas minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples.

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2	R3	R4	R5	R6	R7	R8
100095	Z97171	Hs.78454	myocilin; trabecular meshwork inducible	40.20							
100115	NM_002084	Hs.336920	glutathione peroxidase 3 (plasma)								3.46
100138	U83508	Hs.2463	angiopoietin 1			2.30					
100299	D49493	Hs.2171	growth differentiation factor 10		11.00						
100306	U86749	Hs.80598	transcription elongation factor A (SII);						3.06		
100447	NM_014767	Hs.74583	KIAA0275 gene product								3.16
100458	S74019	Hs.247979	Vpre-B	42.40							
100862	AA005247	Hs.285754	Hepatocyte Growth Factor Receptor						4.13		
100959	AA359129	Hs.118127	actin; alpha; cardiac muscle				125.60				
101032	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	36.40							
101081	AF047347	Hs.4880	amyloid beta (A4) precursor protein-bind				34.60				
101088	X70697	Hs.553	solute carrier family 6 (neurotransmitte				193.20				
101125	AJ250562	Hs.82749	transmembrane 4 superfamily member 2						3.10		
101180	U11874	Hs.846	interleukin 8 receptor; beta				54.86				
101308	L41390		"Homo sapiens core 2 beta-1,6-N-acetylgl	33.20							
101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do				36.40				
101345	NM_005795	Hs.152175	Calcitonin receptor-like			2.29					
101346	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N				70.55				
101397	M26380	Hs.180878	lipoprotein lipase								3.54
101414	NM_000066	Hs.38069	complement component 8; beta polypeptide							3.81	
101435	NM_001100	Hs.1288	actin; alpha 1; skeletal muscle				34.60				
101507	X16896	Hs.82112	interleukin 1 receptor; type I				37.60				
101530	M29874	Hs.1360	cytochrome P450; subfamily IIB (phenobar								4.25
101537	AI469059	Hs.184915	zinc finger protein; Y-linked			2.54					
101542	NM_000102	Hs.1363	cytochrome P450; subfamily XVII (steroid		5.50						
101545	BE246154	Hs.154210	EDG1; endothelial differentiation, sphin	39.40							
101554	BE207611	Hs.123078	thyroid stimulating hormone receptor		13.00						
101560	AW958272	Hs.83733	Intercellular adhesion molecule 2, exon								3.38
101574	M34182	Hs.158029	protein kinase; cAMP-dependent; catalyti						4.37		
101605	M37984	Hs.118845	troponin C; slow								3.80
101621	BE391804	Hs.62661	guanylate binding protein 1; interferon-	30.20							
101680	AA299330	Hs.1042	Sjogren syndrome antigen A1 (52kD; ribon							2.75	
101829	AW452398	Hs.129763	solute carrier family 8 (sodium/calcium						3.37		
101842	M93221	Hs.75182	mannose receptor; C type 1				38.20				
101961	AW004056	Hs.168357	"Hs-TBX2=T-box gene {T-box region} [huma			2.32					
101994	T92248	Hs.2240	uteroglobin								6.85
102020	AU077315	Hs.154970	transcription factor CP2			2.45					
102091	BE280901	Hs.83155	aldehyde dehydrogenase 7								6.75
102112	AW025430	Hs.155591	forkhead box F1	54.60							
102190	AA723157	Hs.73769	folate receptor 1 (adult)								3.98
102202	NM_000507	Hs.574	fructose-bisphosphatase 1								3.62
102241	NM_007351	Hs.268107	Multimerin			2.32					
102310	U33839		Accession not listed in Genbank		7.00						
102397	U41898		"Human sodium cotransporter RKST1 mRNA,	29.40							
102571	U60115	Hs.239069	"Homo sapiens skeletal muscle LIM-protei								3.75
102620	AA976427	Hs.121513	Human clone W2-6 mRNA from chromosome X						3.07		
102636	U67092		"Human ataxia-telangiectasia locus prote			2.40					
102667	U70867	Hs.83974	solute carrier family 21 (prostaglandin			3.15					
102675	U72512	Hs.7771	"Human B-cell receptor associated protei						3.56		
102698	M18667	Hs.1867	progastricsin (pepsinogen C)								4.51
102727	U79251	Hs.99902	opioid-binding protein/cell adhesion mol					12.00			
102852	V00571	Hs.75294	corticotropin releasing hormone	37.40							
103026	X54162	Hs.79386	thyroid and eye muscle autoantigen D1 (6					13.00			
103028	X54380	Hs.74094	pregnancy-zone protein	28.80							
103098	M86361		Human mRNA for T cell receptor; clone IG					10.00			
103117	X63578	Hs.295449	parvalbumin		6.00						
103241	X76223		H.sapiens MAL gene exon 4			2.47					
103280	U84722	Hs.76206	Cadherin 5, VE-cadherin (vascular epithe			2.69					
103360	Y16791	Hs.73082	keratin; hair; acidic; 5							2.16	

103496	Y09267	Hs.132821	flavin containing monooxygenase 2								5.97
103508	Y10141		"H.sapiens DAT1 gene, partial, VNTR"						3.27		
103561	NM_001843	Hs.143434	contactin 1			2.40					
103569	NM_005512	Hs.151641	glycoprotein A repetitions predominant			2.99					
103575	Z26256		"H.sapiens isoform 1 gene for L-type cal						4.18		
103627	Z48513		H.sapiens XG mRNA (clone PEP6)						3.44		
103767	BE244667	Hs.296155	CGI-100 protein							2.25	
103850	AA187101	Hs.213194	Hypothetical protein MGC10895; sim to SR				46.55				
104078	AA402801	Hs.303276	ESTs						3.05		
104326	AW732858	Hs.143067	ESTs						3.54		
104352	BE219898	Hs.173135	dual-specificity tyrosine-(Y)-phosphoryl						3.16		
104398	AI423930	Hs.36790	ESTs; Weakly similar to putative p150 [H	64.80							
104473	AI904823	Hs.31297	ESTs								3.38
104493	AW960427	Hs.79059	ESTs; Moderately similar to TGF-BETA REC			2.47					
104495	AW975687	Hs.292979	ESTs	28.60							
104595	AI799603	Hs.271568	ESTs						3.42		
104597	AI364504	Hs.93967	ESTs; Weakly similar to Slit-1 protein [		6.00						
104659	AW969769	Hs.105201	ESTs	34.00							
104686	AA010539	Hs.18912	ESTs		11.00						
104691	U29690	Hs.37744	ESTs; Beta-1-adrenergic receptor	56.80							
104764	AI039243	Hs.278585	ESTs				60.40				
104776	AA026349		ESTs	34.20							
104825	AA035613	Hs.141883	ESTs			3.03					
104865	T79340	Hs.22575	Homo sapiens cDNA: FLJ21042 fis, clone C	41.20							
104942	NM_016348	Hs.10235	ESTs								3.27
104989	R65998	Hs.285243	ESTs				40.00				
105062	AW954355	Hs.36529	ESTs								3.20
105101	H63202	Hs.38163	ESTs	34.20							
105173	U54617	Hs.8364	ESTs								4.17
105194	R06780	Hs.19800	ESTs		16.00						
105226	R58958	Hs.26608	ESTs			2.34					
105256	AA430650	Hs.16529	transmembrane 4 superfamily member (tetr			2.72					
105394	BE245812	Hs.8941	ESTs			2.61					
105647	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	33.60							
105789	AF106941	Hs.18142	arrestin; beta 2								3.59
105817	AA397825		synaptopodin						4.46		
105847	AW964490	Hs.32241	ESTs				35.40				
105894	AI904740	Hs.25691	calcitonin receptor-like receptor activi			3.43					
105999	BE268786	Hs.21543	ESTs		7.00						
106075	AA045290	Hs.25930	ESTs				42.60				
106178	AL049935	Hs.301763	KIAA0554 protein	34.80							
106381	AB040916	Hs.24106	ESTs					12.00			
106467	AA450040	Hs.154162	ADP-ribosylation factor-like 2						3.69		
106536	AA329648	Hs.23804	ESTs				96.40				
106569	R20909	Hs.300741	sorcin				47.20				
106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr				220.40				
106842	AF124251	Hs.26054	novel SH2-containing protein 3			2.55					
106844	AA485055	Hs.158213	sperm associated antigen 6	39.20							
106870	AI983730	Hs.26530	serum deprivation response (phosphatidyl			2.28					
106943	AW888222	Hs.9973	ESTs								4.28
106954	AF128847	Hs.204038	ESTs								4.32
107106	AA862496	Hs.28482	ESTs					10.45			
107163	AF233588	Hs.27018	ESTs			2.57					
107201	D20378	Hs.30731	EST						3.84		
107238	D59362	Hs.330777	EST		8.00						
107376	U90545	Hs.327179	solute carrier family 17 (sodium phospha		10.67						
107530	Y13622	Hs.85087	latent transforming growth factor beta b			2.32					
107688	AW082221	Hs.60536	ESTs				34.60				
107706	AA015579	Hs.29276	ESTs	28.40							
107723	AA015967		EST						3.29		
107727	AA149707	Hs.173091	DKFZP434K151 protein				80.80				
107750	AA017291	Hs.60781	ESTs				51.40				
107751	AA017301	Hs.235390	ESTs						3.14		
107873	AK000520	Hs.143811	ESTs		9.00						
107899	BE019261	Hs.83869	ESTs; Weakly similar to !!!! ALU SUBFAMI						3.65		
107994	AA036811	Hs.48469	ESTs				44.60				
107997	AL049176	Hs.82223	Human DNA sequence from clone 141H5 on c				32.00				
108041	AW204712	Hs.61957	ESTs				30.80				
108048	AI797341	Hs.165195	ESTs							4.75	
108338	AA070773		"zm53g11.s1 Stratagene fibroblast (#9372			2.33					
108434	AA078899		"zm94b1.s1 Stratagene colon HT29 (#93722							2.92	
108447	AA079126		"zm92a11.s1 Stratagene ovarian cancer (#						3.06		
108480	AL133092	Hs.68055	ESTs				34.00				
108499	AA083103		"zn1b12.s1 Stratagene hNT neuron (#93723								3.36
108535	R13949	Hs.226440	Homo sapiens clone 24881 mRNA sequence					19.00			
108550	AA084867		"zn11f6.s1 Stratagene hNT neuron (#93723					12.00			
108604	AA934589	Hs.49696	ESTs			2.33					
108625	AW972330	Hs.283022	ESTs								5.82
108629	AA102425		"zn24c6.s1 Stratagene neuroepithelium NT							3.42	
108655	AA099960		"zm65c6.s1 Stratagene fibroblast (#93721		7.00						
108756	AA127221	Hs.117037	Homo sapiens mRNA; cDNA DKFZp564N1164 (f		6.05						
108864	AI733852	Hs.199957	ESTs	28.80							
108895	AL138272	Hs.62713	ESTs	32.80							
108921	AI568801	Hs.71721	ESTs				57.80				
108967	AA142989	Hs.71730	ESTs	28.80							

109001	AI056548	Hs.72116	ESTs, Moderately similar to hedgehog-int			2.57					
109003	AA147497	Hs.71825	ESTs							2.11	
109004	AA156235	Hs.139077	EST		5.60						
109065	AA161125	Hs.252739	EST					10.00			
109250	H83784	Hs.62113	ESTs; Weakly similar to PHOSPHATIDYLETHA							3.44	
109490	AA233416	Hs.139202	ESTs							2.92	
109510	AI798863	Hs.87191	ESTs			2.40					
109578	F02208	Hs.27214	ESTs		10.00						
109601	F02695	Hs.311662	EST				40.80				
109613	H47315	Hs.27519	ESTs				54.40				
109650	R31770	Hs.23540	ESTs	31.20							
109682	H18017	Hs.22869	ESTs		8.40						
109724	D59899	Hs.127842	ESTs				29.40				
109782	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene					8.00			
109833	R79864	Hs.29889	ESTs		10.00						
109837	H00656	Hs.29792	ESTs			6.49					
109977	T64183	Hs.282982	ESTs							2.75	
109984	AI796320	Hs.10299	ESTs				107.00				
110146	H41324	Hs.31581	ESTs; Moderately similar to SYNTAXIN 1B							2.22	
110271	H28985	Hs.31330	ESTs						3.48		
110280	AW874263	Hs.32468	ESTs	44.20							
110420	R93141	Hs.184261	ESTs				32.00				
110578	T62507	Hs.11038	ESTs	28.40							
110634	R98905	Hs.35992	ESTs					20.00			
110726	AW961818	Hs.24379	potassium voltage-gated channel; shaker-								4.15
110837	H03109	Hs.108920	ESTs; Weakly similar to semaphorin F [H.				56.80				
110875	N35070	Hs.26401	tumor necrosis factor (ligand) superfami			3.13					
110894	R92356	Hs.66881	ESTs; Moderately similar to cytoplasmic		5.33						
110971	AI760098	Hs.21411	ESTs				44.60				
111023	AV655386	Hs.7645	ESTs	32.40							
111057	T79639	Hs.14629	ESTs					17.14			
111247	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f							4.58	
111330	BE247767	Hs.18166	KIAA0870 protein								3.42
111374	BE250726	Hs.283724	ESTs; Moderately similar to HYA22 [H.sap								3.91
111442	AW449573	Hs.181003	ESTs				33.20				
111737	H04607	Hs.9218	ESTs				53.00				
111747	AI741471	Hs.23666	ESTs	46.20							
111807	R33508	Hs.18827	ESTs		16.00						
111862	R37472	Hs.21559	EST						3.91		
112045	AI372588	Hs.8022	TU3A protein							2.74	
112057	R43713	Hs.22945	EST							4.92	
112214	AW148652	Hs.167398	ESTs					13.00			
112263	R52393	Hs.25917	ESTs			2.43					
112314	AW206093	Hs.748	ESTs		9.00						
112324	R55965	Hs.26479	limbic system-associated membrane protei					14.00			
112362	AW300887	Hs.26638	ESTs; Weakly similar to CD20 receptor [H			2.49					
112380	H63010	Hs.5740	ESTs			2.34					
112425	AA324998	Hs.321677	ESTs; Weakly similar to !!!! ALU SUBFAMI		8.00						
112473	R65993	Hs.279798	pregnancy specific beta-1-glycoprotein 9						4.53		
112492	N51620	Hs.28694	ESTs				29.80				
112541	AF038392	Hs.116674	ESTs						3.62		
112620	R80552	Hs.29040	ESTs			2.37					
112623	AW373104	Hs.25094	ESTs			2.26					
112867	T03254	Hs.167393	ESTs					12.00			
112894	T08188	Hs.3770	ESTs		6.50						
112954	AA928953	Hs.6655	ESTs		7.00						
113029	AW081710	Hs.7369	ESTs; Weakly similar to !!!! ALU SUBFAMI								4.39
113086	AA346839	Hs.209100	DKFZP434C171 protein								4.47
113140	T50405	Hs.175967	ESTs					10.00			
113252	NM_004469	Hs.11392	c-fos induced growth factor (vascular en		14.00						
113257	AI821378	Hs.159367	ESTs						3.72		
113394	T81473	Hs.177894	ESTs						3.60		
113437	T85349	Hs.15923	EST	35.00							
113454	AI022166	Hs.16188	ESTs		6.00						
113502	T89130		ESTs	39.60							
113552	AI654223	Hs.16026	ESTs								3.88
113645	T95358	Hs.333181	ESTs							2.58	
113691	T96935	Hs.17932	EST				38.20				
113706	AA004693	Hs.269192	ESTs						3.09		
113883	U89281	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro			2.31					
113924	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	30.40							
114035	W92798	Hs.269181	ESTs					13.00			
114058	AK002016	Hs.114727	ESTs								5.00
114084	AA708035	Hs.12248	ESTs				40.60				
114121	H05785	Hs.25425	ESTs			2.31					
114124	W57554	Hs.125019	Human lymphoid nuclear protein (LAF-4)		7.00						
114275	AW515443	Hs.306117	interleukin 13 receptor; alpha 1		6.00						
114297	AA149707	Hs.173091	DKFZP434K151 protein				48.80				
114427	AA017176	Hs.33532	ESTs; Highly similar to Miz-1 protein [H						3.45		
114449	AA020736		"ze63b11.s1 Soares retina N2b4HR Homo sa					10.00			
114452	AI369275	Hs.243010	ESTs, Moderately similar to RTC0_HUMAN G		14.00						
114609	AA079505		"zm97a5.s1 Stratagene colon HT29 (#93722						3.13		
114648	AA101056		"zn25b3.s1 Stratagene neuroepithelium NT				35.40				
114731	BE094291	Hs.155651	Homo sapiens HNF-3beta mRNA for hepatocy								3.42
114762	AA146979	Hs.288464	ESTs	33.00							

114776	AA151719	Hs.95834	ESTs	34.40							
115009	AA251561	Hs.48689	ESTs	30.20							
115272	AW015947		ESTs; Weakly similar to hypothetical L1	32.60							
115279	AW964897	Hs.290825	ESTs		6.00						
115302	AL109719	Hs.47578	ESTs					12.00			
115365	AW976252	Hs.268391	ESTs						3.32		
115559	AL079707	Hs.207443	ESTs				48.00				
115566	AI142336	Hs.43977	ESTs				56.20				
115683	AF255910	Hs.54650	ESTs, Weakly similar to (define not ava	31.40							
115744	AA418538	Hs.43945	ESTs; Highly similar to dJ1178H5.3 [H.sa				33.60				
115819	AA486620	Hs.41135	Endomucin 2				74.40				
115949	AI478427	Hs.43125	ESTs			3.18					
115965	AA001732	Hs.173233	ESTs				388.80				
116035	AA621405	Hs.184664	ESTs				33.20				
116049	AA454033	Hs.41644	ESTs				45.80				
116081	AI190071	Hs.55278	ESTs						3.57		
116082	AB029496	Hs.59729	ESTs			3.06					
116213	AA292105	Hs.326740	leucine rich repeat (in FLII) interactin	50.60							
116228	AI767947	Hs.50841	ESTs; Weakly similar to tuftelin [M.musc			3.85					
116250	N76712	Hs.44829	ESTs		6.00						
116419	AI613480	Hs.47152	ESTs; Weakly similar to testicular tekti				30.00				
116617	D80761	Hs.45220	EST			2.27					
116784	AB007979	Hs.301281	tenascin R (restrictin; janusin)	47.20							
116835	N39230	Hs.38218	ESTs				41.20				
116970	AB023179	Hs.9059	KIAA0962 protein					11.00			
117023	AW070211	Hs.102415	ESTs				91.00				
117027	AW085208	Hs.130093	ESTs	49.40							
117036	H88908	Hs.41192	EST				32.60				
117110	AA160079	Hs.172932	ESTs		8.67						
117209	W03011	Hs.306881	ESTs				30.60				
117325	N23599	Hs.43396	ESTs					9.29			
117454	N29569	Hs.44055	ESTs						3.19		
117475	N30205	Hs.93740	ESTs	44.00							
117543	BE219453	Hs.42722	ESTs		16.00						
117567	AW444761	Hs.44565	ESTs					12.00			
117570	N48649	Hs.44583	ESTs					11.00			
117600	N34963	Hs.44676	EST						3.74		
117730	N45513	Hs.46608	ESTs		6.00						
117791	N48325	Hs.93956	EST		9.00						
117929	N51075	Hs.47191	ESTs				29.20				
117990	AA446167	Hs.47385	ESTs		8.00						
118224	N62275	Hs.48503	EST	31.40							
118244	N62516	Hs.48556	ESTs	32.80							
118357	AL109667	Hs.124154	Homo sapiens mRNA full length insert cDN			2.40					
118446	N66361	Hs.269121	ESTs			2.28					
118447	N66399	Hs.49193	EST	30.80							
118530	N67900	Hs.118446	ESTs						3.10		
118549	N68163	Hs.322954	EST						3.41		
118823	W03754	Hs.50813	ESTs; Weakly similar to long chain fatty			3.94					
118862	W17065	Hs.54522	ESTs						3.58		
118935	AI979247	Hs.247043	KIAA0525 protein				33.00				
118944	AI734233	Hs.226142	ESTs; Weakly similar to !!!! ALU SUBFAMI					11.43			
118995	N94591	Hs.323056	ESTs		14.00						
119073	BE245360	Hs.279477	ERG-2/ERG-1; V-ets avian erythroblastosi				52.60				
119268	T16335	Hs.65325	EST	31.40							
119514	W37937		Accession not listed in Genbank						3.50		
119824	W74536	Hs.184	advanced glycosylation end product-speci			2.75					
119831	AL117664	Hs.58419	DKFZP586L2024 protein								3.21
119861	W78816	Hs.49943	ESTs; Moderately similar to !!!! ALU SUB				33.80				
119889	W84346	Hs.58671	ESTs				30.03				
119921	W86192	Hs.58815	ESTs	29.00							
120082	H80286	Hs.40111	ESTs						3.80		
120094	AA811339	Hs.124049	ESTs		6.00						
120132	W57554	Hs.125019	Human lymphoid nuclear protein (LAF-4)				36.60				
120378	AA223249	Hs.285728	ESTs		12.00						
120404	AB023230	Hs.96427	KIAA1013 protein	39.40							
120504	AA256837		ESTs					8.00			
120512	N55761	Hs.194718	ESTs	33.00							
120667	AA287740	Hs.78335	microtubule-associated protein; RP/EB fa								4.18
120777	AA287702	Hs.10031	KIAA0955 protein				46.60				
121082	AA398722		ESTs				39.00				
121191	AA400205	Hs.104447	ESTs	41.60							
121248	AA400914	Hs.97827	EST							5.08	
121363	AI287280	Hs.97933	ESTs					12.00			
121366	AI743515		ESTs					20.00			
121483	AI660332	Hs.25274	ESTs; Moderately similar to putative sev						3.32		
121518	AA412155		ESTs				30.20				
121545	AA412442	Hs.98132	ESTs			2.29					
121622	AA416931	Hs.126065	ESTs		9.00						
121665	AA416556	Hs.98234	ESTs				34.80				
121709	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	34.80							
121730	AI140683	Hs.98328	ESTs	38.80							
121740	AA421138	Hs.98334	EST		7.00						
121772	AI590770	Hs.110347	Homo sapiens mRNA for alpha integrin bin	36.20							
121821	AL040235	Hs.3346	ESTs								3.61

121835	AB033030	Hs.300670	ESTs			2.34					
121841	AA427794	Hs.104864	ESTs			2.61					
121885	AA934883	Hs.98467	ESTs							2.25	
121888	AA426429	Hs.98463	ESTs							2.92	
121938	AA428659	Hs.98610	ESTs				46.80				
121950	AA429515		EST				31.40				
122030	AA431310	Hs.98724	ESTs	34.40							
122054	AA431725	Hs.98746	EST							3.58	
122211	AA300900	Hs.98849	ESTs; Moderately similar to bithoraxoid-	49.40							
122233	AA436455	Hs.98872	EST	29.80							
122247	AA436676	Hs.98890	EST				39.80				
122253	AA436703	Hs.104936	ESTs; Weakly similar to hypothetical pro		9.00						
122266	AA436840	Hs.98907	EST						3.60		
122285	AA436981	Hs.121602	EST						3.14		
122409	AA446830	Hs.99081	ESTs	30.80							
122485	AA524547	Hs.160318	phospholemman			2.65					
122697	AA420683	Hs.98321	Homo sapiens cDNA FLJ14103 fis, clone MA		15.00						
122772	AW117452	Hs.99489	ESTs		6.67						
122831	AI857570	Hs.5120	ESTs						3.37		
122913	AI638774	Hs.105328	ESTs				32.20				
123049	BE047680	Hs.211869	ESTs				41.80				
123076	AI345569	Hs.190046	ESTs	35.80							
123136	AW451999	Hs.194024	ESTs							2.58	
123309	N52937	Hs.102679	ESTs					19.00			
123455	AA353113	Hs.112497	ESTs				82.80				
123691	AA609579	Hs.112724	ESTs						3.95		
123756	AA609971	Hs.112795	EST	35.40							
123802	AA620448		Homo sapiens clone 24760 mRNA sequence	58.00							
123837	AI807243	Hs.112893	ESTs				32.40				
123844	AA938905	Hs.120017	olfactory receptor; family 7; subfamily			2.63					
123936	NM_004673	Hs.241519	ESTs	29.00							
123987	C21171	Hs.95497	ESTs; Weakly similar to GLUCOSE TRANSPOR				70.60				
124013	AI521936	Hs.107149	ESTs; Weakly similar to PTB-ASSOCIATED S	28.40							
124160	R40290	Hs.124685	ESTs					13.00			
124205	H77570	Hs.108135	ESTs						4.74		
124226	AA618527	Hs.190266	ESTs			2.35					
124246	H67680	Hs.270962	ESTs				29.40				
124348	AI796320	Hs.10299	ESTs		17.00						
124358	AW070211	Hs.102415	"yw35g11.s1 Morton Fetal Cochlea Homo sa			3.07					
124409	AI814166	Hs.107197	ESTs						3.14		
124442	AW663632	Hs.285625	TATA box binding protein (TBP)-associate			2.48					
124468	N51413	Hs.109284	ESTs				30.80				
124479	AB011130	Hs.127436	calcium channel; voltage-dependent; alph								6.03
124519	AI670056	Hs.137274	ESTs; Weakly similar to SPLICEOSOME ASSO			2.50					
124711	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	59.20							
124866	AI768289	Hs.304389	ESTs		8.00						
124874	BE550182	Hs.127826	ESTs				37.60				
125097	AW576389	Hs.335774	ESTs					10.00			
125179	AW206468	Hs.103118	ESTs						3.12		
125200	AW836591	Hs.103156	ESTs							2.79	
125299	T32982	Hs.102720	ESTs				34.20				
125400	AL110151	Hs.128797	DKFZP586D0824 protein	29.00							
125810	H00083		aryl hydrocarbon receptor-interacting pr	32.20							
126176	BE242256	Hs.2441	KIAA0022 gene product		12.00						
126303	D78841		HUM525A05B Human placenta polyA+ (TFuji				33.60				
126403	AW629054	Hs.125976	ESTs; Weakly similar to metalloprotease/	35.80							
126507	AL040137	Hs.23964	ESTs; Weakly similar to HC1 ORF [M.muscu				29.80				
126773	AA648284	Hs.187584	ESTs	39.60							
127307	AW962712	Hs.126712	ESTs; Weakly similar to pIL2 hypothetica	28.80							
127462	AA760776	Hs.293977	aa59b04.s1 NCI_CGAP_GCB1 Homo sapiens c				34.40				
127486	AW002846	Hs.105468	ESTs		9.00						
127572	AA594027	Hs.191788	ESTs			2.36					
127609	X80031	Hs.530	ESTs				29.40				
127832	AW976035	Hs.292396	ESTs				37.20				
127898	AA774725	Hs.128970	ESTs							4.42	
128073	AW340720	Hs.125983	ESTs				38.40				
128101	AA905730	Hs.128254	ESTs		7.33						
128149	NM_012214	Hs.177576	mannosyl (alpha-1;3-)-glycoprotein beta-							2.58	
128212	W27411	Hs.336920	glutathione peroxidase 3 (plasma)			3.09					
128333	W68800	Hs.12126	ESTs; Weakly similar to LR8 [H.sapiens]				34.40				
128364	N76462	Hs.269152	ESTs; Weakly similar to ZINC FINGER PROT		10.00						
128426	AI265784	Hs.145197	ESTs							4.31	
128598	AA305407	Hs.102308	potassium inwardly-rectifying channel; s	31.20							
128634	AA464918		ESTs; Moderately similar to !!!! ALU SUB				41.60				
128687	AW271273	Hs.23767	ESTs				87.00				
128726	AI311238	Hs.104476	ESTs								4.02
128773	NM_004131	Hs.1051	granzyme B (granzyme 2; cytotoxic T-lymp					9.00			
128833	W26667	Hs.184581	ESTs								3.76
128870	H39537	Hs.75309	eukaryotic translation elongation factor			2.66					
128878	R25513	Hs.10683	ESTs						3.10		
128885	AF134803	Hs.180141	cofilin 2 (muscle)					11.00			
128998	W04245	Hs.107761	ESTs; Weakly similar to PUTATIVE RHO/RAC							3.21	
129000	AA744902	Hs.107767	ESTs; Moderately similar to CaM-KII inhi								3.68
129038	AW156903	Hs.108124	ribosomal protein L41						3.17		
129098	AW580945	Hs.330466	ESTs	34.60							

129210	AL039940	Hs.202949	KIAA1102 protein								4.09
129240	AA361258	Hs.237868	interleukin 7 receptor			2.29					
129262	BE222198	Hs.109843	ESTs						3.30		
129301	AF182277	Hs.330780	Human cytochrome P450-IIB (hIIB3) mRNA;								4.05
129331	AW167668	Hs.279772	ESTs; Highly similar to CGI-38 protein [								4.09
129381	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted			2.93					
129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1				160.80				
129595	U09550	Hs.1154	oviductal glycoprotein 1; 120kD					10.00			
129613	AW978517	Hs.172847	ESTs; Weakly similar to collagen alpha 1						3.40		
129782	AW016932	Hs.104105	EST		9.00						
129950	F07783	Hs.1369	decay accelerating factor for complement				87.80				
129958	R27496	Hs.1378	annexin A3				44.60				
129959	AL036554	Hs.274463	defensin; alpha 1; myeloid-related seque			2.72					
130160	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1;3-galactosyltr				42.20				
130259	NM_000328	Hs.153614	retinitis pigmentosa GTPase regulator			2.54					
130273	AW972422	Hs.153863	MAD (mothers against decapentaplegic; Dr				51.60				
130312	AF056195	Hs.15430	DKFZP586G1219 protein						3.16		
130436	NM_001928	Hs.155597	D component of complement (adipsin)								4.11
130523	AA999702	Hs.214507	ESTs						4.77		
130799	AB028945	Hs.12696	ESTs		6.00						
130885	NM_005883	Hs.20912	adenomatous polyposis coli like						3.54		
131002	AL050295	Hs.22039	KIAA0758 protein								3.50
131012	AL039940	Hs.202949	KIAA1102 protein		20.00						
131031	NM_001650	Hs.288650	aquaporin 4	41.20							
131061	N64328	Hs.268744	ESTs; Moderately similar to KIAA0273 [H.				31.40				
131066	AW169287	Hs.22588	ESTs				29.60				
131082	AI091121	Hs.246218	ESTs; Weakly similar to zinc finger prot					9.00			
131087	AF147709	Hs.22824	ESTs; Weakly similar to p160 myb-binding								3.86
131161	AF033382	Hs.23735	potassium voltage-gated channel; subfami						3.14		
131179	AA171388	Hs.184482	DKFZP586D0624 protein						3.80		
131182	AI824144	Hs.23912	ESTs								3.67
131205	NM_003102	Hs.2420	superoxide dismutase 3; extracellular			2.98					
131277	AA131466	Hs.23767	ESTs			3.15					
131281	AA251716	Hs.25227	ESTs				32.20				
131282	X03350	Hs.4	alcohol dehydrogenase 3 (class I); gamma								3.44
131285	AI567943	Hs.25274	ESTs; Moderately similar to putative sev						6.40		
131355	R52804	Hs.25956	DKFZP564D206 protein		8.00						
131391	AW085781	Hs.26270	ESTs		10.00						
131461	AA992841	Hs.27263	butyrate response factor 2 (EGF-response	28.80							
131487	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f							4.03	
131517	AB037789	Hs.263395	ESTs; Highly similar to semaphorin VIa [	39.00							
131545	AL137432	Hs.28564	ESTs					11.00			
131583	AK000383	Hs.323092	ESTs; Weakly similar to dual specificity					10.00			
131647	AA359615	Hs.30089	ESTs			2.47					
131675	H15205	Hs.30509	ESTs						3.06		
131676	AI126821	Hs.30514	ESTs	45.80							
131708	S60415	Hs.30941	calcium channel; voltage-dependent; beta			2.28					
131717	X94630	Hs.3107	CD97 antigen								3.78
131756	AA443966	Hs.31595	ESTs				40.60				
131762	AA744902	Hs.107767	ESTs; Moderately similar to CaM-KII inhi								3.67
131821	AA017247	Hs.164577	ESTs			2.87					
131839	AB014533	Hs.33010	KIAA0633 protein							3.48	
131861	AL096858	Hs.184245	KIAA0929 protein Msx2 interacting nuclea	54.00							
132015	AI418006	Hs.3731	ESTs				49.20				
132070	BE622641	Hs.38489	ESTs				34.80				
132242	AA332697	Hs.42721	ESTs			2.68					
132334	AW080704	Hs.45033	lacrimal proline rich protein			4.66					
132476	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	34.20							
132490	NM_001290	Hs.4980	LIM binding domain 2			2.66					
132533	AI922988	Hs.172510	ESTs		13.00						
132598	X80031	Hs.530	collagen; type IV; alpha 3 (Goodpasture				30.60				
132619	H28855	Hs.53447	ESTs; Moderately similar to kinesin ligh						4.02		
132652	N41739	Hs.61260	ESTs						3.18		
132726	N52298	Hs.55608	ESTs; Weakly similar to cDNA EST yk484g1					11.43			
133028	R51604	Hs.300842	ESTs			2.37					
133071	BE384932	Hs.64313	ESTs			2.27					
133120	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein			2.63					
133129	AA428580	Hs.65551	ESTs								5.49
133147	AA026533	Hs.66	interleukin 1 receptor-like 1			6.20					
133151	NM_014051	Hs.94896	ESTs						3.69		
133213	AA903424	Hs.6786	ESTs				31.40				
133276	AW978439	Hs.69504	ESTs					9.00			
133377	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene famil	41.20							
133407	AF017987	Hs.7306	secreted frizzled-related protein 1	50.20							
133535	AL134030	Hs.284180	protocadherin 2 (cadherin-like 2)						3.72		
133537	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr								3.35
133656	BE149455	Hs.75415	Accession not listed in Genbank			2.65					
133689	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)				90.80				
133779	T58486	Hs.222566	ESTs						3.05		
133978	AF035718	Hs.78061	transcription factor 21			2.92					
133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec								3.45
134000	AW175787	Hs.334841	selenium binding protein 1								4.05
134111	AI372588	Hs.8022	TU3A protein			4.49					
134185	AA285136	Hs.301914	Homo sapiens mRNA; cDNA DKFZp586K1220 (f							3.27	
134204	AI873257	Hs.7994	ESTs; Weakly similar to CGI-69 protein [				40.80				

134641	AI092634	Hs.156114	protein tyrosine phosphatase; non-recept					3.76		
134677	AA251363	Hs.177711	ESTs				32.20			
134745	NM_000685	Hs.89472	angiotensin receptor 1B		15.00					
134749	T28499	Hs.89485	carbonic anhydrase IV			3.05				
134786	T29618	Hs.89640	angiopoietin 1 receptor; TEK tyrosine ki				57.80			
134825	U33749	Hs.197764	thyroid transcription factor 1							3.73
134978	AI829008	Hs.333383	ficolin (collagen/fibrinogen domain-cont			2.52				
135010	N50465	Hs.92927	ESTs				31.60			
135053	AW796190	Hs.93678	ESTs					3.21		
135081	AF069517	Hs.173993	RNA binding motif protein 6	28.80						
135091	AA493650	Hs.94367	ESTs							4.24
135135	AA775910	Hs.95011	syntrophin; beta 1 (dystrophin-associate		8.00					
135203	C15737	Hs.269386	ESTs					4.31		
135236	AI636208	Hs.96901	ESTs	43.00						
135266	R41179	Hs.97393	Human mRNA for KIAA0328 gene; partial cd						6.42	
135346	NM_000928	Hs.992	phospholipase A2; group IB (pancreas)			3.82				
135378	AW961818	Hs.24379	potassium voltage-gated channel; shaker-			4.15				
135387	NM_001972	Hs.99863	elastase 2; neutrophil	37.20						
135388	W27965	Hs.99865	EST	38.80						
135402	L12398	Hs.99922	dopamine receptor D4					4.21		

TABLE 2B shows the accession numbers for those primekeys lacking unigeneID's for Table 2A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
108447	43452_-7	AA079126
108550	120073_1	AA084867 AA084996
108655	127522_1	AA099960 AA113013
102397	44371_-1	U41898
126303	1525933_1	D78841 D78880
125810	1554054_1	H00083 R81062
103627	2615_2	Z48513 Z48512
121366	280401_1	AI743515 AA405617 AW276706
114609	116777_1	AA079505 AA079537
115272	172113_1	AW015947 AA211890 AA279425
108338	112186_1	AA070773 AA070774
108434	114012_1	AA078899 AA078782 AA075788
123802	genbank_AA620448	AA620448
102310	NOT_FOUND_entrez_U33839	U33839
102636	entrez_U67092	U67092
104776	genbank_AA026349	AA026349
120504	genbank_AA256837	AA256837
113502	genbank_T89130	T89130
108499	genbank_AA083103	AA083103
101308	entrez_L41390	L41390
108629	genbank_AA102425	AA102425
103098	221_215	M86361 Z26593 X02850 D13070 AE000659 M17649 M87869 M87871 X61077 M16286 AF018169 X61079 S59351 X60142 AF043169
103241	entrez_X76223	X76223
103508	entrez_Y10141	Y10141
103575	entrez_Z26256	Z26256
119514	NOT_FOUND_entrez_W37937	W37937
121082	genbank_AA398722	AA398722
128634	AA464918_at	AA464918
105817	genbank_AA397825	AA397825
121518	genbank_AA412155	AA412155
114449	genbank_AA020736	AA020736
114648	genbank_AA101056	AA101056
121950	genbank_AA429515	AA429515
107723	genbank_AA015967	AA015967

Table 3A shows 452 genes up-regulated in chronically diseased lung relative to normal lung. Chronically diseased lung samples represent chronic non-malignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
ExAccn: Examplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: 80th percentile of AI for chronically diseased lung samples divided by the 90th percentile of AI for normal lung samples.
R2: 80th percentile of AI for chronically diseased lung samples divided by the 90th percentile of normal lung samples, squamous cell carcinomas and adenocarcinomas
R3: 70th percentile of AI for chronically diseased lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of normal lung samples, squamous cell carcinomas and adenocarcinomas minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2	R3
135423	U50531	Hs.138751	Human BRCA2 region, mRNA sequence CG030	12.40		
135378	AW961818	Hs.24379	MUM2 protein			2.13
135346	NM_000928	Hs.992	phospholipase A2, group IB (pancreas)			
135235	AW298244	Hs.293507	ESTs	12.40		
135057	U90268	Hs.93810	cerebral cavernous malformations 1	11.67		
134951	BE305081	Hs.169358	hypothetical protein		8.00	
134799	M36821	Hs.89690	GRO3 oncogene		8.20	
134786	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous			
134772	NM_000829	Hs.163697	glutamate receptor, ionotrophic, AMPA 4	29.80		
134752	BE246762	Hs.89499	arachidonate 5-lipoxygenase			1.93
134749	T28499	Hs.89485	carbonic anhydrase IV			2.07
134696	BE326276	Hs.8861	ESTs			
134636	NM_005582	Hs.87205	lymphocyte antigen 64 (mouse) homolog, r	13.60		
134627	AI018768	Hs.12482	glyceronephosphate O-acyltransferase			1.92
134622	AW975159	Hs.293097	ESTs, Weakly similar to A55380 faciogeni			1.92
134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	13.20		
134561	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h			1.78
134468	NM_001772	Hs.83731	CD33 antigen (gp67)		6.20	
134417	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci			
134343	D50683	Hs.82028	transforming growth factor, beta recepto			
134323	BE170651	Hs.8700	deleted in liver cancer 1			
134300	NM_001430	Hs.8136	endothelial PAS domain protein 1			
134299	AW580939	Hs.97199	complement component C1q receptor			
134253	X52075	Hs.80738	sialophorin (gpL115, leukosialin, CD43)	20.60		
134182	D52059	Hs.7972	KIAA0871 protein	12.20		
133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec			
133978	AF035718	Hs.78061	transcription factor 21			
133835	AI677897	Hs.76640	RGC32 protein			
133651	AI301740	Hs.173381	dihydropyrimidinase-like 2			
133633	D21262	Hs.75337	nucleolar and coiled-body phosphprotein	15.20		
133565	AW955776	Hs.313500	ESTs, Moderately similar to ALU7_HUMAN A			
133548	AW946384	Hs.178112	DNA segment, single copy probe LNS-CAI/L			1.77
133488	AA335295	Hs.74120	adipose specific 2			
133478	X83703	Hs.31432	cardiac ankyrin repeat protein			2.08
133337	AF085983	Hs.293676	ESTs		9.60	
133200	AB037715	Hs.183639	hypothetical protein FLJ10210			1.77
133153	AF070592	Hs.66170	HSKM-B protein	30.60		
133130	AI128606	Hs.6557	zinc finger protein 161	22.60		
133120	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein			
132928	AW168082	Hs.169449	protein kinase C, alpha	13.80		
132836	AB023177	Hs.29900	KIAA0960 protein			
132799	W73311	Hs.169407	SAC2 (suppressor of actin mutations 2,	41.60		
132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	40.40		
132548	X12830	Hs.193400	interleukin 6 receptor		7.20	
132476	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi		4.76	
132439	AK001942	Hs.4863	hypothetical protein DKFZp566A1524			1.88
132240	AB018324	Hs.42676	KIAA0781 protein	21.20		
132210	NM_007203	Hs.42322	A kinase (PRKA) anchor protein 2			1.99
132199	AL041299	Hs.165084	ESTs	15.20		
131751	T96555	Hs.31562	ESTs			1.76
131745	AI828559	Hs.31447	ESTs, Moderately similar to A46010 X-li	27.80		
131694	NM_000246	Hs.3076	MHC class II transactivator		4.00	
131686	NM_012296	Hs.30687	GRB2-associated binding protein 2			
131676	AI126821	Hs.30514	ESTs		6.20	
131629	Z45794	Hs.236809	ESTs	21.40		
131589	C18825	Hs.29191	epithelial membrane protein 2			
131536	AA019201	Hs.269210	ESTs		9.40	
131517	AB037789	Hs.263395	sema domain, transmembrane domain (TM),		3.59	
131355	R52804	Hs.25956	DKFZP564D206 protein		4.48	
131253	R71802	Hs.24853	ESTs	15.00		
131207	AF104266	Hs.24212	latrophilin			1.75
131156	AI472209	Hs.323117	ESTs			1.84
131066	AW169287	Hs.22588	ESTs		3.54	
131061	N64328	Hs.268744	KIAA1796 protein			
131053	AA348541	Hs.296261	guanine nucleotide binding protein (G pr			1.93
130895	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	16.60		
130762	D84371	Hs.1898	paraoxonase 1	12.00		

130657	AW337575	Hs.201591	ESTs			
130655	AI831962	Hs.17409	cysteine-rich protein 1 (intestinal)			
130589	AL110226	Hs.16441	DKFZP434H204 protein			2.08
130562	D50402	Hs.182611	solute carrier family 11 (proton-coupled			1.91
130555	R69743	Hs.116774	integrin, alpha 1		9.60	
130365	W56119	Hs.155103	eukaryotic translation initiation factor	11.60		
130273	AW972422	Hs.153863	MAD (mothers against decapentaplegic, Dr		6.60	
130259	NM_000328	Hs.153614	retinitis pigmentosa GTPase regulator			1.91
130090	H97878	Hs.132390	zinc finger protein 36 (KOX 18)	21.20		
129958	R27496	Hs.1378	annexin A3		5.05	
129898	AI672731	Hs.13256	ESTs			
129875	AA181018	Hs.13056	hypothetical protein FLJ13920	18.60		
129699	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas			
129626	F13272	Hs.111334	ferritin, light polypeptide			
129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	22.63		
129593	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f			
129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1			2.53
129527	AA769221	Hs.270847	delta-tubulin	39.20		
129402	W72062	Hs.11112	ESTs			2.11
129385	AA172106	Hs.110950	Rag C protein	15.20		
129315	NM_014563	Hs.174038	spondyloepiphyseal dysplasia, late	12.40		
129312	T97579	Hs.110334	ESTs, Weakly similar to I78885 serine/th	20.83		
129240	AA361258	Hs.237868	interleukin 7 receptor			1.95
129210	AL039940	Hs.202949	KIAA1102 protein			
129122	AW958473	Hs.301957	nudix (nucleoside diphosphate linked moi		4.20	
129057	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)			
128946	Y13153	Hs.107318	kynurenine 3-monooxygenase (kynurenine 3		5.20	
128798	AF015525	Hs.302043	chemokine (C-C motif) receptor-like 2			
128789	AW368576	Hs.139851	caveolin 2			2.24
128778	AA504776	Hs.186709	ESTs, Weakly similar to I38022 hypothet	12.20		
128766	AW160432	Hs.296460	craniofacial development protein 1	26.40		
128631	R44238	Hs.155546	KIAA1080 protein; Golgi-associated, gamm			1.78
128624	BE154765	Hs.102647	ESTs, Weakly similar to TRHY_HUMAN TRICH			2.51
128609	NM_003616	Hs.102456	survival of motor neuron protein interac	16.00		
128603	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	12.80		
128598	AA305407	Hs.102308	potassium inwardly-rectifying channel, s		4.00	
128458	H55864	Hs.56340	ESTs			
128061	AF150882	Hs.186877	sodium channel, voltage-gated, type XII,	17.20		
127968	AA830201	Hs.124347	ESTs	21.30		
127959	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L			
127944	AI557081	Hs.262476	S-adenosylmethionine decarboxylase 1	10.60		
127925	AA805151	Hs.3628	mitogen-activated protein kinase kinase	13.40		
127896	AI669586	Hs.222194	ESTs		7.00	
127859	AA761802	Hs.291559	ESTs	14.00		
127817	AA836641	Hs.163085	ESTs	14.00		
127742	AW293496	Hs.180138	ESTs	11.00		
127628	AI240102	Hs.322430	NDRG family, member 4	11.10		
127609	X80031	Hs.530	collagen, type IV, alpha 3 (Goodpasture			
127582	AA908954	Hs.130844	ESTs	19.60		
127543	AK000787	Hs.157392	Homo sapiens cDNA FLJ20780 fis, clone CO	15.40		
127535	AA568424	Hs.164450	ESTs	17.50		
127404	AI379920	Hs.270224	ESTs	14.60		
127396	L31968	Hs.187991	DKFZP564A122 protein	15.40		
127374	AA442797	Hs.312110	ESTs, Weakly similar to I38022 hypothet	14.60		
127346	AA203616	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe	21.00		
127340	BE047653	Hs.119183	ESTs, Weakly similar to ZN91_HUMAN ZINC	15.80		
127307	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5			
127242	AW390395	Hs.181301	cathepsin S	22.60		
127167	AA625690	Hs.190272	ESTs	21.40		
127046	AA321948	Hs.293968	ESTs	41.20		
126928	AA480902	Hs.137401	ESTs	11.00		
126900	AF137386	Hs.12701	plasmolipin			1.78
126852	AA399961		gb:zu68c01.r1 Soares_testis_NHT Homo sap		5.60	
126816	AA248234		gb:csg2228.seq.F Human fetal heart, Lamb	12.20		
126812	AB037860	Hs.173933	nuclear factor I/A	17.19		
126666	AA648886	Hs.151999	ESTs	13.57		
126645	AA316181	Hs.61635	six transmembrane epithelial antigen of	15.40		
126592	AI611153	Hs.6093	Homo sapiens cDNA: FLJ22783 fis, clone K		4.67	
126556	AF255303	Hs.112227	membrane-associated nucleic acid binding	18.00		
126433	AA325606		gb:EST28707 Cerebellum II Homo sapiens c	16.77		
126299	AW979155	Hs.298275	amino acid transporter 2	14.60		
126218	AL049801	Hs.13649	Novel human gene mapping to chomosome 13		3.50	
126182	AA721331	Hs.293771	ESTs	13.40		
126177	AW752782	Hs.129750	hypothetical protein FLJ10546	18.20		
126142	H86261	Hs.40568	ESTs	14.00		
126077	M78772	Hs.210836	ESTs	16.59		
125994	AI990529	Hs.270799	ESTs	17.40		
125934	AA193325	Hs.32646	hypothetical protein FLJ21901	13.00		
125847	AW161885	Hs.249034	ESTs	49.57		
125831	H04043		gb:yj45c03.r1 Soares placenta Nb2HP Homo			
125731	R61771	Hs.26912	ESTs	13.20		
125676	BE612918	Hs.151973	hypothetical protein FLJ23511	11.20		
125561	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S			
125552	H09701	Hs.278366	ESTs, Weakly similar to I38022 hypotheti	12.60		
125489	H49193	Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A	33.40		

125422	AA903229	Hs.153717	ESTs			1.80
125331	AI422996	Hs.161378	ESTs	38.00		
125309	T12411	Hs.183745	hypothetical protein FLJ13456	18.20		
125167	AL137540	Hs.102541	netrin 4			1.95
125139	AW194933	Hs.9788	hypothetical protein MGC10924 similar to			1.84
125042	T78906	Hs.269432	ESTs, Moderately similar to ALU1_HUMAN	21.80		
124711	NM_004657	Hs.26530	serum deprivation response (phosphatidyl		10.60	
124631	NM_014053	Hs.270594	FLVCR protein	23.20		
124578	N68321	Hs.231500	EST	21.43		
124574	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2			1.77
124472	N52517	Hs.102670	EST	37.20		
124438	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A			
124357	N22401		gb:yw37g07.s1 Morton Fetal Cochlea Homo	14.64		
124306	AW973078	Hs.293039	ESTs		4.00	
124214	H58608	Hs.151323	ESTs			
124097	AW298235	Hs.101689	ESTs		27.20	
123978	T89832	Hs.170278	ESTs			2.03
123972	T46848	Hs.70337	immunoglobulin superfamily, member 4		6.00	
123961	AL050184	Hs.21610	DKFZP434B203 protein			1.79
123936	NM_004673	Hs.241519	angiopoietin-like 1		15.80	
123802	AA620448		gb:ae58c09.s1 Stratagene lung carcinoma		4.23	
123734	AA609861	Hs.312447	ESTs		4.20	
123619	AA602964		gb:no97c02.s1 NCI_CGAP_Pr2 Homo sapiens	33.60		
123596	AA421130	Hs.112640	EST	10.93		
123476	AA384564	Hs.108829	ESTs			2.18
123340	AA504264	Hs.182937	peptidylprolyl isomerase A (cyclophilin	11.20		
123190	AA489212	Hs.105228	EST	14.20		
123136	AW451999	Hs.194024	ESTs		7.00	
123073	AA485061	Hs.105652	ESTs	31.20		
123055	AA482005	Hs.105102	ESTs, Weakly similar to reverse transcri		4.80	
122699	AA456130	Hs.301721	KIAA1255 protein		5.00	
122679	AA811286	Hs.192837	ESTs, Weakly similar to ALU5_HUMAN ALU S	14.40		
122633	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg			
122553	AA451884	Hs.190121	ESTs	40.00		
122544	AW973253	Hs.292689	ESTs	15.40		
122485	AA524547	Hs.160318	FXYD domain-containing ion transport reg			1.81
122211	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H		12.10	
122127	AW207175	Hs.106771	ESTs			1.95
122011	AA431082		gb:zw78a10.s1 Soares_testis_NHT Homo sap			1.89
121992	AI860775	Hs.98506	ESTs		3.60	
121989	W56487	Hs.193784	Homo sapiens mRNA; cDNA DKFZp586K1922 (f			2.01
121835	AB033030	Hs.300670	KIAA1204 protein			1.85
121726	AF241254	Hs.178098	angiotensin I converting enzyme (peptidy	12.43		
121690	AV660305	Hs.110286	ESTs			1.82
121643	AA640987	Hs.193767	ESTs			
121633	AA417011	Hs.98175	EST	14.00		
121622	AA416931	Hs.126065	ESTs		16.40	
121497	AA412031	Hs.97901	EST	11.20		
121351	AW206227	Hs.287727	hypothetical protein FLJ23132	12.20		
121314	W07343	Hs.182538	phospholipid scramblase 4			1.83
121242	AA400857	Hs.97509	ESTs	22.40		
121059	AA393283		gb:zt74e03.r1 Soares_testis_NHT Homo sap	14.80		
120934	AA226198		gb:nc26a07.s1 NCI_CGAP_Pr1 Homo sapiens	21.20		
120755	AA312934	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone			1.79
120637	AA811804		gb:ob39a05.s1 NCI_CGAP_GCB1 Homo sapiens	20.00		
120484	AA253170	Hs.96473	EST	40.20		
120336	N85785	Hs.181165	eukaryotic translation elongation factor		6.60	
120266	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	16.80		
120132	W57554	Hs.125019	ESTs		4.73	
120041	AA830882	Hs.59368	ESTs			1.75
119996	W88996	Hs.59134	EST		7.20	
119970	AA767718	Hs.93581	hypothetical protein FLJ10512	11.20		
119861	W78816	Hs.49943	ESTs, Weakly similar to S65657 alpha-1C-		3.78	
119824	W74536	Hs.184	advanced glycosylation end product-speci			
119740	AW021407	Hs.21068	hypothetical protein	20.20		
119271	AI061118	Hs.65328	Fanconi anemia, complementation group F	15.20		
119221	C14322	Hs.250700	tryptase beta 1			
119126	R45175	Hs.117183	ESTs	12.60		
119073	BE245360	Hs.279477	ESTs			
118928	AA312799	Hs.283689	activator of CREM in testis		10.00	
118901	AW292577	Hs.94445	ESTs		3.96	
118661	AL137554	Hs.49927	protein kinase NYD-SP15		9.60	
118607	AI377444	Hs.54245	ESTs, Weakly similar to S65824 reverse t	10.40		
118449	AI813865	Hs.164478	hypothetical protein FLJ21939 similar to			1.90
118416	N66028	Hs.49105	FKBP-associated protein	16.20		
118379	N64491	Hs.48990	ESTs		4.00	
118329	N63520		gb:yy62f01.s1 Soares_multiple_sclerosis_		6.60	
118320	N63451	Hs.141600	ESTs, Weakly similar to alternatively s		3.80	
118253	AA497044	Hs.20887	hypothetical protein FLJ10392	17.60		
118124	N56968	Hs.46707	chromosome 21 open reading frame 37	14.00		
118056	AB037746	Hs.42768	hypothetical protein DKFZp761O0113			1.86
118032	N52802	Hs.47544	EST		5.00	
117840	T26379	Hs.48802	Homo sapiens clone 23632 mRNA sequence		4.00	
117404	N39725	Hs.15220	zinc finger protein 106			1.90
117314	N32498	Hs.42829	ESTs	14.20		

117209	W03011	Hs.306881	MSTP043 protein			
117023	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f			2.31
116814	H50834		gb:yp86a10.s1 Soares fetal liver spleen	20.20		
116784	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific		3.51	
116766	AI608657	Hs.95097	ESTs	16.20		
116712	AW901618	Hs.61935	Homo sapiens mRNA; cDNA DKFZp761I071 (fr		6.80	
116707	H10344	Hs.49050	ESTs, Weakly similar to A Chain A, Human	18.60		
116351	AL133623	Hs.82501	similar to mouse Xm1 / Dhm2 protein	19.40		
116279	AW971248	Hs.291289	ESTs, Weakly similar to ALU1_HUMAN ALU S			
116166	AL039940	Hs.202949	KIAA1102 protein			2.13
116152	AL040521	Hs.15220	zinc finger protein 106			1.75
116117	BE613410	Hs.31575	SEC63, endoplasmic reticulum translocon	13.20		
116107	AL133916	Hs.172572	hypothetical protein FLJ20093	30.11		
115965	AA001732	Hs.173233	hypothetical protein FLJ10970			2.36
115955	AF263613	Hs.44198	intracellular membrane-associated calciu	18.20		
115844	AI373062	Hs.332938	hypothetical protein MGC5370	18.57		
115683	AF255910	Hs.54650	junctional adhesion molecule 2		23.00	
115673	AA406341	Hs.269908	Homo sapiens cDNA FLJ11991 fis, clone HE	11.82		
115672	AI889110	Hs.73251	ESTs	10.60		
115566	AI142336	Hs.43977	Human DNA sequence from clone RP11-196N1			1.76
115313	AA808001	Hs.184411	albumin	25.20		
115279	AW964897	Hs.290825	ESTs		8.00	
115230	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L			1.80
115110	AK001671	Hs.11387	KIAA1453 protein	14.20		
114999	BE246481	Hs.87856	ESTs	19.20		
114930	AA237022	Hs.188717	ESTs		5.60	
114922	AA235672	Hs.87491	ESTs		3.60	
114837	BE244930	Hs.166895	ESTs	43.70		
114769	AA149060	Hs.296100	ESTs	11.00		
114761	AA143781	Hs.126280	hypothetical protein FLJ23393	14.00		
114736	AI610347	Hs.103812	ESTs, Moderately similar to ALU1_HUMAN A		4.20	
114596	AA310162	Hs.169248	cytochrome c	10.71		
114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	20.40		
114455	H37908	Hs.271616	ESTs, Weakly similar to ALU8_HUMAN ALU S	20.40		
114452	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE		17.20	
114359	NM_016929	Hs.283021	chloride intracellular channel 5			2.09
114357	R41677	Hs.6107	Homo sapiens cDNA FLJ14839 fis, clone OV	12.40		
114251	H15261	Hs.21948	ESTs			2.00
114138	AW384793	Hs.15740	Homo sapiens mRNA; cDNA DKFZp434E033 (fr		11.40	
114124	W57554	Hs.125019	ESTs		6.04	
113946	AW083883	Hs.37896	Homo sapiens cDNA FLJ13510 fis, clone PL			1.82
113695	T96965	Hs.17948	ESTs, Weakly similar to ALUB_HUMAN !!!!			
113606	NM_013343	Hs.278951	NAG-7 protein			2.15
113590	R49642	Hs.142447	ESTs, Weakly similar to ALU1_HUMAN ALU S		3.60	
113560	T91015	Hs.268626	ESTs	32.00		
113552	AI654223	Hs.16026	hypothetical protein FLJ23191			
113540	AW152618	Hs.16757	ESTs			
113502	T89130		gb:ye12d01.s1 Stratagene lung (937210) H		8.35	
113288	AI076838	Hs.12967	ESTs	12.40		
113252	NM_004469	Hs.11392	c-fos induced growth factor (vascular en		4.27	
113238	R45467	Hs.189813	ESTs			
113203	AA743563	Hs.10305	ESTs	21.20		
113195	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom			1.92
113089	T40707	Hs.270862	ESTs	14.33		
113076	AF033199	Hs.8198	zinc finger protein 204		6.00	
113009	T23699	Hs.7246	ESTs		9.40	
112937	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti		12.20	
112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-li	10.57		
112794	R97018		gb:yq74b08.s1 Soares fetal liver spleen	26.60		
112691	R88708	Hs.220647	ESTs	15.33		
112602	AW004045	Hs.203365	ESTs	15.60		
112366	AF035318	Hs.12533	Homo sapiens clone 23705 mRNA sequence	15.40		
112210	R49645	Hs.7004	ESTs	14.00		
112064	AL049390	Hs.22689	Homo sapiens mRNA; cDNA DKFZp586O1318 (f	13.00		
111998	R42379	Hs.138283	ESTs	11.00		
111987	NM_015310	Hs.6763	KIAA0942 protein	22.40		
111803	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A			1.77
111737	H04607	Hs.9218	ESTs			1.86
111605	T91061	Hs.194178	ESTs, Moderately similar to PC4259 ferri	23.00		
111510	R07856	Hs.16355	ESTs	11.02		
111341	AL157484	Hs.22483	Homo sapiens mRNA; cDNA DKFZp762M127 (fr			1.88
111280	AA373527	Hs.19385	CGI-58 protein	18.40		
111247	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f			
111232	AI247763	Hs.16928	ESTs	27.60		
110942	R63503	Hs.28419	ESTs	14.80		
110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	24.71		
110837	H03109	Hs.108920	HT018 protein			2.18
110824	AI767183	Hs.26942	ESTs	12.20		
110776	AB032417	Hs.19545	frizzled (Drosophila) homolog 4			1.75
110576	H60869	Hs.37889	ESTs	13.00		
110369	AK000768	Hs.107872	hypothetical protein FLJ20761		5.60	
110099	R44557	Hs.23748	ESTs			2.31
109984	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL			
109958	AA001266	Hs.133521	ESTs	11.25		
109893	AA884208	Hs.30484	ESTs			2.68

109842	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	23.83		
109837	H00656	Hs.29792	ESTs, Weakly similar to I38022 hypotheti			3.91
109796	AI800515	Hs.12024	ESTs		17.20	
109688	R41900	Hs.22245	ESTs		9.60	
109648	H17800	Hs.7154	ESTs	22.80		
109613	H47315	Hs.27519	ESTs			
109550	AW021488	Hs.26981	ESTs			
109523	AW193342	Hs.24144	ESTs			1.89
109472	AK001989	Hs.91165	hypothetical protein		6.00	
109355	AA524525	Hs.48297	DKFZP586C1620 protein	15.00		
109260	AW978515	Hs.131915	KIAA0863 protein	25.60		
108781	AA128654		gb:zn98g07.s1 Stratagene fetal retina 93	14.20		
108663	BE219231	Hs.292653	ESTs, Weakly similar to T26845 hypotheti	11.00		
108573	AA086005		gb:zl84c04.s1 Stratagene colon (937204)	26.00		
108480	AL133092	Hs.68055	hypothetical protein DKFZp434I0428			
108382	NM_006770	Hs.67726	macrophage receptor with collagenous str			1.83
108174	AA055632	Hs.303070	ESTs	15.20		
108138	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr		3.60	
108087	AA045708	Hs.40545	ESTs	15.44		
108048	AI797341	Hs.165195	Homo sapiens cDNA FLJ14237 fis, clone NT		11.40	
108041	AW204712	Hs.61957	ESTs			
107997	AL049176	Hs.82223	chordin-like		4.76	
107994	AA036811	Hs.48469	LIM domains containing 1			
107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	14.20		
107681	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	51.80		
107666	AA010611	Hs.60418	EST	29.20		
107332	T87750	Hs.183297	DKFZP566F2124 protein	10.73		
107292	BE166479	Hs.4789	Homo sapiens serologically defined breas	32.00		
107230	AI034467	Hs.34650	ESTs	17.40		
107168	W57578	Hs.237955	RAB7, member RAS oncogene family	10.43		
107160	AA314490	Hs.27669	KIAA1563 protein	11.40		
107054	AI076459	Hs.15978	KIAA1272 protein			
107029	AF264750	Hs.288971	myeloid/lymphoid or mixed-lineage leukem	21.40		
106999	H93281	Hs.10710	hypothetical protein FLJ20417	35.80		
106954	AF128847	Hs.204038	indolethylamine N-methyltransferase			1.76
106870	AI983730	Hs.26530	serum deprivation response (phosphatidyl			
106865	AW192535	Hs.19479	ESTs	13.40		
106844	AA485055	Hs.158213	sperm associated antigen 6		7.13	
106820	NM_016831	Hs.12592	period (Drosophila) homolog 3		7.00	
106818	AK002135	Hs.3542	hypothetical protein FLJ11273	13.00		
106797	AI768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL			2.05
106773	AA478109	Hs.188833	ESTs			
106747	NM_007118	Hs.171957	triple functional domain (PTPRF interact	12.60		
106743	BE613328	Hs.21938	hypothetical protein FLJ12492	10.60		
106667	AW360847	Hs.16578	ESTs			
106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr			2.40
106567	AW450408	Hs.86412	chromosome 9 open reading frame 5			1.78
106562	AL031846	Hs.152151	plakophilin 4			1.76
106536	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot			2.19
106533	AL134708	Hs.145998	ESTs	23.20		
106507	AA259068	Hs.267819	protein phosphatase 1, regulatory (inhib	15.20		
106490	AA404265	Hs.115537	putative dipeptidase			
106474	BE383668	Hs.42484	hypothetical protein FLJ10618	10.44		
106211	AA428240	Hs.126083	ESTs		29.80	
105986	AB037722	Hs.8707	KIAA1301 protein		3.70	
105894	AI904740	Hs.25691	receptor (calcitonin) activity modifying			1.94
105847	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-			1.75
105803	AW747996	Hs.160999	ESTs, Moderately similar to A56194 throm			2.47
105731	AA834664	Hs.29131	nuclear receptor coactivator 2	10.71		
105729	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds			
105688	AI299139	Hs.17517	ESTs	23.40		
105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	37.20		
105101	H63202	Hs.38163	ESTs		8.30	
104989	R65998	Hs.285243	hypothetical protein FLJ22029		8.09	
104986	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1			1.92
104969	AI670947	Hs.78406	phosphatidylinositol-4-phosphate 5-kinas		5.40	
104903	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,		7.60	
104896	AW015318	Hs.23165	ESTs	13.80		
104865	T79340	Hs.22575	Homo sapiens cDNA: FLJ21042 fis, clone C			
104825	AA035613	Hs.141883	ESTs			1.87
104781	AA099904	Hs.21610	DKFZP434B203 protein			1.93
104776	AA026349		gb:zj99f01.s1 Soares_pregnant_uterus_NbH		10.20	
104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor		5.69	
104667	AI239923	Hs.30098	ESTs		3.82	
104404	H58762		gb:EST00057 HE6W Homo sapiens cDNA clone		4.20	
104392	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	27.20		
104212	AB002298	Hs.173035	KIAA0300 protein			1.91
104074	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	11.20		
103749	AL135301	Hs.8768	hypothetical protein FLJ10849	10.86		
103645	AW246253	Hs.7043	succinate-CoA ligase, GDP-forming, alpha	12.00		
103554	AI878826	Hs.323469	caveolin 1, caveolae protein, 22kD			1.80
103541	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i			
103496	Y09267	Hs.132821	flavin containing monooxygenase 2			
103428	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	11.20		
103353	X89399	Hs.119274	RAS p21 protein activator (GTPase activa	19.80		

103295	X81479	Hs.2375	egf-like module containing, mucin-like,		3.60	
103280	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula			
103100	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)			1.76
103025	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t			2.15
102698	M18667	Hs.1867	progastricsin (pepsinogen C)			
102659	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein	11.00		
102580	U60808	Hs.152981	CDP-diacylglycerol synthase (phosphatida	25.40		
102417	AA034127	Hs.153487	signal transducing adaptor molecule (SH3	14.00		
102363	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc			
102302	AA306342	Hs.69171	protein kinase C-like 2	10.86		
102283	AW161552	Hs.83381	guanine nucleotide binding protein 11			
102188	U20350	Hs.78913	chemokine (C-X3-C) receptor 1		7.40	
102151	T27013	Hs.3132	steroidogenic acute regulatory protein	16.40		
101957	L28824	Hs.74101	spleen tyrosine kinase	15.40		
101842	M93221	Hs.75182	mannose receptor, C type 1			
101771	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant			
101764	AI198550	Hs.81256	S100 calcium-binding protein A4 (calcium			1.78
101716	AF050658	Hs.2563	tachykinin, precursor 1 (substance K, su	18.80		
101678	M62505	Hs.2161	complement component 5 receptor 1 (C5a l			2.22
101447	M21305		gb:Human alpha satellite and satellite 3	504.80		
101383	NM_000132	Hs.79345	coagulation factor VIII, procoagulant co		31.00	
101346	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N			1.75
101345	NM_005795	Hs.152175	calcitonin receptor-like			
101336	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h			2.24
101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do			
101277	BE297626	Hs.296049	microfibrillar-associated protein 4			
101262	L35854		gb:Human dystrophin (dp140) mRNA, 5' end	19.00		
101168	NM_005308	Hs.211569	G protein-coupled receptor kinase 5			2.01
101102	NM_003243	Hs.79059	transforming growth factor, beta recepto			
101088	X70697	Hs.553	solute carrier family 6 (neurotransmitte		7.52	
101066	AW970254	Hs.889	Charot-Leyden crystal protein	19.38		
100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte			1.91
100893	BE245294	Hs.180789	S164 protein	15.40		
100770	W25797.comp	Hs.177486	amyloid beta (A4) precursor protein (pro	11.20		
100716	X89887	Hs.172350	HIR (histone cell cycle regulation defec	14.80		
100555	M69181		gb:Human nonmuscle myosin heavy chain-B	33.00		
100425	NM_014747	Hs.78748	KIAA0237 gene product	16.20		
100408	D86640	Hs.56045	src homology three (SH3) and cysteine ri		4.00	
100382	D83407	Hs.156007	Down syndrome critical region gene 1-lik		4.24	
100351	D64158				6.20	
100299	D49493	Hs.2171	growth differentiation factor 10		21.20	
100134	AA305746	Hs.49	macrophage scavenger receptor 1			
100108	U09577	Hs.76873	hyaluronoglucosaminidase 2			1.79
100095	Z97171	Hs.78454	myocilin, trabecular meshwork inducible		5.40	
100066				11.29		

TABLE 3B shows the accession numbers for those primekeys lacking unigeneID's for Table 3A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
123619	371681_1	AA602964 AA609200
126433	127143_1	AA325606 AA099517 N89423
125831	1522905_1	H04043 D60988 D60337
126816	122973_1	AA248234 AA090985
126852	136135_1	AA399961 AA128347
121059	273450_1	AA393283 AA398628
120637	200885_1	AA811804 AA809404 AA286907 AW977624
122011	7617_-2	AA431082
120934	177521_1	AA226198 AA226513 AA383773
123802	genbank_AA620448	AA620448
116814	genbank_H50834	H50834
118329	genbank_N63520	N63520
104404	H58762_at	H58762
104776	genbank_AA026349	AA026349
113502	genbank_T89130	T89130
101262	entrez_L35854	L35854
108573	genbank_AA086005	AA086005
101447	entrez_M21305	M21305
124357	genbank_N22401	N22401
108781	genbank_AA128654	AA128654
112794	genbank_R97018	R97018
100351	entrez_D64158	D64158
100555	tigr_HT2245	M69181 M81105 U51039

Table 4A shows 202 genes up-regulated in samples from patients treated with chemotherapy or radiotherapy. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: average of AI for samples from patients treated with chemotherapy or radiotherapy divided by the average of AI for normal lung samples.

Pkey	ExAccn	UnigeneID	Unigene Title	R1
100113	NM_001269	Hs.84746	chromosome condensation 1	27.20
100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3	20.60
100210	D26361	Hs.3104	KIAA0042 gene product	20.40
100225	D28539	Hs.167185	glutamate receptor, metabotropic 5	20.60
100269	NM_001949	Hs.1189	E2F transcription factor 3	29.40
100438	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	23.50
100877	X80821	Hs.27973	KIAA0874 protein	35.56
100893	BE245294	Hs.180789	S164 protein	43.40
101273	Z11933	Hs.182505	POU domain, class 3, transcription facto	21.80
101447	M21305		gb:Human alpha satellite and satellite 3	193.60
101649	AW959908	Hs.1690	heparin-binding growth factor binding pr	38.40
101724	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	198.80
101748	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	78.60
101809	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	162.20
101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	50.00
101915	AF207881	Hs.155185	cytosolic ovarian carcinoma antigen 1	26.00
101973	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	37.20
102025	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	
102031	U04898	Hs.2156	RAR-related orphan receptor A	32.00
102052	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	51.20
102391	AA296874	Hs.77494	deoxyguanosine kinase	13.90
102420	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	28.80
102610	U65011	Hs.30743	preferentially expressed antigen in mela	110.60
102829	NM_006183	Hs.80962	neurotensin	116.80
103000	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	2.30
103036	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	181.40
103507	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	49.20
103587	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	86.60
104660	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	42.60
104896	AW015318	Hs.23165	ESTs	29.40
105038	AW503733	Hs.9414	KIAA1488 protein	21.50
105298	BE387790	Hs.26369	hypothetical protein FLJ20287	32.80
105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	20.20
105667	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	28.40
106073	AL157441	Hs.17834	downstream neighbor of SON	25.40
106205	AW965058	Hs.111583	ESTs, Weakly similar to I38022 hypotheti	32.00
106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (	40.60
106533	AL134708	Hs.145998	ESTs	59.80
106575	AW970602	Hs.105421	ESTs	43.40
106654	AW075485	Hs.286049	phosphoserine aminotransferase	50.80
106851	AI458623		gb:tk04g09.x1 NCI_CGAP_Lu24 Homo sapiens	53.40
106995	AB023139	Hs.37892	KIAA0922 protein	20.88
107332	T87750	Hs.183297	DKFZP566F2124 protein	23.60
107532	AA443473	Hs.173684	Homo sapiens mRNA; cDNA DKFZp762G207 (fr	57.20
107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	49.00
108609	BE409857	Hs.69499	hypothetical protein	19.67
108780	AU076442	Hs.117938	collagen, type XVII, alpha 1	48.17
109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	59.20
109260	AW978515	Hs.131915	KIAA0863 protein	28.60
109280	AK001355	Hs.279610	hypothetical protein FLJ10493	22.80
109292	AW975746	Hs.188662	KIAA1702 protein	
109384	AA219172	Hs.86849	ESTs	21.00
109415	U80736	Hs.110826	trinucleotide repeat containing 9	31.60
109445	AA232103	Hs.189915	ESTs	24.20
109502	AW967069	Hs.211556	hypothetical protein MGC5487	21.40
109633	AW003785	Hs.170267	ESTs	20.40
109786	AI989482	Hs.146286	kinesin family member 13A	19.60
109958	AA001266	Hs.133521	ESTs	24.00
110920	N47224	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	28.40
110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	36.00
111084	H44186	Hs.15456	PDZ domain containing 1	61.20
111132	AB037807	Hs.83293	hypothetical protein	24.60
111229	AW389845	Hs.110855	ESTs	27.20
111337	AA837396	Hs.263925	LIS1-interacting protein NUDE1, rat homo	48.00
111987	NM_015310	Hs.6763	KIAA0942 protein	37.80
112046	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	26.80
112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	63.80
112685	R87650	Hs.33439	ESTs, Weakly similar to ALU1_HUMAN ALU	26.40
112871	AL110216	Hs.12285	ESTs, Weakly similar to I55214 salivary	47.64
112897	AW206453	Hs.3782	ESTs	22.00
112973	AB033023	Hs.318127	hypothetical protein FLJ10201	65.00
112992	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	42.00
113073	N39342	Hs.103042	microtubule-associated protein 1B	55.40

113494	T91451	Hs.86538	ESTs	22.80
113560	T91015	Hs.268626	ESTs	22.80
113849	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	51.80
113950	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	28.20
114339	AA782845	Hs.22790	ESTs	20.20
114365	H42169	Hs.18653	hypothetical protein FLJ14627	21.00
114455	H37908	Hs.271616	ESTs, Weakly similar to ALU8_HUMAN ALU S	25.80
114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	23.60
114824	AA960961	Hs.305953	zinc finger protein 83 (HPF1)	27.20
114837	BE244930	Hs.166895	ESTs	30.20
114974	AW966931	Hs.179662	nucleosome assembly protein 1-like 1	20.80
115075	AA814043	Hs.88045	ESTs	30.60
115084	BE383668	Hs.42484	hypothetical protein FLJ10618	28.86
115291	BE545072	Hs.122579	hypothetical protein FLJ10461	38.00
115313	AA808001	Hs.184411	albumin	22.60
115697	D31382	Hs.63325	transmembrane protease, serine 4	173.60
115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	27.77
116090	AI591147	Hs.61232	ESTs	20.80
116107	AL133916	Hs.172572	hypothetical protein FLJ20093	164.20
116399	AA889120	Hs.110637	homeo box A10	38.00
117099	H93699		gb:yv16a11.s1 Soares fetal liver spleen	21.60
117881	AF161470	Hs.260622	butyrate-induced transcript 1	49.40
118091	AW005054	Hs.47883	ESTs, Weakly similar to KCC1_HUMAN CALCI	22.40
118138	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	22.00
118720	N73515		gb:za49d07.s1 Soares fetal liver spleen	20.00
118873	AI824009	Hs.44577	ESTs	19.40
119126	R45175	Hs.117183	ESTs	111.20
119717	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	33.00
119940	AL050097	Hs.272531	DKFZP586B0319 protein	31.00
120266	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	20.20
120515	AA258355		gb:zr59c10.s1 Soares_NhHMPu_S1 Homo sapi	25.00
120859	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	95.40
120983	AA398209	Hs.97587	EST	105.20
121054	AW976570	Hs.97387	ESTs	38.80
121369	AW450737	Hs.128791	CGI-09 protein	41.60
122335	AA443258	Hs.241551	chloride channel, calcium activated, fam	30.80
122612	AA974832	Hs.128708	ESTs	19.60
123130	AA487200		gb:ab19f02.s1 Stratagene lung (937210) H	33.20
123440	AI733692	Hs.112488	ESTs	23.17
123596	AA421130	Hs.112640	EST	23.00
123619	AA602964		gb:no97c02.s1 NCI_CGAP_Pr2 Homo sapiens	28.80
124006	AI147155	Hs.270016	ESTs	77.60
124169	BE079334	Hs.271630	ESTs	22.20
124281	AI333756	Hs.111801	arsenate resistance protein ARS2	42.20
124472	N52517	Hs.102670	EST	32.60
124617	AW628168	Hs.152684	ESTs	21.80
124631	NM_014053	Hs.270594	FLVCR protein	30.40
124839	R55784	Hs.140942	ESTs	21.20
125186	AA610620	Hs.181244	major histocompatibility complex, class	42.80
125321	T86652	Hs.178294	ESTs	27.00
125535	NM_013243	Hs.22215	secretogranin III	23.80
125646	AA628962	Hs.75209	protein kinase (cAMP-dependent, catalyti	23.20
125684	AW589427	Hs.158849	Homo sapiens cDNA: FLJ21663 fis, clone C	21.20
125724	AL360190	Hs.295978	Homo sapiens mRNA full length insert cDN	48.80
125847	AW161885	Hs.249034	ESTs	31.00
125934	AA193325	Hs.32646	hypothetical protein FLJ21901	21.20
126077	M78772	Hs.210836	ESTs	49.80
126299	AW979155	Hs.298275	amino acid transporter 2	21.80
126395	AI468004	Hs.278956	hypothetical protein FLJ12929	71.00
126433	AA325606		gb:EST28707 Cerebellum II Homo sapiens c	23.20
126509	R47400	Hs.23850	ESTs	23.80
126538	AB030656	Hs.17377	coronin, actin-binding protein, 1C	23.10
126666	AA648886	Hs.151999	ESTs	36.00
126812	AB037860	Hs.173933	nuclear factor I/A	20.80
126872	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	46.29
127046	AA321948	Hs.293968	ESTs	22.80
127431	AW771958	Hs.175437	ESTs, Moderately similar to PC4259 ferri	30.00
127489	AA650250	Hs.272076	ESTs	20.80
127521	AW297206	Hs.164018	ESTs	25.20
127742	AW293496	Hs.180138	ESTs	28.00
127925	AA805151	Hs.3628	mitogen-activated protein kinase kinase	21.20
127930	AA809572	Hs.123304	ESTs	20.54
127968	AA830201	Hs.124347	ESTs	28.20
127987	AI022103	Hs.124511	ESTs	19.60
128116	H07103	Hs.286014	Homo sapiens, clone IMAGE:3867243, mRNA	20.40
128609	NM_003616	Hs.102456	survival of motor neuron protein interac	34.40
128777	AI878918	Hs.10526	cysteine and glycine-rich protein 2	53.80
128949	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	23.00
129168	AI132988	Hs.109052	chromosome 14 open reading frame 2	37.60
129404	AI267700	Hs.317584	ESTs	28.60
129527	AA769221	Hs.270847	delta-tubulin	40.80
129574	AA026815	Hs.11463	UMP-CMP kinase	31.20
129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	29.60
129785	H19006	Hs.184780	ESTs	72.20
129970	AV655806	Hs.296198	chromosome 12 open reading frame 4	22.20

130149	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	29.60
130199	Z48579	Hs.172028	a disintegrin and metalloproteinase doma	27.60
130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	28.36
130466	W19744	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	20.20
130482	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	22.40
130617	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	19.60
130703	R77776	Hs.18103	ESTs	19.40
130732	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	21.40
130867	NM_001072	Hs.284239	UDP glycosyltransferase 1 family, polype	110.00
131028	AI879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	25.20
131086	AL035461	Hs.2281	chromogranin B (secretogranin 1)	40.60
131284	NM_001429	Hs.25272	E1A binding protein p300	24.60
131775	AB014548	Hs.31921	KIAA0648 protein	21.00
131860	BE383676	Hs.334	Rho guanine nucleotide exchange factor (	33.40
131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	60.80
132040	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	20.40
132084	NM_002267	Hs.3886	karyopherin alpha 3 (importin alpha 4)	29.40
132389	AA310393	Hs.190044	ESTs	32.40
132437	AA152106	Hs.4859	cyclin L ania-6a	27.40
132550	AW969253	Hs.170195	bone morphogenetic protein 7 (osteogenic	75.60
132617	AF037335	Hs.5338	carbonic anhydrase XII	31.36
132632	AU076916	Hs.5398	guanine monphosphate synthetase	32.40
132672	W27721	Hs.54697	Cdc42 guanine exchange factor (GEF) 9	23.40
132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	61.20
132771	Y10275	Hs.56407	phosphoserine phosphatase	22.33
133070	U92649	Hs.64311	a disintegrin and metalloproteinase doma	23.50
133153	AF070592	Hs.66170	HSKM-B protein	30.00
133181	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	23.80
133282	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	51.60
133350	AI499220	Hs.71573	hypothetical protein FLJ10074	33.00
133592	AV652066	Hs.75113	general transcription factor IIIA	82.00
133658	AA319146	Hs.75426	secretogranin II (chromogranin C)	
133865	AB011155	Hs.170290	discs, large (Drosophila) homolog 5	69.33
134032	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	33.20
134125	NM_014781	Hs.50421	KIAA0203 gene product	31.60
134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	30.60
134321	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-lin	23.40
134367	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	49.20
134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	20.20
134753	NM_006482	Hs.173135	dual-specificity tyrosine-(Y)-phosphoryl	20.80
135002	AA448542	Hs.251677	G antigen 7B	37.60
135029	H58818	Hs.187579	hydroxysteroid (17-beta) dehydrogenase	53.40
135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	31.60
135345	X53655	Hs.99171	neurotrophin 3	26.80

TABLE 4B shows the accession numbers for those primekeys lacking unigeneID's for Table 4A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
123619	371681_1	AA602964 AA609200
126433	127143_1	AA325606 AA099517 N89423
126872	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011362 BE011215 BE011365 BE011363
106851	322947_1	AI458623 AA639708 AA485409 R22065 AA485570
118720	genbank_N73515	N73515
120515	genbank_AA258356	AA258356
117099	321871_1	H93699 H97976 H80036
101447	entrez_M21305	M21305
123130	genbank_AA487200	AA487200

Table 5A shows 680 genes up-regulated in squamous cell carcinoma or adenocarcinoma lung tumors relative to normal lung and chronically diseased lung. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number
UnigeneID:	Unigene number
Unigene Title:	Unigene gene title
R1:	70th percentile of AI for squamous cell carcinoma and adenocarcinoma lung tumor samples divided by the 90th percentile of AI for normal and chronically diseased lung samples.
R2:	80th percentile of AI adenocarcinoma lung tumor samples divided by the 90th percentile of AI for normal and chronically diseased lung samples.
R3:	80th percentile of AI squamous cell carcinoma lung tumor samples divided by the 90th percentile of AI for normal and chronically diseased lung samples.
R4:	80th percentile of AI adenocarcinoma lung tumor samples divided by the 80th percentile of AI for squamous cell carcinoma lung tumor samples.
R5:	70th percentile of AI for squamous cell carcinoma and adenocarcinoma lung tumor samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by 90th percentile of AI for normal and chronically diseased lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2	R3	R4	R5
100035			AFFX control: GAPDH					6.76
100036			AFFX control: GAPDH					5.77
100037			AFFX control: GAPDH					5.75
100071	A28102		Human GABAa receptor alpha-3 subunit		8.00			
100114	X02308	Hs.82962	thymidylate synthetase					5.71
100154	H60720	Hs.81892	KIAA0101 gene product	3.84				
100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3	3.33				
100188	AW247090	Hs.57101	minichromosome maintenance deficient (S.					4.52
100202	BE294407	Hs.99910	phosphofructokinase, platelet					5.49
100216	AA489908	Hs.1390	proteasome (prosome, macropain) subunit,					5.67
100269	NM_001949	Hs.1189	E2F transcription factor 3	2.55				
100287	AU076657	Hs.1600	chaperonin containing TCP1, subunit 5 (e					5.66
100297	AU077258	Hs.182429	protein disulfide isomerase-related prot					3.81
100330	AW410976	Hs.77152	minichromosome maintenance deficient (S.					4.50
100335	AW247529	Hs.6793	platelet-activating factor acetylhydrola	5.07				
100360	W70171	Hs.75939	uridine monophosphate kinase					4.82
100372	NM_014791	Hs.184339	KIAA0175 gene product					3.79
100474	NM_000699	Hs.300280	amylase, alpha 2A; pancreatic				15.65	
100486	T19006	Hs.10842	RAN, member RAS oncogene family					5.49
100491	D56165	Hs.275163	non-metastatic cells 2, protein (NM23B)					4.17
100516	D90278	Hs.11	carcinoembryonic antigen-related cell ad		7.20			
100522	X51501	Hs.99949	prolactin-induced protein				14.20	
100559	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	3.10				
100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid				9.30	
100629	AA015693	Hs.21291	mitogen-activated protein kinase kinase				20.60	
100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	3.85				
100677	AA353686	Hs.57813	zinc ribbon domain containing, 1		8.60			
100696	D14887	Hs.121686	general transcription factor IIA, 1 (37k				10.00	
100709	N26539	Hs.100469	myeloid/lymphoid or mixed-lineage leukem			24.80		
100761	BE208491	Hs.295112	KIAA0618 gene product		7.60			
100830	AC004770	Hs.4756	flap structure-specific endonuclease 1					7.99
100867	U14622		gb:Human transketolase-like protein gene		10.20			
100902	M16029	Hs.287270	ret proto-oncogene (multiple endocrine n		8.00			
100906	AU076916	Hs.5398	guanine monphosphate synthetase					5.16
100960	J00124	Hs.117729	keratin 14 (epidermolysis bullosa simple	2.57				
101045	J05614		gb:Human proliferating cell nuclear anti					4.69
101061	NM_000175	Hs.180532	glucose phosphate isomerase					4.19
101071	L02840	Hs.84244	potassium voltage-gated channel, Shab-re		12.91			
101124	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	3.12				
101175	U82671	Hs.36980	melanoma antigen, family A, 2	3.50				
101181	BE262621	Hs.73798	macrophage migration inhibitory factor (					5.69
101204	L24203	Hs.82237	ataxia-telangiectasia group D-associated	4.08				
101210	L29301	Hs.2353	opioid receptor, mu 1			6.40		
101216	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	2.53				
101228	AA333387	Hs.82916	chaperonin containing TCP1, subunit 6A (					7.90
101233	AL135173	Hs.878	sorbitol dehydrogenase					4.45
101273	Z11933	Hs.182505	POU domain, class 3, transcription facto	8.50				
101342	U52112	Hs.182018	interleukin-1 receptor-associated kinase					4.17
101346	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N				21.89	
101389	NM_000892	Hs.1901	kallikrein B, plasma (Fletcher factor) 1				12.80	
101396	BE267931	Hs.78996	proliferating cell nuclear antigen	3.24				
101431	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)					7.90
101448	NM_000424	Hs.195850	keratin 5 (epidermolysis bullosa simplex	8.31				
101462	AL035668	Hs.73853	bone morphogenetic protein 2				38.80	
101466	BE262660	Hs.170197	glutamic-oxaloacetic transaminase 2, mit					4.01
101484	AA053486	Hs.20315	interferon-induced protein with tetratri				12.00	
101502	M26958		gb:Human parathyroid hormone-related pro.	10.50				
101505	AA307680	Hs.75692	asparagine synthetase					4.46
101526	NM_002197	Hs.154721	aconitase 1, soluble	4.02				
101535	X57152	Hs.99853	fibrillarin					4.65
101577	M34353	Hs.1041	v-ros avian UR2 sarcoma virus oncogene h				9.09	
101649	AW959908	Hs.1690	heparin-binding growth factor binding pr	54.00				
101663	NM_003528	Hs.2178	H2B histone family, member Q	5.59				
101664	AA436989	Hs.121017	H2A histone family, member A	7.00				
101669	L24498	Hs.80409	growth arrest and DNA-damage-inducible,		7.60			

101695	M69136	Hs.135626	chymase 1, mast cell	4.79				
101724	L11690	Hs.620	*bullous pemphigoid antigen 1 (230/240kD)*	15.21				
101748	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	55.50				
101759	M80244	Hs.184601	solute carrier family 7 (cationic amino					4.10
101771	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant				18.57	
101804	M86699	Hs.169840	TTK protein kinase	4.50				
101809	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	140.00				
101833	AU076442	Hs.117938	collagen, type XVII, alpha 1	2.56				
101842	M93221	Hs.75182	*mannose receptor*, C type 1				12.80	
101851	BE260964	Hs.82045	midkine (neurite growth-promoting factor					5.88
102002	NM_002484	Hs.81469	nucleotide binding protein 1 (E.coli Min		7.80			
102039	AL134223	Hs.306098	aldo-keto reductase family 1, member C1					4.35
102072	U09410	Hs.78743	zinc finger protein 131 (clone pHZ-10)			7.40		
102083	T35901	Hs.75117	interleukin enhancer binding factor 2, 4					5.12
102111	L36196	Hs.81884	sulfotransferase family, cytosolic, 2A,				12.00	
102123	NM_001809	Hs.1594	centromere protein A (17kD)	6.20				
102154	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	2.62				
102193	AL036335	Hs.313	secreted phosphoprotein 1 (osteopontin,	5.85				
102217	AA829978	Hs.301613	JTV1 gene					6.18
102224	NM_002810	Hs.148495	proteasome (prosome, macropain) 26S subu					4.49
102234	AW163390	Hs.278554	heterochromatin-like protein 1					5.80
102251	NM_004398	Hs.41706	*DEAD/H (Asp-Glu-Ala-Asp/His) box polypep*	4.50				
102305	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)					5.15
102330	BE298063	Hs.77254	chromobox homolog 1 (Drosophila HP1 beta					4.17
102340	U37055	Hs.278657	macrophage stimulating 1 (hepatocyte gro				9.33	
102348	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	8.87				
102368	U39817	Hs.36820	Bloom syndrome	15.91				
102394	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma			19.20		
102404	NM_005429	Hs.79141	*vascular endothelial growth factor C*				14.00	
102537	U57094	Hs.50477	RAB27A, member RAS oncogene family				12.00	
102581	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2					4.57
102605	AI435128	Hs.181369	ubiquitin fusion degradation 1-like					3.98
102610	U65011	Hs.30743	preferentially expressed antigen in mela	77.50				
102623	AW249285	Hs.37110	melanoma antigen, family A, 9	12.50				
102642	AA205847	Hs.23016	G protein-coupled receptor			22.00		
102654	AV649989	Hs.24385	Human hbc647 mRNA sequence		12.00			
102659	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein				12.80	
102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	6.50				
102672	U72066	Hs.29287	retinoblastoma-binding protein 8	8.50				
102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C					9.24
102696	BE540274	Hs.239	forkhead box M1					5.54
102768	U82321		*gb:Homo sapiens clone 14.9B mRNA sequenc*		6.60			
102781	BE258778	Hs.108809	chaperonin containing TCP1, subunit 7 (e					3.78
102784	U85658	Hs.61796	transcription factor AP-2 gamma (activat					4.26
102824	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H			14.40		
102829	NM_006183	Hs.80962	neurotensin	8.00				
102888	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1					5.50
102892	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin			6.70		
102913	NM_002275	Hs.80342	*keratin 15*	4.64				
102935	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	2.93				
102951	X15218	Hs.2969	v-ski avian sarcoma viral oncogene homol				11.40	
102983	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)					7.26
103023	AW500470	Hs.117950	multifunctional polypeptide similar to S	3.01				
103036	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	27.90				
103038	AA926960	Hs.334883	CDC28 protein kinase 1					8.79
103060	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin					4.27
103099	AI693251	Hs.8248	NADH dehydrogenase (ubiquinone) Fe-S pro		9.80			
103119	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	4.05				
103168	X53463	Hs.2704	glutathione peroxidase 2 (gastrointestin	3.07				
103185	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmi					5.62
103192	M22440	Hs.170009	transforming growth factor, alpha		7.40			
103223	BE275607	Hs.1708	*chaperonin containing TCP1, subunit 3 (g*					4.70
103242	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o			100.00		
103316	X83301	Hs.324728	SMA5				9.80	
103375	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	9.71				
103376	AL036166	Hs.323378	coated vesicle membrane protein	14.00				
103385	NM_007069	Hs.37189	similar to rat HREV107				11.00	
103391	X94453	Hs.114366	pyrroline-5-carboxylate synthetase (glut	2.93				
103404	BE394784	Hs.78596	proteasome (prosome, *macropain*) subunit,					5.15
103430	BE564090	Hs.20716	translocase of inner mitochondrial membr					3.98
103446	X98834	Hs.79971	sal (Drosophila)-like 2				21.40	
103476	Y07701	Hs.293007	aminopeptidase puromycin sensitive		13.00			
103477	AJ011812	Hs.119018	transcription factor NRF			6.40		
103478	BE514982	Hs.38991	S100 calcium-binding protein A2	5.02				
103515	Y10275	Hs.56407	phosphoserine phosphatase	10.50				
103558	BE616547	Hs.2785	keratin 17	6.41				
103580	AA328046	Hs.46405	polymerase (RNA) II (DNA directed) polyp					3.84
103587	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	78.50				
103594	AI368680	Hs.816	SRY (sex determining region Y)-box 2	6.51				
103636	NM_006235	Hs.2407	POU domain, class 2, associating factor	3.50				
103768	AF086009		gb:Homo sapiens full length insert cDNA					4.48
103841	AA314821	Hs.38178	*hypothetical protein FLJ23468*		8.00			
103847	AF219946	Hs.102237	tubby super-family protein		10.40			
103913	AW967500	Hs.133543	ESTs				15.60	
104094	AA418187	Hs.330515	ESTs			6.60		

104150	AL122044	Hs.331633	hypothetical protein DKFZp566N034				26.00	
104257	BE560621	Hs.9222	estrogen receptor binding site associate		6.80			
104261	AW248364	Hs.5409	RNA polymerase I subunit					3.98
104331	AB040450	Hs.279862	cdk inhibitor p21 binding protein		6.80			
104415	BE410992	Hs.258730	heme-regulated initiation factor 2-alpha		10.29			
104558	R56678	Hs.88959	hypothetical protein MGC4816	4.21				
104590	AW373062	Hs.83623	nuclear receptor subfamily 1, group I, m				15.79	
104658	AA360954	Hs.27268	Homo sapiens cDNA: FLJ21933 fis, clone H				17.40	
104660	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	6.40				
104689	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr					6.55
104754	AI206234	Hs.155924	cAMP responsive element modulator				10.00	
104758	BE560269	Hs.7010	NPD002 protein					4.47
104971	BE311926	Hs.15830	hypothetical protein FLJ12691	2.87				
105011	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	3.83				
105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	2.86				
105026	AA809485	Hs.124219	hypothetical protein FLJ12934		11.00			
105076	AI598252	Hs.37810	hypothetical protein MGC14833					5.01
105132	AA148164	Hs.247280	HBV associated factor					3.99
105143	AI368836	Hs.24808	ESTs, Weakly similar to I38022 hypotheti			11.00		
105158	AW976357	Hs.234545	hypothetical protein NUF2R		16.00			
105175	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	4.32				
105200	AA328102	Hs.24641	cytoskeleton associated protein 2	3.00				
105264	AA227934		gb:zr57e08.s1 Soares_NhHMPu_S1 Homo sapi				10.00	
105298	BE387790	Hs.26369	hypothetical protein FLJ20287	3.69				
105409	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8				9.20	
105460	AW296078	Hs.271721	Homo sapiens, clone IMAGE:4179986, mRNA,			7.80		
105667	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	4.12				
105743	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	3.82				
105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro			27.00		
105848	AW954064	Hs.24951	ESTs			7.60		
105891	U55984	Hs.289088	heat shock 90kD protein 1, alpha					4.14
106019	AF221993	Hs.46743	McKusick-Kaufman syndrome			16.80		
106069	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip			23.40		
106073	AL157441	Hs.17834	downstream neighbor of SON	9.50				
106126	AA576953	Hs.22972	hypothetical protein FLJ13352	6.00				
106159	AK001301	Hs.3487	hypothetical protein FLJ10439					3.95
106220	D61329	Hs.32196	mitochondrial ribosomal protein L36					6.04
106260	AI097144	Hs.5250	ESTs, Weakly similar to ALU1_HUMAN ALU S			13.20		
106300	Y10043	Hs.19114	high-mobility group (nonhistone chromoso					5.02
106307	AA436174	Hs.37751	ESTs, Weakly similar to putative p150 [		6.60			
106318	AA025610	Hs.9605	cleavage and polyadenylation specific fa					5.04
106341	AF191020	Hs.5243	hypothetical protein, estradiol-induced					7.25
106440	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub			13.80		
106481	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	4.75				
106586	AA243837	Hs.57787	ESTs				10.84	
106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr				45.60	
106654	AW075485	Hs.286049	phosphoserine aminotransferase	28.00				
106785	Y15227	Hs.20149	deleted in lymphocytic leukemia, 1	3.00				
106813	C05766	Hs.181022	CGI-07 protein			11.40		
106895	AK001826	Hs.25245	hypothetical protein FLJ11269			6.00		
106913	AI219346	Hs.86178	M-phase phosphoprotein 9		6.56			
106919	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU S					4.27
107054	AI076459	Hs.15978	KIAA1272 protein				34.80	
107059	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	4.71				
107098	AI823593	Hs.27688	ESTs				24.80	
107104	AU076640	Hs.15243	nucleolar protein 1 (120kD)					7.05
107129	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.60				
107198	AV657225	Hs.9846	KIAA1040 protein		19.20			
107203	D20426	Hs.41639	programmed cell death 2		7.60			
107217	AL080235	Hs.35861	DKFZP586E1621 protein	9.50				
107284	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	2.71				
107318	T74445	Hs.5957	Homo sapiens clone 24416 mRNA sequence			8.71		
107516	X57152	Hs.99853	fibrillarin					4.33
107529	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)					4.00
107728	AA019551	Hs.294151	Homo sapiens, clone IMAGE:3603836, mRNA,		10.80			
107851	AA022953	Hs.61172	EST			8.00		
107901	L42612	Hs.335952	keratin 6B	3.40				
107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	2.88				
107932	AW392555	Hs.18878	hypothetical protein FLJ21620	7.50				
108015	AW298357	Hs.49927	protein kinase NYD-SP15				23.40	
108056	AA043675	Hs.62633	ESTs				12.80	
108075	AI867370	Hs.139709	hypothetical protein FLJ12572				12.80	
108187	BE245374	Hs.27842	hypothetical protein FLJ11210		7.00			
108296	N31256	Hs.161623	ESTs		6.60			
108305	AA071391		gb:zm61e06.r1 Stratagene fibroblast (937				11.80	
108393	AA075211		gb:zm86a08.r1 Stratagene ovarian cancer				11.80	
108480	AL133092	Hs.68055	hypothetical protein DKFZp434I0428				20.80	
108554	AA084948		gb:zn13b09.s1 Stratagene hNT neuron (937		6.40			
108573	AA086005		gb:zl84c04.s1 Stratagene colon (937204)				25.40	
108584	AA088326	Hs.120905	Homo sapiens cDNA FLJ11448 fis, clone HE		9.60			
108597	AK000292	Hs.278732	hypothetical protein FLJ20285				14.60	
108695	AB029000	Hs.70823	KIAA1077 protein	3.00				
108699	AA121514	Hs.70832	ESTs				10.00	
108700	AA121518	Hs.193540	ESTs, Moderately similar to 2109260A B c			11.00		
108780	AU076442	Hs.117938	collagen, type XVII, alpha 1	11.21				

108810	AW295647	Hs.71331	hypothetical protein MGC5350	8.50				
108816	AA130884	Hs.270501	ESTs, Moderately similar to ALU2_HUMAN		7.40			
108857	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	4.00				
108860	AA133334	Hs.129911	ESTs	6.09				
108937	AL050107	Hs.24341	transcriptional co-activator with PDZ-bi	3.00				
109010	NM_007240	Hs.44229	dual specificity phosphatase 12	2.69				
109121	BE389387	Hs.49767	NADH dehydrogenase (ubiquinone) Fe-S pro					4.53
109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	10.58				
109227	AA766998	Hs.85874	Human DNA sequence from clone RP11-16L21		9.00			
109415	U80736	Hs.110826	trinucleotide repeat containing 9		51.40			
109418	AI866946	Hs.161707	ESTs				11.00	
109454	AA232255	Hs.295232	ESTs, Moderately similar to A46010 X-li			17.60		
109502	AW967069	Hs.211556	hypothetical protein MGC5487			9.49		
109543	AA564994	Hs.222851	ESTs		12.67			
109648	H17800	Hs.7154	ESTs				10.40	
109680	AB037734	Hs.4993	KIAA1313 protein			33.20		
109700	F09609		gb:HSC33H092 normalized infant brain cDN				16.00	
109704	AI743880	Hs.12876	ESTs			11.00		
109792	R49625		gb:yg61f03.s1 Soares infant brain 1NIB H				12.60	
109981	BE546208	Hs.26090	hypothetical protein FLJ20272	4.00				
109998	AL042201	Hs.21273	transcription factor NYD-sp10		7.80			
110039	H11938	Hs.21907	histone acetyltransferase		7.00			
110156	AA581322	Hs.4213	hypothetical protein MGC16207					4.24
110500	AA907723	Hs.36962	ESTs	4.50				
110551	AW450381	Hs.14529	ESTs		8.60			
110561	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.06				
110854	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to		6.80			
110886	AW274992	Hs.72249	three-PDZ containing protein similar to			8.80		
110916	BE178102	Hs.24349	ESTs		6.80			
111003	N52980	Hs.83765	dihydrofolate reductase				16.80	
111337	AA837396	Hs.263925	LIS1-interacting protein NUDE1, rat homo	2.54				
111434	R01608	Hs.142736	ESTs				9.80	
111439	AI476429	Hs.19238	ESTs				10.40	
111540	U82670	Hs.9786	zinc finger protein 275			15.40		
111597	R11499	Hs.189716	ESTs				9.20	
111895	T80581	Hs.12723	Homo sapiens clone 25153 mRNA sequence		6.80			
111929	AF027208	Hs.112360	prominin (mouse)-like 1				14.67	
112054	R43590		gb:yc85g02.s1 Soares infant brain 1NIB H		10.80			
112210	R49645	Hs.7004	ESTs				10.20	
112244	AB029000	Hs.70823	KIAA1077 protein	2.99				
112382	R59904		gb:yh07g12.s1 Soares infant brain 1NIB H		6.60			
112392	R60763	Hs.193274	ESTs, Moderately similar to I57588 HSrel			7.10		
112442	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	3.00				
112539	R70318	Hs.339730	ESTs				37.20	
112772	AI992283	Hs.35437	ESTs, Moderately similar to I38026 MLN 6				14.60	
112869	BE261750	Hs.4747	dyskeratosis congenita 1, dyskerin					4.83
112935	R71449	Hs.268760	ESTs	2.73				
112970	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence				12.00	
112973	AB033023	Hs.318127	hypothetical protein FLJ10201	11.50				
112992	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f			10.89		
113063	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	15.00				
113073	N39342	Hs.103042	microtubule-associated protein 1B			15.31		
113078	T40444	Hs.118354	CAT56 protein		7.00			
113238	R45467	Hs.189813	ESTs				41.20	
113591	T91881	Hs.200597	KIAA0563 gene product				9.40	
113702	T97307		gb:ye53h05.s1 Soares fetal liver spleen	25.00				
113844	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE				13.91	
113984	R96696	Hs.35598	ESTs		7.80			
114073	R44953	Hs.22908	Homo sapiens mRNA; cDNA DKFZp434J1027 (f		7.20			
114162	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	3.42				
114208	AL049466	Hs.7859	ESTs			6.74		
114251	H15261	Hs.21948	ESTs				33.20	
114285	R44338	Hs.22974	ESTs				13.20	
114313	H18456	Hs.27946	ESTs				10.00	
114339	AA782845	Hs.22790	ESTs		7.80			
114407	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f					4.14
114560	AI452469	Hs.165221	ESTs				9.80	
114699	AA127386		gb:zn90d09.r1 Stratagene lung carcinoma		7.60			
114767	AI859865	Hs.154443	minichromosome maintenance deficient (S	3.21				
114793	AA158245		gb:zo76c03.s1 Stratagene pancreas (93720			6.00		
114833	AI417215	Hs.87159	hypothetical protein FLJ12577				11.40	
115047	BE270930	Hs.82916	chaperonin containing TCP1, subunit 6A (					4.31
115060	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3					4.03
115097	AA256213	Hs.72010	ESTs				35.40	
115113	AA256460		gb:zr81a04.s1 Soares_NhHMPu_S1 Homo sapi				15.20	
115123	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m					4.19
115134	AW968073	Hs.194331	ESTs, Highly similar to A55713 inositol				12.40	
115291	BE545072	Hs.122579	hypothetical protein FLJ10461	25.00				
115347	AA356792	Hs.334824	hypothetical protein FLJ14825		7.00			
115414	AA662240	Hs.283099	AF15q14 protein	3.25				
115522	BE614387	Hs.333893	c-Myc target JPO1	3.68				
115536	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	10.50				
115566	AI142336	Hs.43977	Human DNA sequence from clone RP11-196N1				24.40	
115645	AI207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	4.17				
115648	AW016811	Hs.234478	Homo sapiens cDNA: FLJ22648 fis, clone H			6.00		

115652	BE093589	Hs.38178	hypothetical protein FLJ23468	3.81				
115697	D31382	Hs.63325	transmembrane protease, serine 4	62.14				
115793	AA424883	Hs.70333	hypothetical protein MGC10753				11.80	
115816	BE042915	Hs.287588	Homo sapiens cDNA FLJ13675 fis, clone PL				9.71	
115892	AA291377	Hs.50831	ESTs			27.40		
115906	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	2.53				
115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	11.82				
115965	AA001732	Hs.173233	hypothetical protein FLJ10970				34.29	
115978	AL035864	Hs.69517	cDNA for differentially expressed CO16 g					8.23
115985	AA447709	Hs.268115	ESTs, Weakly similar to T08599 probable	3.00				
116090	AI591147	Hs.61232	ESTs	5.17				
116096	AA682382	Hs.59982	ESTs			8.20		
116127	AF126743	Hs.279884	DNAJ domain-containing		10.60			
116157	BE439838	Hs.44298	mitochondrial ribosomal protein S17					5.82
116190	AI949095	Hs.67776	ESTs, Weakly similar to T22341 hypotheti					4.08
116278	NM_003686	Hs.47504	exonuclease 1	9.50				
116335	AK001100	Hs.41690	desmocollin 3	3.67				
116496	AW450694	Hs.21433	hypothetical protein DKFZp547J036		7.00			
116503	AI925316	Hs.212617	ESTs				12.60	
116674	AI768015	Hs.92127	ESTs			32.00		
116929	AA586922	Hs.80475	polymerase (RNA) II (DNA directed) polyp		7.60			
116973	AI702054	Hs.166982	phosphatidylinositol glycan, class F		9.80			
116993	AI417023	Hs.40478	ESTs				10.20	
117079	H92325		gb:ys85f05.s1 Soares retina N2b4HR Homo				15.20	
117317	AI263517	Hs.43322	ESTs				13.40	
117326	N23629	Hs.241420	Homo sapiens mRNA for KIAA1756 protein,				20.60	
117396	W20128	Hs.296039	ESTs				10.60	
117412	N32536	Hs.42645	ESTs				16.00	
117519	N32528	Hs.146286	kinesin family member 13A				9.11	
117693	AW179019	Hs.112110	mitochondrial ribosomal protein L42					4.01
117721	N46100	Hs.93939	EST				19.80	
117881	AF161470	Hs.260622	butyrate-induced transcript 1	2.71				
117903	AA768283	Hs.47111	ESTs				17.80	
117992	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586I2022 (f					4.17
118013	AI674126	Hs.94031	ESTs				10.60	
118017	AI813444	Hs.42197	ESTs			8.82		
118186	N22886	Hs.42380	ESTs		7.00			
118325	AI868065	Hs.166184	intersectin 2				13.80	
118367	N64269	Hs.48946	EST			6.14		
118368	N64339	Hs.48956	gap junction protein, beta 6 (connexin 3	3.14				
118472	AL157545	Hs.42179	bromodomain and PHD finger containing, 3			12.40		
118709	AA232970	Hs.293774	ESTs				12.20	
119025	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	4.50				
119027	AF086161	Hs.114611	hypothetical protein FLJ11808	3.22				
119052	R10889		gb:yf38d02.s1 Soares fetal liver spleen		9.60			
119164	AF221993	Hs.46743	McKusick-Kaufman syndrome			6.60		
119186	AI979147	Hs.101265	hypothetical protein FLJ22593				10.80	
119243	T12603		gb:CHR90123 *Chromosome 9 exon II Homo sa*				9.44	
119490	AA195276	Hs.263858	ESTs, Moderately similar to B34087 hypot				11.80	
119499	AI918906	Hs.55080	ESTs			14.80		
119599	W45552		gb:zc26d03.s1 Soares_senescent_fibroblas		12.60			
119780	NM_016625	Hs.191381	hypothetical protein	17.00				
119845	W79123	Hs.58561	G protein-coupled receptor 87	13.50				
119941	AA699485	Hs.58896	ESTs		8.00			
119994	AA642402	Hs.59142	ESTs	7.73				
120102	W67353	Hs.170218	KIAA0251 protein			39.60		
120104	AK000123	Hs.180479	hypothetical protein FLJ20116	2.91				
120294	AK000059	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par			8.20		
120486	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	8.73				
120599	AA804448	Hs.104463	ESTs		7.00			
120699	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos				10.00	
120715	AA292700		gb:zs59a06.s1 NCI_CGAP_GCB1 Homo sapiens		9.40			
120821	Y19062	Hs.96870	staufen (Drosophila, RNA-binding protein				13.80	
120859	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol		9.00			
120880	AA360240	Hs.97019	EST		15.60			
120983	AA398209	Hs.97587	EST			27.66		
121034	AL389951	Hs.271623	nucleoporin 50kD			20.80		
121121	AA399371	Hs.189095	similar to SALL1 (sal (Drosophila)-like		22.80			
121313	AA402713	Hs.97872	ESTs				10.00	
121369	AW450737	Hs.128791	CGI-09 protein	25.71				
121376	AA448103	Hs.187958	solute carrier family 6 (neurotransmitte					5.42
121476	AA412311	Hs.97903	ESTs		8.30			
121509	AA868939	Hs.97888	ESTs		8.59			
121553	AA412488	Hs.48820	TATA box binding protein (TBP)-associat	18.50				
121753	AK000552	Hs.323518	WD repeat domain 5	7.00				
121838	AA425680	Hs.98441	ESTs				10.40	
121857	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	6.00				
121991	AA430058	Hs.98649	EST				12.20	
122089	AW016543	Hs.98682	hypothetical protein FKSG32			8.60		
122105	AW241685	Hs.98699	ESTs			6.14		
122163	AA435702	Hs.98829	EST				10.40	
122318	AA429743		gb:zv60b05.r1 Soares_testis_NHT Homo sap				18.20	
122335	AA443258	Hs.241551	chloride channel, calcium activated, fam	13.50				
122338	AA443311	Hs.98998	ESTs	4.80				
122414	AI313473	Hs.99087	ESTs, Weakly similar to S47073 finger pr		8.00			

122512	AF053305	Hs.98658	budding uninhibited by benzimidazoles 1			8.80		
122516	AA449352	Hs.99217	ESTs				9.40	
122702	AI220089	Hs.99439	ESTs		9.20			
122852	AI580056	Hs.98992	ESTs				10.40	
122925	AW268962	Hs.111335	ESTs		6.80			
123005	AW369771	Hs.52620	Integrin, beta 8			12.60		
123044	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro					5.35
123160	AA488687	Hs.284235	ESTs, Weakly similar to I38022 hypotheti			6.06		
123315	AA496369		gb:zv37d10.s1 Soares ovary tumor NbHOT H			12.40		
123329	Z47542	Hs.179312	small nuclear RNA activating complex, po			11.80		
123497	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein		12.00			
123518	AL035414	Hs.21068	hypothetical protein			13.00		
123519	AW015887	Hs.112574	ESTs		12.20			
123614	AK000492	Hs.98806	hypothetical protein			7.80		
123616	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L				10.60	
123673	BE550112	Hs.158549	ESTs, Weakly similar to T2D3_HUMAN TRANS	23.00				
123727	AI083986	Hs.282977	hypothetical protein FLJ13490		7.00			
123731	AA609839		gb:ae62f01.s1 Stratagene lung carcinoma			9.80		
123752	AA227714	Hs.179703	KIAA0129 gene product	3.50				
123900	AA621223	Hs.112953	EST				12.80	
124006	AI147155	Hs.270016	ESTs	97.00				
124059	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	3.02				
124069	AF134160	Hs.7327	claudin 1			27.80		
124191	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha				35.80	
124273	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma		7.20			
124297	AL080215	Hs.102301	Homo sapiens mRNA; cDNA DKFZp586J0323 (f				11.00	
124305	AW963221		gb:EST375294 MAGE resequences, MAGH Homo				16.00	
124676	AI360119.comp	Hs.181013	phosphoglycerate mutase 1 (brain)					6.08
124874	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog				21.00	
124904	AK000483	Hs.93872	KIAA1682 protein		9.40			
124969	AI650360	Hs.100256	ESTs				10.80	
125000	T58615	Hs.110640	ESTs				9.80	
125201	AA693960	Hs.103158	ESTs, Weakly similar to T33296 hypotheti		7.60			
125266	W90022	Hs.186809	ESTs, Highly similar to LCT2_HUMAN LEUKO		6.59			
125299	T32982	Hs.102720	ESTs				9.57	
125356	AI057052	Hs.133554	ESTs, Weakly similar to Z195_HUMAN ZINC				14.00	
125370	AA256743	Hs.134158	Homo sapiens, Similar to KIAA0092 gene p			8.20		
125418	AA777690	Hs.188501	ESTs				13.20	
125433	AL162066	Hs.54320	hypothetical protein DKFZp762D096		21.40			
125437	AI609449	Hs.140197	ESTs		6.96			
125446	BE219987	Hs.166982	phosphatidylinositol glycan, class F		8.80			
125711	AA305800	Hs.5672	hypothetical protein AF140225				11.20	
125756	BE174587	Hs.289721	growth arrest specific transcript 5					4.31
125757	AI274906	Hs.166835	ESTs, Highly similar to 1814460A p53-ass				15.60	
125769	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	3.20				
125839	AW836261	Hs.337717	ESTs		8.20			
125850	W85858	Hs.99804	ESTs	2.65				
125875	H14480		gb:ym18b09.r1 Soares infant brain 1NIB H		7.40			
125924	BE272506	Hs.82109	syndecan 1					4.23
125972	AI927475	Hs.35406	ESTs, Highly similar to unnamed protein					3.98
126034	H60340		gb:yr39b04.r1 Soares fetal liver spleen				10.60	
126327	AA432266	Hs.44648	ESTs		11.60			
126345	N49713		gb:yv23f06.s1 Soares fetal liver spleen		6.67			
126435	AW614529	Hs.285847	CGI-19 protein				10.60	
126487	AA283809	Hs.184601	solute carrier family 7 (cationic amino					4.38
126521	AI475110	Hs.203933	ESTs		6.60			
126522	W31912		gb:zc76d03.s1 Pancreatic Islet Homo sapi				14.80	
126543	AL035864	Hs.69517	cDNA for differentially expressed CO16 g					4.01
126567	AA058394	Hs.57887	ESTs, Weakly similar to KIAA0758 protein			7.80		
126605	AA676910		gb:zj65h07.s1 Soares_fetal_liver_spleen_				11.60	
126627	AA497044	Hs.20887	hypothetical protein FLJ10392				14.60	
126628	N49776	Hs.170994	hypothetical protein MGC10946	8.00				
126737	AW976516	Hs.283707	Homo sapiens cDNA: FLJ21354 fis, clone C	2.92				
126795	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cer	7.50				
126802	AW805510	Hs.97056	hypothetical protein FLJ21634		11.60			
126892	AF121856	Hs.284291	sorting nexin 6	3.50				
126928	AA480902	Hs.137401	ESTs				22.83	
126979	AA210954		gb:zq89h10.r1 Stratagene hNT neuron (937				11.80	
126986	AI279892	Hs.46801	sorting nexin 14				11.60	
126992	AI809521		gb:wf30e03.x1 Soares_NFL_T_GBC_S1 Homo s				20.80	
127066	R25066		gb:yg42c07.r1 Soares infant brain 1NIB H				27.60	
127099	AA347668		gb:EST54026 Fetal heart II Homo sapiens				21.60	
127139	AA830233	Hs.293585	ESTs				11.20	
127209	AA305023	Hs.81964	SEC24 (S. cerevisiae) related gene famil	3.10				
127221	BE062109	Hs.241551	chloride channel, calcium activated, fam	2.76				
127225	AA315933	Hs.120879	ESTs				16.80	
127313	AK002014	Hs.47546	Homo sapiens cDNA FLJ11458 fis, clone HE	14.00				
127444	AW978474	Hs.7560	Homo sapiens mRNA for KIAA1729 protein,				13.60	
127500	AW971353	Hs.162115	ESTs		11.20			
127524	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin			7.80		
127540	N45572	Hs.105362	Homo sapiens, clone MGC:18257, mRNA, com	3.53				
127599	AA613204	Hs.150399	ESTs				13.80	
127609	X80031	Hs.530	collagen, type IV, alpha 3 (Goodpasture				28.00	
127662	W80755	Hs.8294	KIAA0196 gene product				19.80	
127668	AI343257	Hs.139993	ESTs				11.20	

127746	AI239495	Hs.120189	ESTs				14.18	
127812	AA741368	Hs.291434	ESTs	4.50				
127817	AA836641	Hs.163085	ESTs				24.60	
127959	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L				9.20	
127960	AI613226	Hs.41569	phosphatidic acid phosphatase type 2A				16.83	
127969	F06498	Hs.93748	Homo sapiens cDNA FLJ14676 fis, clone NT		13.60			
128015	Z21169	Hs.334659	hypothetical protein MGC14139		7.00			
128027	AI433721	Hs.164153	ESTs				37.40	
128077	AI310330	Hs.128720	ESTs				9.60	
128166	NM_006147	Hs.11801	Interferon regulatory factor 6				9.24	
128226	AI284940	Hs.289082	GM2 ganglioside activator protein	19.00				
128305	AI954968	Hs.279009	matrix Gla protein				10.40	
128341	AA191420	Hs.185030	ESTs		9.00			
128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul					4.30
128539	R46163	Hs.258618	ESTs		12.60			
128568	H12912	Hs.274691	adenylate kinase 3					4.56
128572	AA933022	Hs.256583	interleukin enhancer binding factor 3, 9				10.00	
128777	AI878918	Hs.10526	cysteine and glycine-rich protein 2			16.80		
128781	N71826	Hs.105465	small nuclear ribonucleoprotein polypept					4.48
128796	AJ000152	Hs.105924	defensin, beta 2		8.12			
128920	AA622037	Hs.166468	programmed cell death 5					4.62
128924	BE279383	Hs.26557	plakophilin 3					4.04
128971	H05132	Hs.107510	ESTs		12.60			
129008	AL079648	Hs.301088	ESTs		8.80			
129041	BE382756	Hs.169902	solute carrier family 2 (facilitated glu					6.05
129075	BE250162	Hs.83765	dihydrofolate reductase	2.59				
129105	AI769160	Hs.108681	Homo sapiens brain tumor associated prot			6.67		
129189	AB023179	Hs.9059	KIAA0952 protein		8.00			
129229	AF013758	Hs.109643	polyadenylate binding protein-interactin	4.00				
129241	AI878857	Hs.109706	hematological and neurological expressed					4.06
129300	W94197	Hs.110165	ribosomal protein L26 homolog	2.55				
129404	AI267700	Hs.317584	ESTs	18.00				
129457	X61959	Hs.207776	aspartylglucosaminidase	6.50				
129466	L42583	Hs.334309	keratin 6A	12.94				
129494	AI148976	Hs.112062	ESTs				11.00	
129605	AF061812	Hs.115947	keratin 16 (focal non-epidermolytic palm					4.46
129641	AI911527	Hs.11805	ESTs				12.00	
129665	AW163331	Hs.118778	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic					4.70
129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA					4.02
129720	AA156214	Hs.12152	APMCF1 protein					5.71
129748	M16707	Hs.123053	H4 histone, family 2	3.50				
129890	AI868872	Hs.282804	hypothetical protein FLJ22704					4.21
129896	BE295568	Hs.13225	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	2.56				
129945	BE514376	Hs.165998	PAI-1 mRNA-binding protein					4.03
130010	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34			7.00		
130026	T40480	Hs.332112	EST		6.40			
130080	X14850	Hs.147097	H2A histone family, member X					4.65
130149	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	2.74				
130285	AA063546	Hs.75981	ubiquitin specific protease 14 (tRNA-gua			7.40		
130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic					3.91
130482	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	4.87				
130500	AB007913	Hs.158291	KIAA0444 protein				9.60	
130524	U89995	Hs.159234	forkhead box E1 (thyroid transcription f			13.40		
130541	X05608	Hs.211584	neurofilament, light polypeptide (68kD)			8.20		
130553	AF062649	Hs.252587	pituitary tumor-transforming 1					6.06
130567	AA383092	Hs.1608	replication protein A3 (14kD)			7.00		
130577	M69241	Hs.162	insulin-like growth factor binding prote	3.04				
130627	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	3.87				
130648	AI458165	Hs.17296	hypothetical protein MGC2376				16.20	
130697	L29472	Hs.1802	major histocompatibility complex, class				17.80	
130744	H59696	Hs.18747	POP7 (processing of precursor, S. cerevi					5.28
130800	AI187292	Hs.19574	hypothetical protein MGC5469					4.43
130867	NM_001072	Hs.284239	UDP glycosyltransferase 1 family, polype	16.84				
130869	J03626	Hs.2057	uridine monophosphate synthetase (orotat					4.92
130925	AF093419	Hs.169378	multiple PDZ domain protein				9.60	
130994	W17044	Hs.327337	ESTs		12.40			
131028	AI879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	10.21				
131031	NM_001650	Hs.288650	aquaporin 4				9.80	
131041	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,				9.60	
131058	W28545	Hs.101514	hypothetical protein FLJ10342				17.00	
131090	AI143139	Hs.2288	visinin-like 1	2.74				
131112	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f			8.80		
131148	AW953575	Hs.303125	p53-induced protein PIGPC1	3.12				
131185	BE280074	Hs.23960	cyclin B1	3.07				
131200	BE540516	Hs.293732	hypothetical protein MGC3195	3.07				
131219	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	2.87				
131257	AW339037	Hs.24908	ESTs				14.67	
131375	AW293165	Hs.143134	ESTs			19.20		
131460	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	3.50				
131476	AI521663	Hs.334644	hypothetical protein FLJ14668	15.00				
131510	BE245374	Hs.27842	hypothetical protein FLJ11210			7.80		
131646	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom			7.00		
131786	BE000971	Hs.306083	Novel human gene mapping to chomosome 22	2.65				
131839	AB014533	Hs.33010	KIAA0633 protein				35.20	
131843	AA192315	Hs.184062	putative Rab5-interacting protein					4.11

131877	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	19.00				
131885	BE502341	Hs.3402	ESTs	6.48				
131921	AA456093	Hs.34720	ESTs			8.40		
131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	56.00				
131958	NM_014062	Hs.3566	ART-4 protein					3.82
131965	W79283	Hs.35962	ESTs	3.03				
132000	AW247017	Hs.36978	melanoma antigen, family A, 3		9.80			
132040	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	3.30				
132109	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	21.00				
132114	NM_006152	Hs.40202	lymphoid-restricted membrane protein		8.40			
132162	AA315805	Hs.94560	desmoglein 2					12.25
132164	AI752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio	2.70				
132180	NM_004460	Hs.418	fibroblast activation protein, alpha	2.71				
132181	AW961231	Hs.16773	Homo sapiens clone TCCCIA00427 mRNA sequ	3.83				
132182	NM_014210	Hs.70499	ecotropic viral integration site 2A				13.20	
132231	AA662910	Hs.42635	hypothetical protein DKFZp434K2435	9.50				
132277	AK001745	Hs.184628	hypothetical protein FLJ10883	4.50				
132328	NM_014787	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe				9.20	
132394	AK001680	Hs.30488	DKFZP434F091 protein				19.80	
132424	AA417878	Hs.48401	ESTs, Moderately similar to ALU8_HUMAN A			8.60		
132528	T78736	Hs.50758	SMC4 (structural maintenance of chromoso			27.40		
132543	BE568452	Hs.5101	protein regulator of cytokinesis 1	4.38				
132544	L19778	Hs.51011	H2A histone family, member P		7.00			
132550	AW969253	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.64				
132552	BE621985	Hs.296922	thiopurine S-methyltransferase				15.83	
132581	AK000631	Hs.52256	hypothetical protein FLJ20624			6.60		
132617	AF037335	Hs.5338	carbonic anhydrase XII	4.95				
132638	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992		8.20			
132653	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	4.38				
132669	W38586	Hs.293981	guanine nucleotide binding protein (G pr					4.36
132710	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	4.60				
132771	Y10275	Hs.56407	phosphoserine phosphatase	3.71				
132799	W73311	Hs.169407	SAC2 (suppressor of actin mutations 2,				9.48	
132833	U78525	Hs.57783	eukaryotic translation initiation factor					5.83
132892	AW834050	Hs.9973	tensin				12.00	
132906	BE613337	Hs.234896	geminin	3.09				
132959	AW014195	Hs.61472	ESTs, Weakly similar to YAE6_YEAST HYPOT					3.87
132962	AA576635	Hs.6153	CGI-48 protein	3.50				
132990	X77343	Hs.334334	transcription factor AP-2 alpha (activat	6.18				
132994	AA112748	Hs.279905	clone HQ0310 PRO0310p1	3.19				
133000	AL042444	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	2.96				
133050	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	2.55				
133083	BE244588	Hs.6456	chaperonin containing TCP1, subunit 2 (b					4.00
133086	L17131	Hs.139800	high-mobility group (nonhistone chromoso					8.96
133134	AF198620	Hs.65648	RNA binding motif protein 8A					4.28
133155	M58583	Hs.662	cerebellin 1 precursor				10.80	
133181	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	3.00				
133204	BE267696	Hs.254105	enolase 1, (alpha)					4.63
133412	U41493	Hs.73112	guanine nucleotide binding protein (G pr		12.50			
133421	AF134160	Hs.7327	claudin 1	2.85				
133451	AW970026	Hs.73818	ubiquinol-cytochrome c reductase hinge p					4.66
133453	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept		6.80			
133504	NM_004415	Hs.74316	desmoplakin (DPI, DPII)	6.14				
133506	BE562958	Hs.74346	hypothetical protein MGC14353					4.55
133615	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,				17.80	
133627	NM_002047	Hs.75280	glycyl-tRNA synthetase					4.85
133649	U25849	Hs.75393	acid phosphatase 1, soluble					6.34
133669	NM_006925	Hs.166975	splicing factor, arginine/serine-rich 5				14.00	
133749	L20852	Hs.10018	solute carrier family 20 (phosphate tran			6.11		
133776	BE268649	Hs.177766	ADP-ribosyltransferase (NAD+; poly (ADP-					4.91
133865	AB011155	Hs.170290	discs, large (Drosophila) homolog 5	3.07				
133946	AJ001258	Hs.173878	NIPSNAP, C. elegans, homolog 1					4.60
133973	N55540	Hs.78026	ESTs, Weakly similar to similar to ankyr				13.00	
134047	BE262529	Hs.78771	phosphoglycerate kinase 1					3.85
134098	BE513171	Hs.79086	mitochondrial ribosomal protein L3	2.56				
134107	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte			8.20		
134112	AW449809	Hs.79150	chaperonin containing TCP1, subunit 4 (d					4.08
134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	31.00				
134160	T98152	Hs.79432	fibrillin 2 (congenital contractural ara			24.60		
134168	AA398908	Hs.181634	Homo sapiens cDNA: FLJ23602 fis, clone L					6.71
134185	AA285136	Hs.301914	neuronal specific transcription factor D				14.74	
134201	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5		8.40			
134272	X76040	Hs.278614	protease, serine, 15	4.50				
134276	BE083936	Hs.80976	antigen identified by monoclonal antibod		9.00			
134353	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m				16.40	
134367	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	2.80				
134380	AU077143	Hs.179565	minichromosome maintenance deficient (S.	4.68				
134423	H53497	Hs.83006	CGI-139 protein					3.84
134469	AA279661	Hs.83753	small nuclear ribonucleoprotein polypept					5.81
134470	X54942	Hs.83758	CDC28 protein kinase 2					4.21
134498	AW246273	Hs.84131	threonyl-tRNA synthetase					7.30
134502	BE148534	Hs.84168	UV-B repressed sequence, HUR 7		13.60			
134510	NM_002757	Hs.250870	mitogen-activated protein kinase kinase				9.70	
134548	N95406	Hs.333495	Deleted in split-hand/split-foot 1 regio					4.63
134654	AK001741	Hs.8739	hypothetical protein FLJ10879	6.00				

134724	AF045239	Hs.321576	ring finger protein 22				12.00	
134743	AA044163	Hs.89463	potassium large conductance calcium-acti	4.00				
134781	AA374372	Hs.89626	parathyroid hormone-like hormone			25.20		
134806	AD001528	Hs.89718	spermine synthase					4.58
134853	BE268326	Hs.90280	5-aminoimidazole-4-carboxamide ribonucle					4.79
134859	D26488	Hs.90315	KIAA0007 protein			6.20		
134891	R51083	Hs.90787	ESTs			7.40		
134960	BE246400	Hs.285176	acetyl-Coenzyme A transporter	4.00				
134993	BE409809	Hs.301005	purine-rich element binding protein B					4.48
135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	9.50				
135080	AI761180	Hs.94211	rcd1 (required for cell differentiation,	5.00				
135103	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)		11.00			
135145	AW014729	Hs.95262	nuclear factor related to kappa B bindin					4.01
135184	U13222	Hs.96028	forkhead box D1			7.00		
135242	AI583187	Hs.9700	cyclin E1	13.50				
135286	AW023482	Hs.97849	ESTs	6.46				
135289	AW372569	Hs.9788	hypothetical protein MGC10924 similar to		8.80			
135355	AK001652	Hs.99423	ATP-dependent RNA helicase	10.00				
135371	NM_006025	Hs.997	protease, serine, 22	8.00				
135393	L11244	Hs.99886	complement component 4-binding protein,				14.60	

TABLE 5B shows the accession numbers for those primekeys lacking unigeneID's for Table 5A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
117079	1621717_1	H92325 T97125
124305	242183_1	AW963221 AA344870 AA344871 H93331
101502	18202_-6	M26958
109792	754958_1	R49625 F10674
126034	1598157_1	H60340 N91637
102768	44641_1	U82321 H66077
126345	1653833_1	N49713 N49819 W03810
127066	1703458_1	R25066 R20144 R20145 Z43845
127099	244301_1	AA347668 AW956810 Z44271 F07065 F07064 R13506
119243	1774795_1	T12603 T12604
125875	1566433_1	H14480 N98295
112054	1538292_1	R43590 F10439
126979	171411_1	AA210954 AA211007
126992	880655_1	AI809521 H12174 Z42556
122318	292419_1	AA429743 AA442754
114699	135322_1	AA127386 R15644 AA127404
114793	150742_1	AA158245 AA158235
108305	111550_1	AA071391 AA069892 AA069891
108393	113411_1	AA075211 AA075245 AA075126 AA074946
100867	tigr_HT4586	U14622
123731	genbank_AA609839	AA609839
109700	genbank_F09609	F09609
120715	genbank_AA292700	AA292700
113702	genbank_T97307	T97307
115113	genbank_AA256460	AA256460
101045	entrez_J05614	J05614
108554	genbank_AA084948	AA084948
108573	genbank_AA086005	AA086005
119052	149538_1	R10889 R10888
126522	416020_1	W31912 AI167491
126605	439280_1	AA676910 AA778853 AA778865 W86800
103768	46922_1	W42667 AI560740 AI690440 AI561350 AW467906 AW151450 AI625927 AL041716 AI885600 AI742213 AW248624 AI955498 AA033947 AA845593 AI623711 N68583 C00064 AA193567 AW083868 AW163216 AA191595 AA522778 AI628008 AI915518 AA843508 AI926195 AA176265 AW167963 AA992115 W93647 AW103572 AI862994 AI342059 AA911719 AA176155 AA024712 AA069988 AA205591 AI591107 AI199673 AI811766 AI275832 AI422233 AI191852 AI096682 AI580124 AI683612 AA582453 AA927559 AA486415 T32414 AI084978 H44849 H44848 H20477 T91695 W47039 AA070055 AA024795 AA328855 AA379248 AA379330 AA385580 W25920 W03688 AA448359 AA093881 AW362477 AA089997 AI350265 W93479 N99688 AA932257 AW351469 H68590 AA663402 AA069771 AW087986 AI858420 AA600214 AI970774 AI857712 AI683081 AI885584 AW131150 AI567981 AW002714 AW189973 AW075495 AW168303 AA953714 AW516881 AI357375 AI566663 AW512676 AI570580 AI023690 AA448216 AI079853 AI422707 AA779516 AW026972 AW130082 AW162307 AW438646 AA709332 AW192394 AI167350 AI217879 AI129152 AA719509 AI350480 AA663418 AI003634 AW118546 AA180261 AA442833 AI268625 AA888881 AI038759 AA846723 AI248770 AA993694 AI280335 AI885107 AW518649 AA641563 AA995835 AA582521 AI276744 AA436478 AI017360 AI620763 AI859887 N73926 AI076327 AI741615 AI160617 AW172819 AI492005 AA677429 AA996334 AI693771 AI950039 AI245629 AI288515 AI866186 T93293 AA173262 AA599779 AI680092 AW439316 AI084555 AI272672 AI583507 AW473219 AA738132 AW473283 AI367492 AA995410 AI689624 AA206353 AI033095 AI040382 AA873630 AI221074 AI934840 AI418680 AA844306 R94503 AA773520 AA843169 AA219425 AA629658 AI811719 AW411275 AI590981 W37907 AI591178 AI684051 AA983238 AA669347 AA976239 AA704570 AI628339 AI884391 AI241580 AI003539 AW176687 AA009650 N34566 AI333493 AI186070 AA070827 AA411683 AI280884 AA872023 AA207255 AA021576 N71953 AI885888 AW076039 T15777 AI537673 AW248048 H09554 W93480 W47001 AW079114 AA063160 AA757453 R60788 AI859431 H20478 AA218882 AA757465 AA100995 AI864135 AI934209 AA070503 H47008 AA219646 W61039 W93907 AW385050 W37967 W78028 AA189007 AA479136 R93650 AA442312 T30287 AA847628 AA180262 AA009649 C03892 AW149464 AA310963 AA219693 AA069747 R29207 AA094784 AA293615 AA447848 AI984167 N90393 C05097 N56499 AW292351 AW149681 AW473258 AA629322 AI004409 AW105577 AI954937 AI811070 AA902422 AW514437 AA535460 AA916877 AW517122 AA974657 AA975649 AW517130 AW517129 F31737 W07688 AA193645 AA378994 AA489273 F32267 W39303 AA021181 N86810 AA406524 AA062553 AA436801 H08985 H15979 N40310

AA436789 AA232172 AW360778 W25862 R60282 AA436530 AA378894 AA187461 AI940535 AA604210 AA089514 AA360421 N88243 N84281 AA209340 N56174 N88374 AA191088 AW247691 AA249013 AA093111 AA972536 AW298594 AA375893 T12139 W28186 AW243849 AI288629 AA843996 W15260 AI188286 AW248079 R15836

119599	genbank_W45552	W45552
112382	genbank_R59904	R59904
105264	genbank_AA227934	AA227934
100071	entrez_A28102	A28102
123315	714071_1	AA496369 AA496646

Table 6A shows 99 genes up-regulated nonsmokers with lung cancer relative to smokers with lung cancer. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: average of AI for samples from non-smokers with adenocarcinoma divided by the 90th percentile of AI for samples from smokers with adenocarcinoma
R2: average of AI for samples from non-smokers with squamous cell carcinoma divided by the 90th percentile of AI for samples from smokers with squamous cell carcinoma

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte		3.64
101174	L17330	Hs.280	pre-T/NK cell associated protein	15.00	
101296	Y12490	Hs.85092	thyroid hormone receptor interactor 11		2.46
101304	AA001021	Hs.6685	thyroid hormone receptor interactor 8		12.00
101806	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias		2.68
101972	S82472		gb:beta -pol=DNA polymerase beta {exon a		2.11
102274	U30930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose	7.50	
102394	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.50	
102832	U92015		gb:Human clone 143789 defective mariner	13.50	
103010	X52509	Hs.161640	tyrosine aminotransferase	9.50	
103439	X98266		gb:H.sapiens mRNA for ligase like protei		2.50
103563	L02911	Hs.150402	activin A receptor, type I	9.00	
103857	AI076795	Hs.45033	lacrimal proline rich protein		3.94
104239	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	13.50	
104590	AW373062	Hs.83623	nuclear receptor subfamily 1, group I, m		12.66
104907	AA055829	Hs.196701	ESTs, Weakly similar to ALU1_HUMAN ALU	16.50	
106131	BE514788	Hs.296244	SNARE protein		2.17
106672	H47233	Hs.30643	ESTs	7.00	
106872	T56887	Hs.18282	KIAA1134 protein	11.50	
106960	AA156238	Hs.32501	ESTs		2.38
106971	Z43846	Hs.194478	Homo sapiens mRNA; cDNA DKFZp434O1572 (f	9.50	
107982	AA035375	Hs.57887	ESTs, Weakly similar to KIAA0758 protei		2.95
108562	AA100796		gb:zm26c06.s1 Stratagene pancreas (93720	16.50	
108599	AB018549	Hs.69328	MD-2 protein	13.00	
108663	BE219231	Hs.292653	ESTs, Weakly similar to T26845 hypotheti		2.40
109247	AA314907	Hs.85950	ESTs	7.00	
109630	R44607	Hs.22672	ESTs		5.00
110193	AI004874	Hs.310764	Homo sapiens mRNA; cDNA DKFZp434M082 (fr	12.50	
110234	H24458	Hs.32085	EST	16.50	
110644	R94207	Hs.268989	ESTs, Highly similar to type II CALM/AF1	8.00	
110886	AW274992	Hs.72249	three-PDZ containing protein similar to	17.00	
111057	T79639	Hs.14629	ESTs	16.50	
111950	AF071594	Hs.110457	Wolf-Hirschhorn syndrome candidate 1	11.00	
112291	R53972	Hs.26026	ESTs		3.00
112956	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)		2.79
113009	T23699	Hs.7246	ESTs		4.50
113060	BE564162	Hs.250820	hypothetical protein FLJ14827	9.79	
113073	N39342	Hs.103042	microtubule-associated protein 1B	32.50	
113074	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t		3.82
113121	T48011	Hs.8764	EST		2.21
113125	AA968672	Hs.8929	hypothetical protein FLJ11362	19.50	
113757	AA703095	Hs.18631	ESTs		2.65
113848	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	6.00	
113884	AI333076	Hs.28529	chromosome 12 open reading frame 2		6.00
113936	W17056	Hs.83623	nuclear receptor subfamily 1, group I, m		4.63
114875	AA235609	Hs.236443	Homo sapiens mRNA; cDNA DKFZp564N1063 (		7.00
114987	AA251016	Hs.87808	EST		6.00
115460	AW958439	Hs.38613	ESTs		2.27
115722	W91892	Hs.59609	ESTs		9.00
116261	AA481788	Hs.190150	ESTs	9.50	
116830	H61037	Hs.70404	ESTs, Weakly similar to ALU2_HUMAN ALU	8.50	
116970	AB023179	Hs.9059	KIAA0962 protein	7.50	
117178	H98675	Hs.269034	ESTs		2.68
117757	AF088019	Hs.46732	EST	7.50	
118283	AA287747	Hs.173012	ESTs, Weakly similar to A46010 X-linked	16.50	
118384	AF217525	Hs.49002	Down syndrome cell adhesion molecule		2.50
118657	AI822106	Hs.49902	ESTs		2.39
120328	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi		3.50
120404	AB023230	Hs.96427	KIAA1013 protein	7.00	
120524	AA261852	Hs.192905	ESTs	6.00	
120688	AW207555	Hs.97093	Homo sapiens cDNA: FLJ23004 fis, clone L	17.92	

121558	AA412497		gb:zt95g12.s1 Soares_testis_NHT Homo sap		2.95
121676	H56037	Hs.108146	ESTs	10.00	
121936	AI024600	Hs.98612	ESTs	15.00	
121938	AA428659	Hs.98610	ESTs	14.00	
122177	AA435789	Hs.98833	EST	8.93	
123442	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	13.04	
123551	AA608837		gb:af03h12.s1 Soares_testis_NHT Homo sap	11.50	
123756	AA609971	Hs.112795	EST	11.00	
123861	AA620840		gb:af89g01.s1 Soares_testis_NHT Homo sap		2.50
124371	N24924	Hs.188601	ESTs	6.50	
127477	BE328720	Hs.280651	ESTs		4.33
127591	AI190540	Hs.131092	ESTs		3.02
128252	AA455924	Hs.192228	ESTs	7.00	
128426	AI265784	Hs.145197	ESTs		2.08
128925	R67419	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT		2.11
128945	AI990506	Hs.8077	Homo sapiens mRNA; cDNA DKFZp547E184 (fr	10.00	
129105	AI769160	Hs.108681	Homo sapiens brain tumor associated prot	15.50	
129235	AW977238	Hs.126084	KIAA1055 protein		4.25
129506	AB020684	Hs.11217	KIAA0877 protein	6.50	
129595	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9		10.00
130160	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	20.00	
130340	D82326	Hs.239106	solute carrier family 3 (cystine, dibasi	11.50	
131220	AB023194	Hs.300855	KIAA0977 protein	17.50	
131430	AI879148	Hs.26770	fatty acid binding protein 7, brain	6.10	
132114	NM_006152	Hs.40202	lymphoid-restricted membrane protein		6.15
132458	AA935315	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone C		5.58
132647	NM_006927	Hs.54432	sialyltransferase 4B (beta-galactosidase	7.50	
132655	D49372	Hs.54460	small inducible cytokine subfamily A (Cy		2.53
132682	AI077500	Hs.54900	serologically defined colon cancer antig		2.50
132747	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein		2.83
132812	R50333	Hs.92186	Leman coiled-coil protein		3.82
133337	AF085983	Hs.293676	ESTs		5.00
133876	AL134906	Hs.771	phosphorylase, glycogen; liver (Hers dis		3.00
134119	AW157837	Hs.79226	fasciculation and elongation protein zet		2.06
134464	AA302983	Hs.239720	CCR4-NOT transcription complex, subunit		2.27
134542	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi		11.50
135002	AA448542	Hs.251677	G antigen 7B	87.00	
135305	AA203555	Hs.98288	Homo sapiens cDNA FLJ14903 fis, clone PL		6.50

TABLE 6B show the accession numbers for those primekeys lacking unigeneID's for Table 6A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
108562	36375_1	AA100796 AF020589 AA074629 AA075946 AA100849 AA085347 AA126309 AA079311 AA079323 AA085274
103439	35330_1	X98266 N41124
123551	genbank_AA608837	AA608837
123861	genbank_AA620840	AA620840
102832	entrez_U92015	U92015
101972	entrez_S82472	S82472
121558	genbank_AA412497	AA412497

Table 7A shows 98 genes down-regulated in non-smokers with lung cancer relative to smokers with lung cancer. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: 90th percentile of AI for samples from smokers with adenocarcinoma divided by the average of AI for samples from non-smokers with adenocarcinoma.
R2: 90th percentile of AI for samples from smokers with squamous cell carcinoma divided by the average of AI for samples from non-smokers with squamous cell carcinoma.

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3		164.10
100380	D82343	Hs.18551	neuroblastoma (nerve tissue) protein		77.40
100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	102.40	
100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	463.80	
101046	K01160		(NONE)	672.00	
101066	AW970254	Hs.889	Charot-Leyden crystal protein	66.00	
101175	U82671	Hs.36980	melanoma antigen, family A, 2		77.20
101497	W05150	Hs.37034	homeo box A5	62.80	
101663	NM_003528	Hs.2178	H2B histone family, member Q	78.00	
101677	NM_000715	Hs.1012	complement component 4-binding protein,	186.20	
101745	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci	80.08	
101941	S77583		gb:HERVK10/HUMMTV reverse transcriptase	99.20	
102125	NM_006456	Hs.288215	sialyltransferase		103.10
102242	U27185	Hs.82547	retinoic acid receptor responder (tazaro	67.00	
102340	U37055	Hs.278657	macrophage stimulating 1 (hepatocyte gro	71.60	
102369	U39840	Hs.299867	hepatocyte nuclear factor 3, alpha		69.70
102457	NM_001394	Hs.2359	dual specificity phosphatase 4	153.00	
102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2		65.70
102796	AL079646	Hs.107019	symplekin; Huntingtin interacting protei		58.80
102829	NM_006183	Hs.80962	neurotensin		268.80
103207	X72790		gb:Human endogenous retrovirus mRNA for	70.00	
103242	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o		212.10
103260	X78416	Hs.3155	casein, alpha		130.70
103351	X89211		gb:H.sapiens DNA for endogenous retrovir	64.60	
104212	AB002298	Hs.173035	KIAA0300 protein	66.80	
104252	AF002246	Hs.210863	cell adhesion molecule with homology to	63.80	
104258	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	94.40	
105024	AA126311	Hs.9879	ESTs	68.20	
106260	AI097144	Hs.5250	ESTs, Weakly similar to ALU1_HUMAN ALU S		74.60
106440	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub		71.10
106566	BE298210		gb:601118016F1 NIH_MGC_17 Homo sapiens c	73.20	
106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	83.80	
106614	AA648459	Hs.335951	hypothetical protein AF301222		62.30
106654	AW075485	Hs.286049	phosphoserine aminotransferase		202.40
106999	H93281	Hs.10710	hypothetical protein FLJ20417		89.60
108700	AA121518	Hs.193540	ESTs, Moderately similar to 2109260A B c		66.40
108810	AW295647	Hs.71331	hypothetical protein MGC5350		95.50
108857	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act		63.40
109597	AA989362	Hs.293780	ESTs	85.00	
109691	T65568	Hs.12860	ESTs		58.70
109704	AI743880	Hs.12876	ESTs		60.60
110942	R63503	Hs.28419	ESTs	76.40	
111722	R23924	Hs.23596	EST	74.60	
112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-li	64.80	
112992	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f		76.70
113073	N39342	Hs.103042	microtubule-associated protein 1B		120.20
114251	H15261	Hs.21948	ESTs	127.20	
115230	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	174.00	
115291	BE545072	Hs.122579	hypothetical protein FLJ10461		91.00
115815	AW905328	Hs.180842	ribosomal protein L13	66.40	
115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH		226.60
115965	AA001732	Hs.173233	hypothetical protein FLJ10970	82.80	
116107	AL133916	Hs.172572	hypothetical protein FLJ20093		361.60
116552	D20508	Hs.164649	hypothetical protein DKFZp434H247	69.00	
116571	D45652		gb:HUMGS02848 Human adult lung 3' direct	64.20	
118466	N66741		gb:yz33g08.s1 Morton Fetal Cochlea Homo		63.50
120484	AA253170	Hs.96473	EST	81.60	
120983	AA398209	Hs.97587	EST		81.10
121034	AL389951	Hs.271623	nucleoporin 50kD		66.20
121423	AW973352	Hs.290585	ESTs	64.40	
122553	AA451884	Hs.190121	ESTs		60.40
122946	AI718702	Hs.308026	major histocompatibility complex, class	188.60	
123130	AA487200		gb:ab19f02.s1 Stratagene lung (937210) H		80.20
124472	N52517	Hs.102670	EST	71.00	
124526	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci		104.90
125489	H49193	Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A		72.00
125731	R61771	Hs.26912	ESTs		69.90
125747	NM_002884	Hs.865	RAP1A, member of RAS oncogene family	69.00	
126020	H79863	Hs.114243	ESTs		62.40
126547	U47732	Hs.84072	transmembrane 4 superfamily member 3		62.80
126966	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra		60.10

127472	AA761378	Hs.192013	ESTs	70.20	
127610	AA960867	Hs.150271	ESTs, Highly similar to unnamed protein	64.00	
127742	AW293496	Hs.180138	ESTs	85.20	
127987	AI022103	Hs.124511	ESTs	96.60	
128233	AW889132	Hs.11916	ribokinase		78.90
128420	AA650274	Hs.41296	fibronectin leucine rich transmembrane p		106.90
128766	AW160432	Hs.296460	craniofacial development protein 1	66.80	
129014	AW935187	Hs.170162	KIAA1357 protein		58.53
129215	AB040930	Hs.126085	KIAA1497 protein	64.20	
130090	H97878	Hs.132390	zinc finger protein 36 (KOX 18)	63.80	
130385	AW067800	Hs.155223	stanniocalcin 2		139.60
130732	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)		64.60
131025	AB040900	Hs.6189	KIAA1467 protein	64.40	
131241	BE501914	Hs.24654	Homo sapiens cDNA FLJ11640 fis, clone HE	76.20	
131775	AB014548	Hs.31921	KIAA0648 protein	97.80	
132240	AB018324	Hs.42676	KIAA0781 protein		71.00
132856	NM_001448	Hs.58367	glypican 4		88.40
132977	AA093322	Hs.301404	RNA binding motif protein 3	133.20	
133749	L20852	Hs.10018	solute carrier family 20 (phosphate tran		59.30
133818	AI110684	Hs.7645	fibrinogen, B beta polypeptide	341.00	
134264	AF149297	Hs.8087	NAG-5 protein		64.30
134265	M83772	Hs.80876	flavin containing monooxygenase 3		232.53
134346	X84002	Hs.82037	TATA box binding protein (TBP)-associate	66.00	
134395	AA456539	Hs.8262	lysosomal-associated membrane protein 2		75.80
135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su		108.30
135056	N75765	Hs.93765	lipoma HMGIC fusion partner	71.40	
135309	AI564123	Hs.42500	ADP-ribosylation factor-like 5	70.40	

TABLE 7B shows the accession numbers for those primekeys lacking unigeneID's for Table 7A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
103207	30635_-4	X72790
106566	120358_1	BE298210 AI672315 AW086489 BE298417 AA455921 AA902537 BE327124 R14963 AA085210 AW274273 AI333584 AI369742 AI039658 AI885095 AI476470 AI287650 AI885299 AI985381 AW592624 AW340136 AI266556 AA456390 AI310815 AA484951
116571	genbank_D45652	D45652
118466	genbank_N66741	N66741
101046	entrez_K01160	K01160
101941	entrez_S77583	S77583
103351	entrez_X89211	X89211
123130	genbank_AA487200	AA487200

Table 8A shows 1720 genes either up or down-regulated in lung tumors or chronically diseased lung relative to a broad collection of over 40 distinct normal body tissues. Chronically diseased lung samples represent chronic non-malignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 39494 probesets on the Eos/Affymetrix Hu02 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: 70th percentile of AI for lung tumors divided by 90th percentile of AI for normal lung
R2: 70th percentile of AI for chronically diseased lung divided by 90th percentile of AI for normal lung

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
300097	AI916973	Hs.213603	ESTs	5.46	4.69
300117	AW189787	Hs.147474	ESTs	0.58	0.56
300197	AI686661	Hs.218286	ESTs	4.26	5.44
300201	AI308300		gb:ta90c06.x1 NCI_CGAP_Bm20 Homo sapien	0.62	0.83
300225	AI989963	Hs.197505	ESTs	1.68	1.75
300247	AW274682	Hs.161394	ESTs	1.08	2.28
300256	AI469095	Hs.298241	Transmembrane protease, serine 3	0.86	1.00
300337	AI707881	Hs.202090	ESTs	5.80	9.09
300362	Z42308		gb:HSC0FB121 normalized infant brain cDN	4.18	12.78
300374	AI859947	Hs.314158	ESTs	2.99	4.38
300387	AW270150	Hs.254516	ESTs	1.50	2.53
300440	AI421541	Hs.146164	ESTs	3.98	5.25
300441	R10367	Hs.307921	EST, Weakly similar to Z232_HUMAN ZINC F	3.18	6.80
300449	AI362967	Hs.132221	hypothetical protein FLJ12401	0.43	0.62
300469	AW135830	Hs.233955	hypothetical protein FLJ20401	0.16	0.83
300552	X85711	Hs.21838	hypothetical protein FLJ11191	4.10	9.75
300627	W27363		gb:ab37d01.r1 Stratagene HeLa cell s3 93	4.60	12.60
300630	AW118822	Hs.128757	ESTs	2.91	5.86
300716	AI216113	Hs.126280	hypothetical protein FLJ23393	1.00	0.92
300738	AI623332	Hs.130541	KIAA1542 protein	1.82	1.71
300777	AA235361	Hs.96840	KIAA1527 protein	4.48	8.22
300790	AI492471	Hs.188270	ESTs	1.29	1.18
300832	AI688147	Hs.220615	ESTs, Weakly similar to T03829 transcrip	5.51	8.56
300836	Z44942	Hs.22958	calcium channel alpha2-delta3 subunit	4.90	6.34
300838	AI582897	Hs.192570	hypothetical protein FLJ22028	1.70	2.81
300878	AW449802	Hs.285901	Homo sapiens cDNA FLJ20428 fis, clone KA	4.56	7.91
300897	AI890356	Hs.127804	ESTs, Weakly similar to T17233 hypotheti	2.23	1.58
300926	AA504860		gb:ab03a10.s1 Stratagene fetal retina 93	2.13	3.50
300960	AI041019	Hs.152454	ESTs	2.74	4.46
300961	AW204069	Hs.312716	ESTs, Weakly similar to unnamed protein	1.00	1.00
300962	AA593373	Hs.293744	ESTs	1.46	1.51
300967	AA565209	Hs.269439	ESTs	0.39	1.30
300987	AW450840	Hs.148590	ESTs, Weakly similar to AF208846 1 BM-00	1.49	1.08
300988	AI927208	Hs.208952	ESTs	0.16	0.37
301050	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen i	3.23	1.94
301098	AA677570	Hs.185918	ESTs	6.76	14.28
301157	AA729905	Hs.231916	ESTs	3.16	8.85
301162	AI142118	Hs.129004	ESTs	1.68	7.18
301170	AA737594	Hs.247606	ESTs	4.40	6.42
301192	AI808751	Hs.121188	ESTs	6.38	11.59
301193	AA758115	Hs.128350	ESTs, Weakly similar to JC5423 2-hydroxy	4.35	7.78
301267	AW297762	Hs.255690	ESTs	1.56	1.61
301281	AA843986	Hs.190586	ESTs	2.19	1.78
301341	AI819198	Hs.208229	ESTs	0.76	0.76
301382	AA912839	Hs.163369	ESTs	1.00	1.81
301407	AW450466	Hs.126830	ESTs	1.48	1.51
301452	AA975688	Hs.159955	ESTs	0.51	1.46
301483	AW272467	Hs.254655	Untitled	2.40	5.02
301494	AI678034	Hs.131099	ESTs	2.79	3.41
301521	AI733621	Hs.133011	zinc finger protein 117 (HPF9)	0.67	0.67
301531	AI077462	Hs.134084	ESTs	2.52	3.76
301580	AI878959	Hs.73737	splicing factor, arginine/serine-rich 1	7.41	11.92
301676	Z43570	Hs.27453	ESTs, Moderately similar to G01251 Rar p	8.31	10.70
301690	F05865	Hs.108323	ubiquitin-conjugating enzyme E2E 2 (homo	2.70	4.22
301718	F07744	Hs.7987	DKFZP434F162 protein	4.20	8.78
301799	AA384252	Hs.286132	D15F37 (pseudogene)	5.93	7.04
301804	AA581004	Hs.62180	anillin (Drosophila Scraps homolog), act	1.70	0.76
301822	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	1.58	1.36
301846	R20002	Hs.6823	hypothetical protein FLJ10430	1.00	1.00
301868	T71508	Hs.13861	ESTs, Weakly similar to pH sensitive max	2.88	5.49
301882	T78054		gb:yc97g09.r1 Soares infant brain 1NIB H	2.28	3.80
301905	AI991127	Hs.117202	ESTs	1.00	1.00
301948	AA344647	Hs.116724	aldo-keto reductase family 1, member B11	5.28	2.28
301960	AW070252	Hs.27973	KIAA0874 protein	5.38	6.48
302011	T91418	Hs.125156	transcriptional adaptor 2 (ADA2, yeast,	3.03	3.42
302016	N40834	Hs.23495	hypothetical protein FLJ11252	1.00	1.25
302041	NM_001501	Hs.129715	gonadotropin-releasing hormone 2	0.71	0.99
302072	AJ238381	Hs.132576	paired box gene 9	1.60	1.71
302094	AI286176	Hs.6786	ESTs	0.52	1.20
302095	AW044300	Hs.137506	Homo sapiens BAC clone RP11-120J2 from 7	2.75	4.93
302148	AW269618	Hs.23244	ESTs	3.04	3.87

302155	AI088485	Hs.144759	ESTs	0.45	1.15
302201	AJ006276	Hs.159003	transient receptor potential channel 6	0.33	0.84
302202	AF097159	Hs.159140	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	0.52	0.94
302206	AI937193	Hs.41143	phosphoinositide-specific phospholipase	2.76	3.65
302209	AF047445	Hs.159297	killer cell lectin-like receptor subfami	1.00	1.00
302235	AL049987	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	1.68	1.50
302290	AL117607	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	1.00	2.11
302328	AA354849	Hs.23240	Homo sapiens cDNA FLJ13496 fis, clone PL	9.38	13.08
302346	AL039101	Hs.194625	dynein, cytoplasmic, light intermediate	3.27	7.24
302360	AJ010901	Hs.198267	mucin 4, tracheobronchial	2.54	1.88
302384	Y08982	Hs.202676	synaptonemal complex protein 2	1.00	0.91
302406	U86751	Hs.211956	CD3-epsilon-associated protein; antisens	2.63	2.67
302409	AF155156	Hs.218028	adaptor-related protein complex 4, epsil	5.82	9.34
302423	AB028977	Hs.225974	KIAA1054 protein	3.66	3.18
302432	AL080068	Hs.272534	Homo sapiens mRNA; cDNA DKFZp564J062 (fr	2.44	6.77
302435	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	0.44	0.84
302437	AB024730	Hs.227473	UDP-N-acetylglucosamine:a-1,3-D-mannosid	4.18	5.64
302455	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	1.85	0.92
302472	AA317451	Hs.6335	SWI/SNF related, matrix associated, acti	2.04	2.13
302476	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSm8	1.44	1.89
302489	T80660	Hs.230424	Homo sapiens cDNA FLJ13540 fis, clone PL	0.51	1.10
302490	AA885502	Hs.187032	ESTs	2.64	4.87
302562	AJ005585	Hs.48956	gap junction protein, beta 6 (connexin 3	5.34	2.68
302566	AA085996	Hs.248572	hypothetical protein FLJ22965	1.00	1.21
302630	AB029488	Hs.272100	SMS3 protein	0.52	1.24
302634	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	1.00	1.00
302638	AA463798	Hs.102696	MCT-1 protein	1.58	1.02
302647	X57723	Hs.198273	NADH dehydrogenase (ubiquinone) 1 beta s	2.72	6.85
302655	AJ227892	Hs.146274	ESTs	1.00	4.32
302656	AW293005	Hs.70704	Homo sapiens, clone IMAGE:2823731, mRNA,	2.97	0.93
302668	AA580691	Hs.180789	S164 protein	0.80	0.95
302679	H65022		gb:yu66g11.r1 Weizmann Olfactory Epithel	1.68	5.04
302680	AW192334	Hs.38218	ESTs	2.70	7.98
302697	AJ001408		gb:Homo sapiens mRNA for immunoglobulin	4.25	8.13
302705	U09060		gb:Human immunoglobulin heavy chain, V-r	3.91	8.68
302711	L08442		gb:Human autonomously replicating sequen	2.20	2.73
302719	W69724	Hs.288959	hypothetical protein FLJ20920	0.54	1.02
302742	L12069		gb:Homo sapiens (clone WR4.10VH) anti-th	4.28	11.57
302755	AW384815	Hs.149208	KIAA1555 protein	1.57	2.38
302771	H98476	Hs.42522	ESTs	2.94	4.68
302789	AJ245067		gb:Homo sapiens mRNA for immunoglobulin	3.49	6.31
302795	AJ245313	Hs.272838	hypothetical protein FLJ10494	0.80	2.74
302802	Y08250		gb:H.sapiens mRNA for variable region of	1.13	0.77
302803	AA442824	Hs.293961	ESTs, Moderately similar to putative DNA	3.14	10.68
302812	N31301	Hs.152664	hypothetical protein FLJ20051	3.04	8.24
302847	X98940		gb:H.sapiens rearranged Ig heavy chain (	1.80	1.92
302885	AL137763	Hs.132127	hypothetical protein LOC57822	1.00	1.00
302943	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	0.53	0.67
302977	AW263124	Hs.315111	hypothetical protein FLJ12894	2.45	2.62
303006	AF078950	Hs.24139	Homo sapiens cDNA: FLJ23137 fis, clone L	4.88	8.61
303011	AF090405		gb:Homo sapiens clone 2A1 scFV antibody	1.41	1.86
303013	F07898	Hs.288968	RAB22A, member RAS oncogene family	1.51	1.19
303061	AF151882	Hs.27693	peptidylprolyl isomerase (cyclophilin)-l	0.72	0.76
303077	AF163305		gb:H.sapiens T-cell receptor mRNA	1.17	3.90
303090	AA443259	Hs.146286	kinesin family member 13A	4.08	6.46
303091	AF192913	Hs.130683	zinc finger protein 180 (HHZ168)	2.50	4.37
303094	AF195513	Hs.278953	Pur-gamma	5.38	8.38
303095	AF202051	Hs.134079	NM23-H8	3.26	4.08
303131	AW081061	Hs.103180	DC2 protein	2.02	1.83
303195	AA082211	Hs.233936	myosin, light polypeptide, regulatory, n	1.32	3.95
303196	AA082298	Hs.59710	ESTs	0.77	0.53
303216	AA581439	Hs.152328	ESTs	0.24	0.63
303222	AA333538	Hs.204501	hypothetical protein FLJ10534	3.56	6.22
303234	AA132255	Hs.143951	ESTs	2.28	3.17
303251	AW340037	Hs.115897	protocadherin 12	0.38	1.02
303295	AA205625	Hs.208067	ESTs	2.30	1.00
303297	T80072	Hs.13423	Homo sapiens clone 24468 mRNA sequence	1.86	4.48
303316	AF033122	Hs.14125	p53 regulated PA26 nuclear protein	0.10	0.80
303467	AA398801	Hs.323397	ESTs	4.54	9.65
303506	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	0.09	0.04
303552	AA359799	Hs.224662	ESTs, Weakly similar to unnamed protein	1.00	1.72
303598	AA382814		gb:EST96097 Testis I Homo sapiens cDNA 5	4.96	9.14
303637	AF056083	Hs.24879	phosphatidic acid phosphatase type 2C	2.06	2.02
303655	AA504702	Hs.258802	ATPase, (Na+)/K+ transporting, beta 4 po	1.00	1.24
303756	AI738488	Hs.115838	ESTs	1.08	1.43
303856	AA968589	Hs.180532	glucose phosphate isomerase	1.76	1.31
303893	N88597	Hs.113503	karyopherin (importin) beta 3	2.30	2.57
303907	AW467774	Hs.171880	polymerase (RNA) II (DNA directed) polyp	3.10	5.79
303946	AW474196	Hs.306637	Homo sapiens cDNA FLJ12363 fis, clone MA	5.06	11.86
303978	AW513315		gb:xo43c12.x1 NCI_CGAP_Ut1 Homo sapiens	5.14	7.31
303981	AW513804	Hs.278834	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.83	4.06
303990	AW515465		gb:xu71a11.x1 NCI_CGAP_Kid8 Homo sapiens	1.15	2.35
303998	AW516449		gb:xt68f05.x1 NCI_CGAP_Ut2 Homo sapiens	2.20	9.35
303999	AW516611		gb:xp70b11.x1 NCI_CGAP_Ov39 Homo sapiens	4.85	6.28
304006	AW517947		gb:xt66h02.x1 NCI_CGAP_Ut2 Homo sapiens	3.21	4.07

304008	AW518198	Hs.3297	ribosomal protein S27a	6.50	11.08
304009	AW518206	Hs.181165	eukaryotic translation elongation factor	1.88	3.27
304024	T03036		gb:FB21B7 Fetal brain, Stratagene Homo s	2.15	3.55
304026	T03160		gb:FB26F2 Fetal brain, Stratagene Homo s	5.88	11.80
304028	T03266		gb:FB7C1 Fetal brain, Stratagene Homo sa	5.59	13.46
304036	T16855	Hs.244621	ribosomal protein S14	6.55	14.43
304046	T54803		gb:yb42d06.s1 Stratagene fetal spleen (9	6.18	12.19
304061	T61521		gb:yb73g01.s1 Stratagene ovary (937217)	2.64	8.23
304063	T62536		gb:yc04c12.s1 Stratagene lung (937210) H	0.53	1.61
304097	R25376	Hs.177592	ribosomal protein, large, P1	6.49	11.67
304114	R78946		gb:yi87g02.s1 Soares placenta Nb2HP Homo	2.90	4.18
304122	H28966		gb:ym31a06.s1 Soares infant brain 1NIB H	1.00	2.76
304155	H68696		gb:yr78b06.s1 Soares fetal liver spleen	0.79	1.18
304203	N56929		gb:yy82d08.s1 Soares_multiple_sclerosis_	4.28	11.34
304234	W81608		gb:zd88h06.s1 Soares_fetal_heart_NbHH19W	6.47	11.03
304267	AA064862	Hs.73742	ribosomal protein, large, P0	1.34	1.16
304270	AA069711	Hs.297753	vimentin	3.40	5.40
304287	AA079286	Hs.78466	proteasome (prosome, macropain) 26S sub	2.93	4.42
304348	AA179868		gb:zp38g12.s1 Stratagene muscle 937209 H	3.98	10.96
304415	AA290747	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	3.32	5.99
304430	AA347682		gb:EST54044 Fetal heart II Homo sapiens	1.00	1.00
304456	AA411240		gb:zv26g05.s1 Soares_NhHMPu_S1 Homo sapi	1.42	3.33
304521	AA464716		gb:zx82c11.s1 Soares ovary tumor NbHOT H	2.18	1.15
304526	AA476427		gb:zx02c05.s1 Soares_total_fetus_Nb2HF8_	5.38	14.11
304542	AA482602	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.16	8.23
304546	AA486074	Hs.297681	serine (or cysteine) proteinase inhibito	0.55	1.20
304607	AA513322		gb:nh85e08.s1 NCI_CGAP_Br1.1 Homo sapien	1.95	2.10
304640	AA524440	Hs.111334	ferritin, light polypeptide	2.10	2.83
304650	AA527489	Hs.3463	ribosomal protein S23	3.33	12.62
304735	AA576453		gb:nm75h11.s1 NCI_CGAP_Co9 Homo sapiens	1.33	0.88
304760	AA580401		gb:nn13g09.s1 NCI_CGAP_Co12 Homo sapiens	3.68	8.14
304849	AA588157	Hs.13801	KIAA1685 protein	2.77	3.70
304917	AA602585	Hs.284136	PRO2047 protein	7.16	11.01
304921	AA603092	Hs.297753	vimentin	2.47	4.24
304966	AA613893	Hs.282435	ESTs	6.78	11.66
304987	AA618044	Hs.300697	immunoglobulin heavy constant gamma 3 (G	0.90	1.23
305016	AA626876		gb:zu89h05.s1 Soares_testis_NHT Homo sap	6.46	10.17
305034	AA630128		gb:ab99c04.s1 Stratagene lung (937210) H	1.00	1.00
305072	AA641012		gb:nr72a12.s1 NCI_CGAP_Pr24 Homo sapiens	5.68	11.59
305111	AA644187	Hs.303405	ESTs	1.48	1.37
305148	AA654070		gb:nt01g08.s1 NCI_CGAP_Lym3 Homo sapiens	1.76	4.61
305159	AA659166	Hs.275668	EST, Weakly similar to EF1D_HUMAN ELONG	1.00	2.15
305190	AA665955		gb:ag57d12.s1 Gessler Wilms tumor Homo s	5.31	8.14
305232	AA670052	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	0.78	1.18
305235	AA670480		gb:ag37e01.s1 Jia bone marrow stroma Hom	3.11	8.66
305245	AA676695	Hs.81328	nuclear factor of kappa light polypeptid	4.38	7.53
305312	AA700201		gb:zj44f07.s1 Soares_fetal_liver_spleen_	2.13	2.66
305322	AA701597	Hs.163019	EST	1.20	1.40
305394	AA720942	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.16	0.68
305413	AA724659		gb:ai10f08.s1 Soares_parathyroid_tumor_N	5.86	9.87
305447	AA737856		gb:nx10c08.s1 NCI_CGAP_GC3 Homo sapiens	2.21	2.86
305476	AA745664	Hs.287445	hypothetical protein FLJ11726	3.36	6.54
305483	AA748030	Hs.303512	EST	1.00	2.02
305528	AA769156		gb:nz12e05.s1 NCI_CGAP_GCB1 Homo sapiens	6.44	9.10
305612	AA782347	Hs.272572	hemoglobin, alpha 2	0.19	0.79
305614	AA782866		gb:aj09h02.s1 Soares_parathyroid_tumor_N	1.00	1.00
305616	AA782884	Hs.275865	ribosomal protein S18	7.57	10.20
305637	AA806124		gb:oe29a12.s1 NCI_CGAP_Pr25 Homo sapiens	4.78	12.42
305639	AA806138		gb:oe29c12.s1 NCI_CGAP_Pr25 Homo sapiens	0.89	0.70
305650	AA807709		gb:nw31e04.s1 NCI_CGAP_GCB0 Homo sapiens	4.49	8.71
305690	AA813477		gb:ai67a05.s1 Soares_testis_NHT Homo sap	4.91	9.40
305726	AA828156	Hs.73742	ribosomal protein, large, P0	0.19	0.81
305728	AA828209		gb:of34a02.s1 NCI_CGAP_Kid6 Homo sapiens	5.12	9.29
305759	AA835353		gb:ak72b06.s1 Barstead spleen HPLRB2 Hom	1.66	4.11
305792	AA845256		gb:ak84a08.s1 Barstead spleen HPLRB2 Hom	2.34	4.25
305864	AA864374	Hs.73742	ribosomal protein, large, P0	0.30	1.40
305901	AA872968		gb:oh63h08.s1 NCI_CGAP_Kid5 Homo sapiens	2.10	5.21
305910	AA875981		gb:nx21h02.s1 NCI_CGAP_GC3 Homo sapiens	0.32	1.01
306015	AA897116		gb:am08b07.s1 Soares_NFL_T_GBC_S1 Homo s	1.56	1.12
306017	AA897221	Hs.109058	ribosomal protein S6 kinase, 90kD, polyp	5.21	7.90
306020	AA897630	Hs.130027	EST	1.96	6.59
306063	AA906316		gb:ok03g03.s1 Soares_NFL_T_GBC_S1 Homo s	7.38	20.69
306065	AA906725		gb:ok78g02.s1 NCI_CGAP_GC4 Homo sapiens	7.19	13.48
306104	AA910956		gb:ok85h11.s1 NCI_CGAP_Kid3 Homo sapiens	6.50	9.13
306109	AA911861		gb:og21a07.s1 NCI_CGAP_PNS1 Homo sapiens	4.21	5.25
306148	AA917409	Hs.288036	tRNA isopentenylpyrophosphate transferas	2.20	2.70
306242	AA932805		gb:oo60g04.s1 NCI_CGAP_Lu5 Homo sapiens	2.84	5.35
306288	AA936900		gb:oi53h05.s1 NCI_CGAP_HN3 Homo sapiens	1.60	1.12
306325	AA953072	Hs.210546	interleukin 21 receptor	1.65	2.26
306353	AA961382	Hs.275865	ribosomal protein S18	3.78	6.32
306375	AA968650	Hs.276018	EST, Moderately similar to JC4662 ribos	4.30	5.74
306396	AA970223		gb:op09d05.s1 NCI_CGAP_Kid6 Homo sapiens	0.95	2.45
306428	AA975110	Hs.191228	hypothetical protein FLJ20284	3.19	4.10
306442	AA976899		gb:oq35e09.s1 NCI_CGAP_GC4 Homo sapiens	4.67	7.44
306446	AA977348		gb:oq72e12.s1 NCI_CGAP_Kid6 Homo sapiens	3.92	6.27

306458	AA978186		gb:op33c06.s1 Soares_NFL_T_GBC_S1 Homo s	3.35	5.77
306467	AA983508	Hs.163593	ribosomal protein L18a	3.72	5.37
306510	AA988546		gb:or84d07.s1 NCI_CGAP_Lu5 Homo sapiens	1.00	1.00
306555	AA994304	Hs.276083	EST, Weakly similar to RL23_HUMAN 60S R	6.61	10.91
306557	AA994530		gb:ou57e08.s1 NCI_CGAP_Br2 Homo sapiens	16.20	31.83
306572	AA995686		gb:os25c12.s1 NCI_CGAP_Kid5 Homo sapiens	2.51	6.52
306582	AA996248		gb:os18c10.s1 NCI_CGAP_Kid5 Homo sapiens	1.42	3.13
306598	AI000320	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.91	8.68
306605	AI000497	Hs.119500	ribosomal protein, large P2	1.96	8.60
306656	AI004024		gb:ou11b07.x1 Soares_NFL_T_GBC_S1 Homo s	0.11	0.45
306676	AI005603	Hs.284136	PRO2047 protein	9.56	17.28
306686	AI015615		gb:ov29f10.x1 Soares_testis_NHT Homo sap	1.86	3.60
306702	AI022565	Hs.307670	EST	1.47	1.19
306728	AI027359	Hs.272572	hemoglobin, alpha 2	1.28	2.83
306751	AI032589		gb:ow70h12.s1 Soares_fetal_liver_spleen_	3.91	5.21
306767	AI038963	Hs.249118	ESTs	3.33	6.06
306892	AI092465		gb:qa75h12.x1 Soares_fetal_heart_NbHH19W	3.77	7.46
306897	AI093967		gb:qa33c06.s1 Soares_NhHMPu_S1 Homo sapi	2.12	2.85
306956	AI125111		gb:am66f03.s1 Barstead spleen HPLRB2 Hom	6.10	10.52
306958	AI125152		gb:am55e09.x1 Johnston frontal cortex Ho	1.72	1.56
307035	AI142774	Hs.119122	ribosomal protein L13a	2.00	4.70
307041	AI144243		gb:qb85b12.x1 Soares_fetal_heart_NbHH19W	9.12	12.56
307091	AI167439		gb:ox70h06.s1 Soares_NhHMPu_S1 Homo sapi	4.88	8.52
307181	AI189251		gb:qc99g06.x1 Soares_pregnant_uterus_NbH	3.55	6.44
307297	AI205798	Hs.111334	ferritin, light polypeptide	2.46	4.65
307317	AI208303	Hs.147333	EST	5.64	10.13
307327	AI214142	Hs.246381	CD68 antigen	3.18	5.15
307382	AI223158	Hs.147885	ESTs	2.02	3.73
307410	AI241715	Hs.77039	ribosomal protein S3A	0.72	0.48
307415	AI242118		gb:qh92b02.x1 Soares_NFL_T_GBC_S1 Homo s	2.38	3.51
307423	AI243206	Hs.179573	collagen, type I, alpha 2	2.60	5.44
307426	AI243364		gb:qh30g11.x1 Soares_NFL_T_GBC_S1 Homo s	3.18	7.67
307517	AI275055		gb:ql72d03.x1 Soares_NhHMPu_S1 Homo sapi	1.00	1.00
307551	AI281556		gb:qu52f11.x1 NCI_CGAP_Lym6 Homo sapiens	3.40	11.20
307561	AI282207		gb:qp65a12.x1 Soares_fetal_lung_NbHL19W	4.74	15.51
307608	AI290295		gb:qm01f02.x1 Soares_NhHMPu_S1 Homo sapi	3.50	7.19
307657	AI306428	Hs.298262	ribosomal protein S19	1.76	2.44
307691	AI318285		gb:tb17b01.x1 NCI_CGAP_Ov37 Homo sapiens	1.59	1.31
307701	AI318583	Hs.276672	EST, Weakly similar to RL6_HUMAN 60S RI	1.90	2.13
307718	AI333406	Hs.83753	small nuclear ribonucleoprotein polypept	0.45	0.99
307730	AI336092		gb:qt43b07.x1 Soares_fetal_lung_NbHL19W	1.51	0.99
307760	AI342387		gb:qt27f07.x1 Soares_pregnant_uterus_NbH	1.00	1.00
307764	AI342731		gb:qo26a07.x1 NCI_CGAP_Lu5 Homo sapiens	4.52	12.58
307783	AI347274		gb:tc05d02.x1 NCI_CGAP_Co16 Homo sapiens	1.42	1.00
307796	AI350556		gb:qt18f09.x1 NCI_CGAP_GC4 Homo sapiens	6.57	9.61
307807	AI351799		gb:qt09d02.x1 NCI_CGAP_GC4 Homo sapiens	3.38	7.68
307808	AI351826		gb:qt09g03.x1 NCI_CGAP_GC4 Homo sapiens	0.33	0.86
307820	AI355761		gb:qt94a11.x1 NCI_CGAP_Co14 Homo sapiens	7.94	21.57
307830	AI358722	Hs.276737	EST, Weakly similar to R5HU22 ribosomal	2.05	3.32
307852	AI365541		gb:qz08g05.x1 NCI_CGAP_CLL1 Homo sapiens	3.18	5.21
307902	AI380462		gb:tg02h05.x1 NCI_CGAP_CLL1 Homo sapiens	3.13	4.99
307997	AI434512	Hs.181165	eukaryotic translation elongation factor	1.00	3.01
308002	AI435240	Hs.283442	ESTs	5.86	12.64
308011	AI439473		gb:ti60a08.x1 NCI_CGAP_Lym12 Homo sapien	3.79	5.83
308023	AI452732	Hs.251577	hemoglobin, alpha 1	0.38	0.88
308041	AI458824	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.36	6.06
308059	AI468938	Hs.276877	EST, Weakly similar to RL10_HUMAN 60S R	1.80	1.98
308085	AI474135	Hs.181165	eukaryotic translation elongation factor	3.38	4.14
308101	AI475950	Hs.181165	eukaryotic translation elongation factor	1.30	3.87
308106	AI476803		gb:tj77e12.x1 Soares_NSF_F8_9W_OT_PA_P_S2.38		8.72
308122	AI480123	Hs.309411	EST	2.70	3.86
308154	AI500600		gb:tn93d08.x1 NCI_CGAP_Ut2 Homo sapiens	0.66	1.33
308171	AI523632	Hs.298766	ESTs, Weakly similar to schlafen4 [M.mu	2.48	4.86
308211	AI557029	Hs.278572	anaplastic lymphoma kinase (Ki-1)	2.43	2.14
308213	AI557041		gb:PT2.1_12_E04.r tumor2 Homo sapiens cD	3.34	3.79
308216	AI557135		gb:PT2.1_13_H06.r tumor2 Homo sapiens cD	4.61	4.78
308219	AI557246		gb:PT2.1_15_D07.r tumor2 Homo sapiens cD	4.87	7.94
308271	AI567844	Hs.252259	ribosomal protein S3	2.40	6.35
308319	AI583983	Hs.181165	eukaryotic translation elongation factor	2.45	3.33
308362	AI613519	Hs.105749	KIAA0553 protein	1.24	1.41
308413	AI636253	Hs.196511	ESTs	3.16	4.82
308450	AI650860	Hs.96840	KIAA1527 protein	1.79	2.68
308464	AI672425	Hs.277117	EST, Moderately similar to I38055 myosi	4.87	8.27
308588	AI718299		gb:as51g12.x1 Barstead aorta HPLRB6 Homo	3.90	5.64
308599	AI719893		gb:as47d07.x1 Barstead aorta HPLRB6 Homo	3.32	5.12
308615	AI738593	Hs.101774	hypothetical protein FLJ23045	3.11	2.36
308643	AI745040		gb:tr19a12.x1 NCI_CGAP_Ov23 Homo sapiens	3.98	3.69
308673	AI760864		gb:wi09c10.x1 NCI_CGAP_CLL1 Homo sapiens	0.82	0.99
308697	AI767143		gb:wi97a07.x1 NCI_CGAP_Kid12 Homo sapien	2.76	5.59
308762	AI807405	Hs.259408	ESTs	3.17	6.30
308778	AI811109		gb:tr04c11.x1 NCI_CGAP_Ov23 Homo sapiens	1.00	1.00
308782	AI811767	Hs.2186	eukaryotic translation elongation factor	2.94	5.15
308808	AI818289		gb:wk52c01.x1 NCI_CGAP_Pr22 Homo sapiens	4.41	8.34
308823	AI824118	Hs.217493	annexin A2	1.85	1.92
308875	AI832332		gb:at48g03.x1 Barstead colon HPLRB7 Homo	2.52	3.80

308879	AI832763	Hs.75968	thymosin, beta 4, X chromosome	3.38	7.96
308886	AI833240		gb:at76d10.x1 Barstead colon HPLRB7 Homo	3.06	2.65
308898	AI858845		gb:wl32d10.x1 NCI_CGAP_Ut1 Homo sapiens	2.45	3.44
308934	AI865023	Hs.177	phosphatidylinositol glycan, class H	4.14	6.76
308966	AI870704		gb:wl47h01.x1 NCI_CGAP_Ut1 Homo sapiens	1.00	1.00
308979	AI873111		gb:wl52h05.x1 NCI_CGAP_Brn25 Homo sapien	7.15	11.10
309045	AI910902		gb:tq39f01.x1 NCI_CGAP_Ut1 Homo sapiens	0.61	0.59
309051	AI911975		gb:wd78d01.x1 NCI_CGAP_Lu24 Homo sapiens	1.78	4.42
309069	AI917366	Hs.78202	SWI/SNF related, matrix associated, act	3.27	5.88
309083	AI922426	Hs.119598	ribosomal protein L3	2.39	3.34
309105	AI925503	Hs.265884	ESTs	5.54	17.78
309122	AI928178		gb:wo95a11.x1 NCI_CGAP_Kid11 Homo sapien	1.00	2.92
309128	AI928816	Hs.180842	ribosomal protein L13	1.38	5.55
309164	AI937761		gb:wp84b09.x1 NCI_CGAP_Brn25 Homo sapien	2.43	3.11
309177	AI951118		gb:wx63g05.x1 NCI_CGAP_Br18 Homo sapiens	0.81	0.97
309288	AI991525	Hs.299426	ESTs	4.86	7.46
309299	AW003478		gb:wq66c06.x1 NCI_CGAP_GC6 Homo sapiens	4.36	9.43
309303	AW004823		gb:ws93a08.x1 NCI_CGAP_Co3 Homo sapiens	2.88	7.54
309411	AW085201	Hs.244144	EST	4.30	7.14
309437	AW090702	Hs.278242	tubulin, alpha, ubiquitous	2.49	3.11
309459	AW117645	Hs.65114	keratin 18	2.88	4.55
309476	AW129368		gb:xe14b05.x1 NCI_CGAP_Ut4 Homo sapiens	2.08	6.60
309499	AW136325	Hs.279771	Homo sapiens clone PP1596 unknown mRNA	2.82	3.55
309529	AW150807	Hs.181357	laminin receptor 1 (67kD, ribosomal pro	4.78	3.95
309532	AW151119		gb:xg33e10.x1 NCI_CGAP_Ut1 Homo sapiens	1.18	4.40
309626	AW192004	Hs.297681	serine (or cysteine) proteinase inhibit	4.46	12.06
309641	AW194230	Hs.253100	EST, Moderately similar to GHHU Ig gamm	1.47	1.39
309675	AW205681	Hs.253506	EST, Moderately similar to ATPN_HUMAN A	5.68	15.20
309693	AW237221	Hs.181357	laminin receptor 1 (67kD, ribosomal prot	1.00	1.00
309695	AW238011	Hs.295605	mannosidase, alpha, class 2A, member 2	5.45	9.61
309700	AW241170	Hs.179661	tubulin, beta polypeptide	1.41	1.25
309747	AW264889		gb:xq36h02.x1 NCI_CGAP_Lu28 Homo sapiens	5.00	8.35
309769	AW272346		gb:xs13c10.x1 NCI_CGAP_Kid11 Homo sapien	5.76	11.90
309782	AW275156	Hs.156110	immunoglobulin kappa constant	0.42	0.69
309783	AW275401	Hs.254798	EST	1.00	4.11
309799	AW276964		gb:xp58h01.x1 NCI_CGAP_Ov39 Homo sapiens	1.68	1.44
309866	AW299916		gb:xs44c01.x1 NCI_CGAP_Kid11 Homo sapien	3.02	5.04
309903	AW339071	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.05	1.18
309923	AW340684		gb:hd05g08.x1 Soares_NFL_T_GBC_S1 Homo s	2.30	3.67
309928	AW341418		gb:hd08c03.x1 Soares_NFL_T_GBC_S1 Homo s	7.41	13.71
309931	AW341683		gb:hd13d01.x1 Soares_NFL_T_GBC_S1 Homo s	1.20	12.70
309933	AW341936		gb:hb73f10.x1 NCI_CGAP_Ut2 Homo sapiens	4.90	18.29
309964	AW449111	Hs.257111	hypothetical protein MGC3265	1.99	3.07
310002	AI439096	Hs.323079	Homo sapiens mRNA; cDNA DKFZp564P116 (fr	0.20	0.47
310096	AW136822	Hs.172824	ESTs, Weakly similar to B48013 proline-r	1.51	1.22
310098	AI685841	Hs.161354	ESTs	0.31	0.76
310109	AI203094	Hs.148633	ESTs	2.06	5.83
310112	AW197233	Hs.147253	ESTs	2.92	3.55
310115	AI611317	Hs.223796	ESTs	1.25	0.84
310121	AW195642	Hs.148901	ESTs	1.00	2.71
310146	AI206614	Hs.197422	ESTs	9.50	15.31
310193	AI627653	Hs.147562	ESTs	2.85	4.18
310255	AW450439	Hs.153378	ESTs	4.26	10.63
310261	AI240483	Hs.201217	ESTs	3.28	4.40
310264	AI915771	Hs.74170	metallothionein 1E (functional)	0.26	0.86
310275	AI242102	Hs.213636	ESTs	5.43	8.19
310282	AI243332	Hs.156055	ESTs	3.15	8.06
310290	AW013815	Hs.149103	ESTs	2.19	3.12
310333	AI253200	Hs.145402	ESTs	1.17	1.91
310346	AI261340	Hs.145517	ESTs	4.81	9.95
310385	AI263392	Hs.156151	ESTs	5.96	7.79
310443	AW119018	Hs.164231	ESTs	2.90	4.63
310444	AW196632	Hs.252956	ESTs	0.85	1.01
310446	AI275715	Hs.145926	ESTs	2.18	3.85
310468	AI984074	Hs.196398	ESTs	3.39	5.19
310477	AI948801	Hs.171073	ESTs	1.00	1.00
310512	AW275603	Hs.200712	ESTs	3.87	8.12
310514	AI681145	Hs.160724	ESTs	3.30	7.33
310524	AW082270	Hs.12496	ESTs, Highly similar to AC004836 1 simil	0.72	1.44
310547	AI302654	Hs.208024	ESTs	3.26	3.46
310584	AI653007	Hs.156304	ESTs	2.39	4.08
310608	AI962234	Hs.196102	ESTs	5.60	6.49
310624	AI341594		gb:Human endogenous retrovirus H proteas	4.91	9.09
310636	AI814373	Hs.164175	ESTs	1.85	1.71
310648	AI347863	Hs.156672	ESTs	0.17	0.69
310694	AI654370	Hs.157752	Homo sapiens mRNA full length insert cDN	5.40	13.22
310695	AI472124	Hs.157757	ESTs	4.82	6.27
310714	AI418446	Hs.157882	ESTs	1.76	3.51
310722	AI989803	Hs.157289	ESTs	1.14	6.85
310756	AI916560	Hs.158707	ESTs	8.46	13.01
310764	AI376769	Hs.167172	ESTs	4.76	7.37
310848	AI459554	Hs.161286	ESTs	2.84	1.96
310851	AW291714	Hs.221703	ESTs	1.00	2.32
310854	AI421677	Hs.161332	ESTs	6.37	7.94
310858	AI871000	Hs.161330	ESTs	6.07	9.84

310864	AI924558	Hs.161399	ESTs	0.87	0.78
310875	T47764	Hs.132917	ESTs	1.00	3.63
310896	AW157731	Hs.270982	ESTs, Moderately similar to ALU7_HUMAN A	7.07	16.68
310922	AW195634	Hs.170401	ESTs	1.00	1.00
310955	AI560210	Hs.263912	ESTs	10.08	17.66
310957	AW190974	Hs.196918	ESTs	2.18	3.18
311000	AI521830	Hs.171050	ESTs	3.06	6.64
311012	AW298070	Hs.241097	ESTs	1.23	3.77
311034	AI564023	Hs.311389	ESTs, Moderately similar to PT0375 natur	2.44	2.09
311074	AW290922	Hs.199848	ESTs	6.04	14.19
311134	AI990849	Hs.196971	ESTs	3.54	6.96
311174	AW450552	Hs.205457	periaxin	0.65	0.95
311187	AI638374	Hs.224189	ESTs	2.46	2.78
311220	AI656040	Hs.196532	ESTs	1.10	2.52
311230	AI989808	Hs.197663	ESTs	1.41	1.75
311236	AI653378	Hs.197674	ESTs	2.18	2.11
311242	AW016812	Hs.200266	ESTs	0.63	5.11
311258	AI671221	Hs.199887	ESTs	1.00	1.41
311277	AW072813	Hs.270868	ESTs, Moderately similar to ALU4_HUMAN A	2.56	1.94
311294	AA826425	Hs.291829	ESTs	1.04	2.69
311308	F12664	Hs.49000	ESTs	1.96	6.70
311351	AI682303	Hs.201274	ESTs	4.77	9.38
311390	AW392997	Hs.202280	ESTs	2.80	6.06
311405	AW290961	Hs.201815	ESTs	3.80	11.66
311409	AI698839		gb:wd31f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.84	6.94
311420	AI936291	Hs.209867	ESTs	5.30	12.56
311443	AI791521	Hs.192206	ESTs	4.39	6.09
311467	AI934909	Hs.175377	ESTs	1.00	1.04
311479	AI933672	Hs.211399	ESTs	2.76	5.61
311488	R57390	Hs.301064	arfaptin 1	2.50	5.73
311495	AW300077	Hs.221358	ESTs	3.63	6.09
311511	AW444568	Hs.210303	ESTs	2.00	2.87
311534	AW130351	Hs.243549	ESTs	0.31	1.33
311537	AI805121	Hs.211828	ESTs	3.69	5.85
311543	AI681360	Hs.201259	ESTs	1.73	1.34
311551	AW449774	Hs.296380	POM (POM121 rat homolog) and ZP3 fusion	3.31	6.12
311557	AI819230	Hs.211238	interleukin-1 homolog 1	1.00	1.00
311558	Z44432	Hs.63128	KIAA1292 protein	2.25	3.41
311559	AW008271	Hs.265848	similar to rat myomegalin	2.68	5.90
311563	AI922143	Hs.211334	ESTs	2.39	3.32
311586	AI827834	Hs.211227	ESTs	2.47	3.85
311616	AW450675	Hs.212709	ESTs	1.00	1.00
311621	AI924307	Hs.213464	ESTs	4.16	6.74
311635	AI928456	Hs.213081	ESTs	2.17	3.76
311668	AW193674	Hs.240044	ESTs	2.60	3.12
311672	R11807	Hs.20914	hypothetical protein FLJ23056	2.79	5.18
311683	AW183738	Hs.232644	ESTs	0.19	0.96
311700	R49601	Hs.171495	retinoic acid receptor, beta	6.28	8.83
311714	AW131785	Hs.246831	ESTs, Weakly similar to CIKG_HUMAN VOLTA	5.00	8.17
311735	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	0.96	0.72
311743	T99079	Hs.191194	ESTs	1.00	1.95
311783	AI682478	Hs.13528	hypothetical protein FLJ14054	0.16	0.77
311785	AI056769	Hs.133512	ESTs	1.34	3.97
311799	AA780791	Hs.14014	ESTs, Weakly similar to KIAA0973 protein	8.52	13.32
311819	AW265275	Hs.254325	ESTs	3.58	3.91
311823	AI089422	Hs.131297	ESTs	1.40	1.72
311877	AA349893	Hs.85339	G protein-coupled receptor 39	0.95	0.91
311886	AA522738	Hs.132554	ESTs	0.88	0.87
311896	AW206447		gb:UI-H-BI1-afg-g-02-0-UI.s1 NCI_CGAP_Su	1.66	1.13
311910	N28365	Hs.22579	Homo sapiens clone CDABP0036 mRNA sequen	1.66	2.30
311923	T60843	Hs.189679	ESTs	0.42	2.63
311933	AI597963	Hs.118726	ESTs	1.88	3.02
311959	T67262	Hs.124733	ESTs	2.02	2.33
311960	AW440133	Hs.189690	ESTs	3.87	6.62
311967	AI382726	Hs.182434	ESTs	5.80	8.14
311975	AA804374	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	0.98	3.26
312005	T78450	Hs.13941	ESTs	0.12	1.39
312028	T78886	Hs.284450	ESTs	3.78	4.92
312046	AI580018	Hs.268591	ESTs	4.11	7.32
312056	T83748	Hs.268594	ESTs	2.36	3.08
312064	AA676713	Hs.191155	ESTs	3.34	5.28
312088	AW303760	Hs.13685	ESTs	1.60	1.15
312093	T91809	Hs.121296	ESTs	0.68	0.85
312094	Z78390		gb:HSZ78390 Human fetal brain S. Meier-E	3.05	4.48
312097	AI352096	Hs.112180	zinc finger protein 148 (pHZ-52)	4.52	9.70
312118	T85332	Hs.178294	ESTs	2.40	2.60
312128	AI052609	Hs.17631	Homo sapiens cDNA FLJ20118 fis, clone CO	2.39	3.53
312147	T89855	Hs.195648	ESTs	0.67	1.03
312175	AA953383	Hs.127554	ESTs	5.85	10.60
312179	AI052572	Hs.269864	ESTs	2.41	3.32
312201	AI928365	Hs.91139	solute carrier family 1 (neuronal/epithe	0.24	0.89
312207	H90213	Hs.191330	ESTs	2.20	4.55
312220	N74613		gb:za55a07.s1 Soares fetal liver spleen	4.28	11.13
312252	AI128388	Hs.143655	ESTs	1.64	1.57
312304	AA491949	Hs.269392	ESTs	0.12	2.47

312318	AW235092	Hs.143981	ESTs	3.46	5.69
312319	AA216698	Hs.180780	TERA protein	5.78	4.46
312321	R66210	Hs.186937	ESTs	0.44	1.74
312331	AA825512	Hs.289101	glucose regulated protein, 58kD	3.73	5.96
312339	AA524394	Hs.165544	ESTs	3.07	0.95
312363	AI675558	Hs.181867	ESTs	10.08	16.73
312375	AI375096	Hs.172405	cell division cycle 27	2.78	3.71
312376	R52089	Hs.172717	ESTs	1.00	1.00
312389	AI863140		gb:tz43h12.x1 NCI_CGAP_Brn52 Homo sapien	2.37	3.98
312437	AA995028		gb:RC4-BT0629-120200-011-b10 BT0629 Homo	4.06	5.41
312440	AI051133	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	1.00	1.00
312451	R59969	Hs.176539	ESTs	4.96	10.04
312458	AI167637	Hs.146924	ESTs	1.11	1.00
312507	AI168177	Hs.143653	ESTs	5.89	8.24
312520	AI742591	Hs.205392	ESTs	3.30	8.92
312548	AI566228	Hs.159426	hypothetical protein PRO2121	1.38	1.65
312564	H21520	Hs.35088	ESTs	0.40	0.77
312583	AI193122	Hs.124141	ESTs	0.13	0.94
312599	AI865073	Hs.125720	ESTs	3.75	5.29
312602	AA046451	Hs.165200	ESTs	6.78	12.93
312645	H52121	Hs.193007	ESTs	0.38	1.13
312666	AI240582	Hs.214678	ESTs	0.98	2.03
312689	AW450461	Hs.203965	ESTs	0.21	0.61
312817	H75459	Hs.233425	ESTs	1.51	0.85
312846	AW152104	Hs.200879	ESTs	8.93	13.78
312873	AI690071	Hs.283552	ESTs, Weakly similar to unnamed protein	4.20	6.23
312893	AI016204	Hs.172922	ESTs	2.67	3.15
312902	AW292797	Hs.130316	ESTs, Weakly similar to T2D3_HUMAN TRANS	1.19	0.71
312925	N90868	Hs.271695	ESTs	2.50	4.25
312936	AI681581	Hs.121525	ESTs	1.00	1.17
312975	AI640506	Hs.293119	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.30	4.80
312978	N24887	Hs.292500	ESTs	0.80	1.05
312980	AA497043	Hs.115685	ESTs	3.12	3.60
312984	N25871	Hs.177337	ESTs	2.03	2.13
313000	AI147412	Hs.146657	ESTs	5.52	8.42
313029	AA731520	Hs.170504	ESTs	0.96	1.39
313039	AI419290	Hs.149990	ESTs, Weakly similar to unnamed protein	6.48	13.20
313049	AW293055	Hs.119357	ESTs	6.44	10.73
313056	AI651930	Hs.135684	ESTs	1.51	2.04
313058	D81015	Hs.125382	ESTs	0.25	1.50
313070	AI422023	Hs.161338	ESTs	8.56	11.60
313097	AI676164	Hs.204339	ESTs	3.72	4.56
313130	AW449171	Hs.168677	ESTs	3.28	5.06
313136	N59284	Hs.288010	ESTs	0.49	1.36
313153	AI240838	Hs.132750	ESTs	5.36	5.52
313210	N74077	Hs.197043	ESTs	0.30	0.66
313236	AW238169	Hs.83513	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.16	8.76
313239	W19632	Hs.124170	ESTs	1.00	3.87
313265	N93466	Hs.121764	ESTs, Weakly similar to testicular tekti	0.74	2.06
313267	AI770008	Hs.129583	ESTs	0.23	1.30
313275	AI027604	Hs.159650	ESTs	6.68	9.57
313290	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	1.34	1.07
313292	AI362991	Hs.202121	ESTs, Weakly similar to env protein [H.s	2.00	4.32
313325	AI420611	Hs.127832	ESTs	1.20	2.27
313357	AW074848	Hs.201501	ESTs	4.02	5.33
313393	AI674685	Hs.200141	ESTs	1.36	2.84
313399	AW376889	Hs.194097	ESTs	2.58	5.26
313414	AI241540	Hs.132933	ESTs	6.57	15.07
313417	AA741151	Hs.137323	ESTs	0.63	3.01
313457	AA576052	Hs.193223	Homo sapiens cDNA FLJ11646 fis, clone HE	2.78	4.70
313499	AI261390	Hs.146085	KIAA1345 protein	0.91	2.37
313516	AA029058	Hs.135145	ESTs	3.41	7.08
313556	AA628517	Hs.118502	ESTs	0.23	0.70
313569	AI273419	Hs.135146	hypothetical protein FLJ13984	1.88	1.00
313570	AA041455	Hs.209312	ESTs	0.73	2.27
313638	AI753075	Hs.104627	Homo sapiens cDNA FLJ10158 fis, clone HE	1.00	1.72
313662	AA740151	Hs.130425	ESTs	0.20	1.42
313671	W49823	Hs.104613	RP42 homolog	1.00	1.00
313672	AW468891	Hs.122948	ESTs	3.46	5.80
313690	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	0.51	0.97
313711	AA398070	Hs.133471	ESTs	0.18	1.01
313723	AA070412		gb:zm68c10.s1 Stratagene neuroepithelium	1.08	1.03
313726	AI744687	Hs.257806	ESTs	2.13	2.99
313774	AW136836	Hs.144583	ESTs	1.38	1.19
313784	AA910514	Hs.134905	ESTs	3.88	5.78
313790	AW078569	Hs.177043	ESTs	0.22	2.06
313832	AW271022	Hs.133294	ESTs	1.15	0.91
313834	AW418779	Hs.114889	ESTs	0.68	3.14
313835	AI538438	Hs.159087	ESTs	5.74	8.88
313852	H18633	Hs.123641	protein tyrosine phosphatase, receptor t	0.16	1.14
313854	AW470806	Hs.275002	ESTs	2.09	4.05
313865	AA731470	Hs.163839	ESTs	3.41	4.09
313871	AW471088	Hs.145950	ESTs	5.28	6.83
313883	AI949384		gb:nu76d01.s1 NCI_CGAP_Alv1 Homo sapiens	2.90	10.91
313915	AI969390	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	1.00	1.00

313926	AW473830	Hs.171442	ESTs	3.40	4.11
313948	AW452823	Hs.135268	ESTs	5.77	9.15
313978	AI870175	Hs.13957	ESTs	0.46	0.75
313983	AI829133	Hs.226780	ESTs	4.10	6.40
314035	AA164199	Hs.270152	ESTs	5.88	7.90
314037	AW300048	Hs.275272	ESTs	1.00	3.79
314040	AA166970	Hs.118748	ESTs	7.60	11.33
314067	AW293538	Hs.51743	KIAA1340 protein	1.86	1.21
314103	AI028477	Hs.132775	ESTs	2.90	5.29
314107	AA806113	Hs.189025	ESTs	2.00	1.66
314113	AA218986	Hs.118854	ESTs	0.91	4.17
314124	AW118745	Hs.9460	Homo sapiens mRNA; cDNA DKFZp547C244 (fr	2.53	3.32
314126	AA226431		gb:nc18b12.s1 NCI_CGAP_Pr1 Homo sapiens	3.13	5.08
314128	AA935633	Hs.194628	ESTs	2.90	6.35
314151	AA236163	Hs.202430	ESTs	4.15	6.45
314184	AW081795	Hs.233465	ESTs	3.44	4.65
314192	AW290975	Hs.118923	ESTs	1.00	1.23
314244	AL036450	Hs.103238	ESTs	2.88	3.67
314253	AA278679	Hs.189510	ESTs	4.98	7.16
314262	AW086215	Hs.246096	ESTs	0.38	1.94
314320	AA811598	Hs.275809	ESTs	3.34	5.66
314332	AL037551	Hs.95612	ESTs	2.85	2.09
314335	AA287443	Hs.142570	Homo sapiens clone 24629 mRNA sequence	4.35	4.78
314340	AW304350	Hs.130879	ESTs, Moderately similar to putative p15	0.77	0.86
314351	AA292275	Hs.193746	ESTs	3.07	3.77
314376	AI628633	Hs.324679	ESTs	4.10	6.11
314443	AA827125	Hs.192043	ESTs	6.20	13.67
314458	AI217440	Hs.143873	ESTs	0.58	2.49
314466	AA767818	Hs.122707	ESTs	2.53	2.62
314478	AI521173	Hs.125507	DEAD-box protein	3.94	5.65
314482	AL043807	Hs.134182	ESTs	1.30	1.44
314506	AA833655	Hs.206868	Homo sapiens cDNA FLJ14056 fis, clone HE	3.28	3.47
314519	R42554	Hs.210862	T-box, brain, 1	3.12	6.16
314529	AL046412	Hs.202151	ESTs	3.43	6.87
314546	AW007211	Hs.16131	hypothetical protein FLJ12876	1.38	1.00
314562	AI564127	Hs.143493	ESTs	2.29	5.27
314579	AW197442	Hs.116998	ESTs	3.87	5.75
314580	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 pro	0.10	0.71
314585	AA918474	Hs.216363	ESTs	1.08	1.40
314589	AW384790	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	1.00	1.00
314592	AA435761	Hs.192148	ESTs	0.90	2.60
314603	AA418024	Hs.270670	ESTs	4.56	6.29
314604	AA946582	Hs.8700	deleted in liver cancer 1	3.42	3.92
314606	AA418241	Hs.188767	ESTs	2.97	4.55
314648	AA878419		gb:EST391378 MAGE resequences, MAGP Homo	1.42	1.36
314699	AI038719	Hs.132801	ESTs	3.66	4.97
314701	AI754634	Hs.131987	ESTs	0.03	0.90
314710	AI669131	Hs.290989	EST	3.40	7.52
314750	AI095005	Hs.135174	ESTs	2.80	6.54
314767	AW135412	Hs.164002	ESTs	3.20	4.26
314801	AA481027	Hs.109045	hypothetical protein FLJ10498	1.00	1.00
314817	AI694139	Hs.192855	ESTs	0.91	0.99
314835	AI281370	Hs.76064	ribosomal protein L27a	5.75	7.44
314852	AI903735		gb:MR-BT035-200199-031 BT035 Homo sapien	1.68	4.34
314853	AA729232	Hs.153279	ESTs	0.60	1.85
314940	AW452768	Hs.162045	ESTs	10.10	16.20
314941	AA515902	Hs.130650	ESTs	0.31	1.02
314943	AI476797	Hs.184572	cell division cycle 2, G1 to S and G2 to	2.18	0.37
314955	AA521382	Hs.192534	ESTs	2.59	3.90
314973	AW273128	Hs.300268	ESTs	1.05	1.25
315004	AA527941	Hs.325351	EST	5.64	13.63
315006	AI538613	Hs.298241	Transmembrane protease, serine 3	0.52	1.78
315033	AI493046	Hs.146133	ESTs	2.46	1.00
315035	AI569476	Hs.177135	ESTs	0.34	1.33
315056	AI202703	Hs.152414	ESTs	2.10	2.64
315069	AI821517	Hs.105866	ESTs	1.00	1.30
315071	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	1.78	1.00
315073	AW452948	Hs.257631	ESTs	1.17	1.52
315078	AA568548	Hs.190616	ESTs	3.00	3.79
315080	AA744550	Hs.136345	ESTs	1.00	1.00
315120	AA564991	Hs.269477	ESTs	0.64	1.44
315175	AI025842	Hs.152530	ESTs	0.61	1.91
315193	AI241331	Hs.131765	ESTs	1.06	0.97
315196	AA972756	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	0.48	1.96
315200	AI808235	Hs.307686	EST	3.76	9.40
315254	AI474433	Hs.179556	ESTs	5.37	9.36
315353	AW452608	Hs.279610	hypothetical protein FLJ10493	1.00	1.30
315397	AA218940	Hs.137516	fidgetin-like 1	3.38	2.24
315403	AW362980	Hs.163924	ESTs	2.04	5.23
315431	AA622104	Hs.184838	ESTs	2.36	8.04
315454	AI239473		gb:qh36f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.46	7.64
315455	AW393391	Hs.156919	ESTs	3.78	5.76
315473	AI681671	Hs.312671	ESTs, Moderately similar to OVCA1	0.89	2.15
315483	AW512763	Hs.222024	transcription factor BMAL2	2.32	1.96
315526	AI193048	Hs.128685	ESTs	1.67	1.78

315530	AI200852	Hs.127780	ESTs	1.05	1.01
315541	AI168233	Hs.123159	sperm associated antigen 4	0.85	0.56
315552	AW445034	Hs.256578	ESTs	1.00	2.22
315562	AA737415	Hs.152826	ESTs	2.66	2.48
315577	AW513545	Hs.17283	hypothetical protein FLJ10890	2.20	2.25
315587	AI268399	Hs.140489	ESTs	1.00	1.04
315589	AW072387	Hs.158258	Homo sapiens mRNA; cDNA DKFZp434B1272 (f	0.14	1.05
315623	AA364078	Hs.258189	ESTs	7.44	12.56
315634	AA837085	Hs.220585	ESTs	0.50	1.40
315668	AA912347	Hs.136585	ESTs	0.43	1.22
315677	AI932662	Hs.164073	ESTs	0.60	1.39
315706	AW440742	Hs.155556	hypothetical protein FLJ20202	2.18	3.77
315707	AI418055	Hs.161160	ESTs	2.88	2.63
315730	H25899	Hs.201591	ESTs	0.11	0.60
315745	AI821759	Hs.191856	ESTs	3.50	7.25
315791	AA678177		gb:zi15a05.s1 Soares_fetal_liver_spleen_	1.78	2.63
315801	AA827752	Hs.266134	ESTs	4.31	6.23
315820	AI652022	Hs.258785	ESTs	2.35	3.01
315878	AA683336	Hs.189046	ESTs	2.12	2.64
315905	AI821911	Hs.209452	ESTs	1.03	1.97
315923	AI052789	Hs.133263	ESTs	2.63	5.06
315954	AW276810	Hs.254859	ESTs, Moderately similar to ALU5_HUMAN A	1.21	0.85
315978	AA830893	Hs.119769	ESTs	3.09	3.41
316001	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	2.20	6.82
316011	AW516953	Hs.201372	ESTs	0.35	1.63
316012	AA764950	Hs.119898	ESTs	6.56	8.13
316040	AI983409	Hs.189226	ESTs	5.69	10.69
316048	AI720759	Hs.224971	ESTs	2.84	10.45
316076	AW297895	Hs.116424	ESTs	0.30	1.05
316124	AI308862	Hs.167028	ESTs	1.00	1.43
316151	AI806016	Hs.156520	ESTs	5.80	9.03
316187	AW518299	Hs.192253	ESTs	1.20	3.96
316204	AA731509	Hs.120257	ESTs	4.92	6.94
316232	AW297853	Hs.251203	ESTs	1.48	1.60
316275	AI671041	Hs.292611	ESTs, Moderately similar to ALU1_HUMAN A	5.86	12.14
316291	AW375974	Hs.156704	ESTs	2.73	2.69
316303	AA740994	Hs.209609	ESTs	1.53	1.26
316344	AA744518	Hs.120610	ESTs	3.66	8.34
316346	AI028478	Hs.157447	ESTs	3.51	6.69
316365	AI627845	Hs.210776	ESTs	2.50	4.33
316380	AI393378	Hs.164496	ESTs	1.16	2.16
316470	AA809902	Hs.243813	ESTs	5.40	10.34
316509	AA767310	Hs.291766	ESTs	2.46	2.89
316514	AA768037	Hs.291671	ESTs	4.70	6.04
316519	AI929097		gb:od10c11.s1 NCI_CGAP_GCB1 Homo sapiens	4.41	9.70
316609	AW292520	Hs.122082	ESTs	1.00	2.89
316633	AI125586	Hs.127955	ESTs	2.61	3.72
316700	AW172316	Hs.252961	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.46	4.64
316711	AI743721	Hs.285316	ESTs, Moderately similar to ALU7_HUMAN A	4.45	6.95
316713	AI090671	Hs.134807	hypothetical protein FLJ12057	0.30	2.40
316715	AI440266	Hs.170673	ESTs, Weakly similar to AF126780 1 retin	0.20	1.45
316787	AW369770	Hs.130351	ESTs	4.05	5.53
316809	AA825839	Hs.202238	ESTs	2.25	3.82
316811	AA922060	Hs.132471	ESTs	1.00	1.32
316812	AW135045	Hs.232001	ESTs	3.28	4.70
316818	AA827176	Hs.124316	ESTs	0.67	1.81
316824	AA837416	Hs.124299	ESTs	3.53	6.00
316827	AI380429	Hs.172445	ESTs	0.72	1.56
316891	AW298119	Hs.202536	ESTs	1.64	2.97
316951	AA134365	Hs.57548	ESTs	1.45	1.08
316970	AA860172	Hs.132406	ESTs	1.00	1.53
316971	AA860212	Hs.170991	ESTs	1.08	1.96
316990	AA861611	Hs.130643	ESTs	5.44	10.04
317001	AI627917	Hs.233694	hypothetical protein FLJ11350	3.56	4.37
317008	AW051597	Hs.143707	ESTs	0.69	1.37
317051	AA873253	Hs.126233	ESTs	6.18	12.72
317128	AA971374	Hs.125674	ESTs	1.87	2.66
317129	H12523	Hs.78521	Homo sapiens cDNA: FLJ21193 fis, clone C	4.12	6.64
317137	AW341567	Hs.125710	ESTs	2.82	5.12
317196	AI348258	Hs.153412	ESTs	1.98	2.51
317212	AI866468	Hs.148294	ESTs	1.86	2.83
317223	AW297920	Hs.130054	ESTs	0.83	1.57
317224	D56760	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	2.74	0.86
317266	AA906289	Hs.203614	ESTs	1.00	1.00
317282	AI807444	Hs.176101	ESTs	2.60	4.21
317285	AW370882	Hs.222080	ESTs	1.96	3.49
317302	AA908709	Hs.135564	ESTs	7.16	8.32
317304	AW449899	Hs.130184	ESTs	1.38	2.28
317320	AA927151	Hs.130452	ESTs	3.58	8.13
317413	AW341701	Hs.126622	ESTs	2.08	4.92
317417	AA918420	Hs.145378	ESTs	3.06	4.79
317452	AA972965	Hs.135568	ESTs	4.22	9.21
317519	AI859695	Hs.126860	ESTs	1.88	4.15
317521	AI824338	Hs.126891	ESTs	3.12	4.55
317529	AI916517	Hs.126865	ESTs	2.73	3.34

317570	AI733361	Hs.127122	ESTs	1.00	2.43
317571	AA938663	Hs.199828	ESTs	5.20	11.95
317598	AW206035	Hs.192123	ESTs	0.33	1.56
317627	AI346110	Hs.132553	ESTs	1.50	1.39
317650	AI733310	Hs.127346	ESTs	0.48	1.46
317659	AA961216	Hs.127785	ESTs	4.18	7.14
317674	AW294909	Hs.132208	ESTs	2.92	3.20
317686	AA969051	Hs.187319	ESTs	1.00	1.01
317692	AI307659	Hs.174794	ESTs	5.33	9.59
317701	AI674774	Hs.128014	ESTs	1.00	1.00
317711	AI733015	Hs.272189	ESTs	5.13	7.81
317722	AI733373	Hs.128119	ESTs	2.50	6.03
317756	AA973667	Hs.128320	ESTs	1.59	1.30
317777	AI143525	Hs.47313	KIAA0258 gene product	1.00	2.48
317799	AI498273	Hs.128808	ESTs	1.78	2.11
317803	AA983251	Hs.128899	ESTs	0.80	1.06
317821	AI368158	Hs.70983	PTPL1-associated RhoGAP 1	0.17	0.68
317848	AI820575	Hs.129086	Homo sapiens cDNA FLJ12007 fis, clone HE	5.30	8.16
317850	N29974	Hs.152982	hypothetical protein FLJ13117	1.30	2.28
317861	AW341064	Hs.129119	ESTs	2.18	5.93
317865	AI298794	Hs.129130	ESTs	4.48	8.20
317869	AW295184	Hs.129142	deoxyribonuclease II beta	0.44	0.99
317881	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	4.06	2.23
317890	AI915599	Hs.129225	ESTs	4.68	7.48
317899	AI952430	Hs.150614	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.14	3.37
317986	AI005163	Hs.201378	ESTs, Weakly similar to T12545 hypotheti	0.28	1.66
318001	AW235697	Hs.130980	ESTs	5.12	9.97
318016	AI016694	Hs.256921	ESTs	1.86	4.50
318023	AW243058	Hs.131155	ESTs	2.92	5.22
318054	AW449270	Hs.232140	ESTs	3.92	6.37
318068	AI024540	Hs.131574	ESTs	1.21	1.27
318117	AI208304	Hs.250114	ESTs	0.86	1.17
318187	AI792585	Hs.133272	ESTs, Weakly similar to ALUC_HUMAN IIII	5.90	6.98
318223	AI077540	Hs.134090	ESTs	1.05	0.90
318240	AI085377	Hs.143610	ESTs	3.10	2.40
318255	AI082692	Hs.134662	ESTs	0.02	1.05
318266	AI554341	Hs.271443	ESTs	6.12	10.55
318330	AI093840	Hs.143758	ESTs	4.98	7.90
318369	AI493501	Hs.170974	ESTs	2.46	5.62
318428	AI949409	Hs.194591	ESTs	0.77	0.45
318458	AI149783	Hs.158438	ESTs	3.54	4.92
318467	AI151395	Hs.144834	ESTs	4.56	5.62
318473	AI939339	Hs.146883	ESTs	2.08	4.05
318476	AI693927	Hs.265165	ESTs	4.22	8.07
318487	AI167877	Hs.143716	ESTs	1.47	1.05
318488	AI217431	Hs.144709	ESTs	1.40	4.14
318491	T26477	Hs.22883	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.84	1.90
318499	T25451		gb:PTHI188 HTCDL1 Homo sapiens cDNA 5/3	2.58	5.20
318537	AA377908	Hs.13254	ESTs	3.26	4.18
318538	N28625	Hs.74034	Homo sapiens clone 24651 mRNA sequence	0.35	1.07
318547	R20578	Hs.90431	ESTs	3.22	4.60
318552	R18364	Hs.90363	ESTs	4.87	9.06
318575	R55102	Hs.107761	ESTs, Weakly similar to unnamed protein	1.91	1.98
318580	T34571	Hs.49007	poly(A) polymerase alpha	2.74	6.22
318587	AA779704	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	0.85	2.46
318596	AI470235	Hs.172698	EST	4.88	4.93
318622	T48325	Hs.237658	apolipoprotein A-II	4.80	12.51
318629	N25163	Hs.8861	ESTs	0.39	1.04
318637	AA243539	Hs.9196	hypothetical protein	1.72	3.57
318648	T77141	Hs.184411	albumin	6.27	9.91
318650	AA393302	Hs.176626	hypothetical protein EDAG-1	3.96	8.84
318671	AA188823	Hs.299254	Homo sapiens cDNA: FLJ23597 fis, clone L	1.53	0.81
318679	T58115	Hs.10336	ESTs	1.00	2.19
318711	AI936475	Hs.101282	Homo sapiens cDNA: FLJ21238 fis, clone C	3.05	3.18
318725	AI962487	Hs.242990	ESTs	1.08	2.46
318728	Z30201	Hs.291289	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.77	1.33
318740	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	0.25	1.49
318776	R24963	Hs.23766	ESTs	1.00	3.01
318784	H00148	Hs.5181	proliferation-associated 2G4, 38kD	2.70	3.86
318816	F07873	Hs.21273	ESTs	3.90	7.13
318865	H10818		gb:ym04f10.r1 Soares infant brain 1NIB H	2.25	3.56
318879	R56332	Hs.18268	adenylate kinase 5	1.78	5.00
318881	Z43224	Hs.124952	ESTs	4.79	14.13
318894	F08138	Hs.7387	DKFZP564B116 protein	5.31	7.00
318901	AW368520	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	1.03	0.91
318925	Z43577	Hs.21470	ESTs	2.23	3.80
318936	AI219221	Hs.308298	ESTs	1.86	7.16
318982	Z44140	Hs.269622	ESTs	5.84	9.79
318986	Z44186	Hs.169161	ESTs, Highly similar to MAON_HUMAN NADP-	1.00	1.00
319041	Z44720	Hs.98365	ESTs, Weakly similar to weak similarity	3.38	6.11
319103	H05896	Hs.4993	KIAA1313 protein	1.00	1.07
319170	R13678	Hs.285306	putative selenocysteine lyase	3.79	5.03
319196	F07953	Hs.16085	putative G-protein coupled receptor	1.00	2.98
319199	F07361	Hs.13306	ESTs	3.53	5.66
319242	F11472	Hs.12839	ESTs	5.87	7.26

319263	T65331	Hs.81360	Homo sapiens cDNA: FLJ21927 fis, clone H	1.81	1.57
319267	F11802	Hs.6818	ESTs	1.10	4.72
319270	R13474	Hs.290263	ESTs	4.80	10.40
319279	T65094	Hs.12677	CGI-147 protein	1.50	2.11
319282	AA461358	Hs.12876	ESTs	1.00	1.00
319289	W07304	Hs.79059	transforming growth factor, beta recepto	0.18	0.68
319291	W86578	Hs.285243	hypothetical protein FLJ22029	0.26	0.62
319293	F12119	Hs.12583	ESTs	3.13	4.50
319312	Z45481		gb:HSC2QE041 normalized infant brain cDN	1.10	1.00
319370	H54254	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	0.16	0.73
319391	R06304	Hs.13911	ESTs	1.26	2.43
319396	H67130	Hs.301743	ESTs	0.70	0.76
319398	AA359754	Hs.191196	ESTs	2.45	3.59
319407	R05329		gb:ye91b04.r1 Soares fetal liver spleen	2.00	3.54
319425	T82930		gb:yd39f07.r1 Soares fetal liver spleen	4.28	8.81
319433	R06050	Hs.191198	ESTs	6.15	14.13
319437	AA282420	Hs.111991	ESTs, Weakly similar to Y48A5A.1 [C.eleg	3.26	5.68
319466	AI809937	Hs.116417	ESTs	1.76	5.65
319471	R06546	Hs.19717	ESTs	4.29	4.84
319480	R06933	Hs.184221	ESTs	1.00	1.00
319484	T91772		gb:yd52a10.s1 Soares fetal liver spleen	2.81	4.88
319486	AI382429	Hs.250799	ESTs	2.08	2.82
319508	T99898	Hs.270104	ESTs, Moderately similar to ALU8_HUMAN A	2.80	4.39
319523	T69499	Hs.191184	ESTs	1.55	3.25
319545	R83716	Hs.14355	Homo sapiens cDNA FLJ13207 fis, clone NT	1.65	1.19
319546	R09692		gb:yf23b12.r1 Soares fetal liver spleen	5.11	8.54
319552	AA096106	Hs.20403	ESTs	1.89	3.36
319582	T82998	Hs.250154	hypothetical protein FLJ12973	3.48	4.82
319586	D78808	Hs.283683	chromosome 8 open reading frame 4	0.26	0.82
319604	R11679	Hs.297753	vimentin	1.68	3.41
319609	AW247514	Hs.12293	hypothetical protein FLJ21103	3.06	4.24
319611	H14957		gb:ym19c10.r1 Soares infant brain 1NIB H	2.76	4.24
319653	AA770183	Hs.173515	uncharacterized hypothalamus protein HT0	2.61	3.55
319657	R19897	Hs.106604	ESTs	5.32	7.68
319658	R13432	Hs.167481	syntrophin, gamma 1	3.35	5.00
319661	H08035	Hs.21398	ESTs, Moderately similar to A Chain A, H	5.18	12.55
319662	H06382	Hs.21400	ESTs	1.58	1.56
319708	R15372	Hs.22664	ESTs	1.00	1.22
319742	T77668	Hs.21162	ESTs	2.48	3.13
319748	R18178	Hs.295866	Homo sapiens mRNA; cDNA DKFZp434N1923 (f	3.02	4.85
319772	R76633	Hs.22646	ESTs	4.36	11.61
319788	AA321932	Hs.117414	KIAA1320 protein	2.56	3.68
319805	R92857	Hs.271350	likely ortholog of mouse polydom	4.63	6.56
319812	N74880	Hs.264330	N-acylsphingosine amidohydrolase (acid c	0.63	1.32
319834	AA071267		gb:zm61g01.r1 Stratagene fibroblast (937	0.30	0.94
319878	T78517	Hs.13941	ESTs	3.99	6.44
319882	AA258981	Hs.291392	ESTs	5.09	7.36
319912	T77559	Hs.94109	Homo sapiens cDNA FLJ13634 fis, clone PL	3.24	3.21
319935	H79460	Hs.271722	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.40	9.42
319944	T79248	Hs.133510	ESTs	3.31	5.39
319947	AA160967	Hs.14479	Homo sapiens cDNA FLJ14199 fis, clone NT	2.90	4.95
319962	H06350	Hs.135056	Human DNA sequence from clone RP5-850E9	1.81	1.57
320007	AA336314		gb:EST40943 Endometrial tumor Homo sapie	3.42	6.29
320018	T83263		gb:yd40h09.r1 Soares fetal liver spleen	2.77	5.14
320030	H63789	Hs.296288	ESTs, Weakly similar to KIAA0638 protein	4.10	6.69
320032	AI699772	Hs.292664	ESTs, Weakly similar to A46010 X-linked	3.27	3.27
320040	AA233671	Hs.87164	hypothetical protein FLJ14001	1.81	1.64
320047	T86564	Hs.302256	EST	3.38	7.36
320063	AA074108	Hs.120844	FOXJ2 forkhead factor	5.90	16.73
320096	H58138	Hs.117915	ESTs	2.08	4.47
320099	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	1.00	1.00
320112	T92107	Hs.188489	ESTs	2.27	2.06
320140	H94179	Hs.119023	SMC2 (structural maintenance of chromoso	1.00	1.00
320188	AW419200	Hs.172318	ESTs	1.26	1.00
320193	AA831259	Hs.17132	ESTs	2.58	6.23
320195	R62203	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	2.85	4.53
320199	R78659	Hs.29792	ESTs	0.40	0.94
320203	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (f	0.84	1.18
320219	AA327564	Hs.127011	tubulointerstitial nephritis antigen	1.00	1.17
320220	AF054910	Hs.127111	tektin 2 (testicular)	0.18	1.09
320225	AF058989	Hs.128231	G antigen, family B, 1 (prostate associa	5.26	13.75
320231	H03139	Hs.24683	ESTs	1.59	1.93
320260	NM_003608	Hs.131924	G protein-coupled receptor 65	1.38	4.56
320267	AL049337	Hs.132571	Homo sapiens mRNA; cDNA DKFZp564P016 (fr	1.00	1.92
320268	H06019	Hs.151293	Homo sapiens cDNA FLJ10664 fis, clone NT	5.58	5.70
320322	AF077374	Hs.139322	small proline-rich protein 3	1.41	1.01
320325	AI167978	Hs.139851	caveolin 2	0.05	0.67
320330	AF026004	Hs.141660	chloride channel 2	2.17	1.26
320339	H10807	Hs.281434	Homo sapiens cDNA FLJ14028 fis, clone HE	1.81	2.32
320388	H16065	Hs.31286	ESTs	1.00	3.22
320402	R22291	Hs.23368	Homo sapiens clone FLC0578 PRO2852 mRNA,	1.41	1.36
320413	AA203711	Hs.173269	ESTs	2.31	3.61
320432	R62786	Hs.124136	ESTs	11.25	20.78
320436	AA253352	Hs.293663	ESTs	2.22	3.49
320438	W24548	Hs.5669	ESTs	3.53	8.14

320448	AI240233	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	1.42	3.46
320451	R26944	Hs.180777	Homo sapiens mRNA; cDNA DKFZp564M0264 (f	0.87	0.81
320484	AA094436	Hs.296267	follistatin-like 1	0.65	1.18
320499	R32555	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	3.44	7.15
320514	AB007978	Hs.158278	KIAA0509 protein	6.44	13.62
320521	N31464	Hs.24743	hypothetical protein FLJ20171	1.48	1.04
320526	AW374205	Hs.111314	ESTs	3.66	7.87
320527	R34672	Hs.324522	ESTs	3.16	5.63
320536	AA331732	Hs.137224	ESTs	2.83	5.83
320556	AF054177	Hs.14570	hypothetical protein FLJ22530	1.28	1.00
320564	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	1.22	0.81
320587	Z44524	Hs.167456	Homo sapiens mRNA full length insert cDN	1.84	2.44
320635	R54159	Hs.80506	small nuclear ribonucleoprotein polypept	1.00	6.25
320639	AA243258	Hs.7395	hypothetical protein FLJ23182	2.60	2.30
320648	N48521	Hs.26549	Homo sapiens mRNA for KIAA1708 protein,	1.00	1.53
320651	AA489268	Hs.111334	ferritin, light polypeptide	0.14	0.79
320664	AI904216	Hs.91251	hypothetical protein FLJ11198	5.02	8.84
320676	AA132650	Hs.300511	ESTs	3.63	5.37
320683	R59291	Hs.26638	ESTs, Weakly similar to unnamed protein	0.37	1.31
320689	AA334609	Hs.171929	ESTs, Weakly similar to A54849 collagen	1.27	1.02
320696	AW135016	Hs.172780	ESTs	3.53	4.60
320714	AI445591		gb:yq04a10.r1 Soares fetal liver spleen	1.06	0.85
320727	U96044	Hs.181125	immunoglobulin lambda locus	1.35	1.49
320771	AI793266	Hs.117176	poly(A)-binding protein, nuclear 1	0.04	0.82
320794	AA281993	Hs.91226	ESTs	2.96	4.33
320822	AF100780	Hs.194679	WNT1 inducible signaling pathway protein	0.10	0.79
320824	AF120274	Hs.194689	artemin	1.16	1.11
320830	AJ132445	Hs.266416	claudin 14	1.06	1.75
320843	AA317372	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	1.36	1.47
320849	D60031	Hs.34771	ESTs	5.30	7.49
320853	AI473796	Hs.135904	ESTs	1.00	1.00
320896	AB002155	Hs.271580	uroplakin 1B	5.90	2.55
320921	R94038	Hs.199538	inhibin, beta C	2.20	1.17
320927	AI205786	Hs.213923	ESTs	0.18	1.46
320957	AI878933	Hs.92023	core histone macroH2A2.2	1.67	2.18
320997	H22544		gb:yn69f11.r1 Soares adult brain N2b5HB5	3.26	3.62
321045	W88483	Hs.293650	ESTs	2.25	4.55
321046	H27794	Hs.269055	ESTs	2.69	4.25
321052	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	2.14	2.56
321059	AI092824	Hs.126465	ESTs	1.69	0.53
321062	R87955	Hs.241411	Homo sapiens mRNA full length insert cDN	2.76	5.20
321067	AF131782	Hs.241438	Homo sapiens clone 24941 mRNA sequence	4.79	7.41
321102	AA018306		gb:ze40d08.r1 Soares retina N2b4HR Homo	1.79	4.27
321130	H43750	Hs.125494	ESTs	1.00	3.14
321142	AI817933	Hs.298351	ASPL protein	8.73	15.36
321155	AA336635	Hs.99598	hypothetical protein MGC5338	3.04	5.03
321158	AA700289		gb:yu76f11.r1 Soares fetal liver spleen	4.62	8.39
321170	N53742	Hs.172982	ESTs	2.21	4.46
321199	AW385512		gb:yy56d10.s1 Soares_multiple_sclerosis_	5.69	8.01
321206	H54178	Hs.226469	Homo sapiens cDNA FLJ12417 fis, clone MA	4.00	7.32
321225	AL080073	Hs.251414	Homo sapiens mRNA; cDNA DKFZp564B1462 (f	4.17	4.63
321236	AW371941	Hs.18192	Ser/Arg-related nuclear matrix protein (	1.00	1.00
321244	AF068654		gb:Homo sapiens isolate AN.1 immunoglobu	2.18	9.13
321270	R83560		gb:yv76c06.s1 Soares fetal liver spleen	3.80	5.26
321317	AI937060	Hs.6298	KIAA1151 protein	1.81	1.65
321318	AB033041	Hs.137507	KIAA1215 protein	1.00	1.00
321325	AB033100	Hs.300646	KIAA protein (similar to mouse paladin)	0.44	0.93
321342	AA127984	Hs.222024	transcription factor BMAL2	4.94	4.93
321356	R93443	Hs.271770	ESTs	3.10	4.66
321418	AI739161	Hs.161075	ESTs	2.28	2.54
321420	AI368667	Hs.132743	ESTs	1.13	0.97
321430	U05890		gb:H.sapiens (DIG3) mRNA for immunoglobu	2.42	3.35
321453	N50080	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	1.60	3.11
321467	X13075		gb:Human 2a12 mRNA for kappa-immunoglobu	0.42	0.72
321468	AA514198	Hs.38540	ESTs	2.46	6.50
321491	H70665	Hs.292549	ESTs	1.00	1.25
321498	AW295517	Hs.255436	ESTs	3.19	6.24
321504	W02356	Hs.268980	ESTs	2.28	3.86
321510	AA703650	Hs.255748	ESTs	2.14	3.94
321513	H84972	Hs.108551	ESTs	2.78	5.37
321516	AI382803	Hs.159235	ESTs	3.06	7.19
321565	AI525773	Hs.266514	hypothetical protein FLJ11342	4.89	7.82
321577	H84260		gb:ys90g04.r1 Soares retina N2b5HR Homo	1.00	1.73
321581	AA019964	Hs.28803	ESTs	4.88	6.73
321582	AA143755	Hs.21858	trinucleotide repeat containing 3	1.00	2.08
321587	H95531		gb:ys76e02.r1 Soares retina N2b4HR Homo	2.26	4.52
321626	AA295430	Hs.96322	hypothetical protein FLJ23560	1.95	3.83
321628	H87064	Hs.161051	ESTs, Moderately similar to ALU6_HUMAN A	0.47	1.02
321642	AW085917	Hs.247084	ESTs	1.52	1.38
321669	H95404	Hs.294110	ESTs	2.17	2.45
321687	AA625149		gb:af70c12.r1 Soares_NhHMPu_S1 Homo sapi	4.31	6.95
321688	H97646	Hs.123158	Homo sapiens cDNA FLJ12830 fis, clone NT	2.82	3.28
321693	AA700017	Hs.173737	ras-related C3 botulinum toxin substrate	0.51	1.08
321700	N55160	Hs.167260	ESTs	4.57	7.46
321701	AW390923	Hs.42568	ESTs	1.00	1.00

321709	N25847	Hs.108923	RAB38, member RAS oncogene family	1.00	1.00
321710	N35682	Hs.259743	ESTs	2.97	5.26
321775	AI694875	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	1.00	1.00
321777	AI637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	1.68	0.45
321779	N42729	Hs.163835	ESTs	0.90	0.90
321829	D81993	Hs.8966	tumor endothelial marker 8	2.69	3.89
321846	AA281594	Hs.87902	ESTs	5.11	7.64
321879	AL109670	Hs.302809	ESTs	6.49	9.58
321883	AA426494	Hs.46901	KIAA1462 protein	0.28	0.95
321899	N55158	Hs.29468	ESTs	0.39	0.95
321911	AF026944	Hs.293797	ESTs	6.20	10.76
321949	R49202	Hs.181694	EST	4.62	10.51
321955	AI651866	Hs.195689	ESTs	2.89	5.47
321956	AL110177	Hs.132882	ESTs	0.32	1.25
321987	AL133612	Hs.272759	KIAA1457 protein	1.00	1.83
321991	AL133627	Hs.158923	Homo sapiens mRNA; cDNA DKFZp434K0722 (f	4.00	6.47
322002	AA328801	Hs.84522	ESTs	2.10	3.48
322035	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	1.00	1.90
322044	AW340926		gb:xy51b10.x1 NCI_CGAP_Lu34.1 Homo sapie	3.20	9.67
322057	N92197	Hs.154679	synaptotagmin 1	1.55	1.07
322060	AI341937		gb:qt10e03.x1 NCI_CGAP_GC4 Homo sapiens	4.59	7.68
322070	U80769	Hs.210322	Homo sapiens mRNA for KIAA1766 protein,	2.78	4.52
322083	AF074982	Hs.226031	ESTs, Highly similar to KIAA0535 protein	3.10	5.52
322091	AI819863	Hs.106243	ESTs	1.59	1.75
322125	R93901		gb:yq16c12.r1 Soares fetal liver spleen	2.06	5.27
322130	R98978	Hs.117767	ESTs	10.12	16.49
322147	AF085919	Hs.114176	ESTs	0.94	0.64
322166	AF085958		gb:yr88b03.r1 Soares fetal liver spleen	4.09	6.67
322173	H52567		gb:yt85d04.r1 Soares_pineal_gland_N3HPG	3.46	4.85
322178	H56535		gb:yt88g03.r1 Soares_pineal_gland_N3HPG	0.44	2.54
322179	H92891		gb:yt94c02.s1 Soares_pineal_gland_N3HPG	4.52	7.50
322186	H67346	Hs.269187	ESTs	0.15	0.98
322196	W87895	Hs.211516	ESTs	2.20	5.04
322212	AF087995	Hs.134877	ESTs	3.42	4.84
322221	AI890619	Hs.179662	nucleosome assembly protein 1-like 1	0.82	2.14
322277	AI640193	Hs.226389	ESTs	3.62	3.98
322278	AF086283		gb:zd46f01.r1 Soares_fetal_heart_NbHH19W	1.00	1.00
322284	AI792140	Hs.49265	ESTs	0.66	2.76
322288	AL037273	Hs.7886	pellino (Drosophila) homolog 1	0.71	0.70
322320	AF086419		gb:zd78d03.r1 Soares_fetal_heart_NbHH19W	2.02	2.76
322336	AA308526	Hs.76152	decorin	2.92	4.44
322339	W17348		gb:zb18c07.x5 Soares_fetal_lung_NbHL19W	8.50	11.56
322366	AW404274	Hs.122492	hypothetical protein	0.61	1.34
322372	W25624	Hs.153943	ESTs	7.37	12.07
322374	AI394663	Hs.122116	ESTs, Moderately similar to Osf2 [M.musc	4.78	10.50
322378	AF064819	Hs.201877	DESC1 protein	1.00	1.00
322388	AI815730	Hs.247474	hypothetical protein FLJ21032	7.09	8.49
322416	AA223183	Hs.298442	adaptor-related protein complex 3, mu 1	3.20	5.80
322419	AA248987	Hs.14084	ring finger protein 7	1.64	1.57
322425	W37943	Hs.34892	KIAA1323 protein	0.83	1.00
322431	AA069222	Hs.141892	ESTs	3.96	5.22
322450	AA040131	Hs.25144	ESTs	5.18	12.67
322465	AA137152	Hs.286049	phosphoserine aminotransferase	3.41	2.23
322467	AF116826	Hs.180340	putative protein-tyrosine kinase	1.00	1.30
322473	AA744286	Hs.266935	tRNA selenocysteine associated protein	1.75	2.03
322509	T52172	Hs.302213	ESTs	1.00	2.27
322523	W80398	Hs.193197	ESTs	2.75	5.49
322527	AF147359		gb:Homo sapiens full length insert cDNA	1.25	1.27
322560	AI916847	Hs.270947	ESTs	4.57	8.81
322566	W87285	Hs.269587	ESTs	1.00	1.42
322585	AA837622		gb:zh69c01.r1 Soares_fetal_liver_spleen_	4.18	6.94
322635	AA679084		gb:zh90h08.r1 Soares_fetal_liver_spleen_	2.40	4.85
322641	AA007352	Hs.256042	ESTs	2.94	4.64
322653	AI828854	Hs.258538	striatin, calmodulin-binding protein	0.48	0.38
322664	AA011522		gb:zi03g07.r1 Soares_fetal_liver_spleen_	1.92	2.18
322687	AI110759		gb:AF074666 Human fetal liver cDNA libra	4.14	6.75
322692	AA018117	Hs.60843	potassium voltage-gated channel, shaker-	3.50	5.00
322694	AI110872	Hs.279812	PRO0327 protein	1.80	1.72
322708	AF113674	Hs.283773	clone FLB1727	1.00	3.43
322712	AA021328	Hs.23607	hypothetical protein FLJ11109	3.28	3.86
322766	AW068805	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	1.63	1.53
322770	AA045796	Hs.122682	ESTs	1.53	1.06
322794	AI608591	Hs.38991	S100 calcium-binding protein A2	12.06	1.94
322810	AI962276	Hs.127444	ESTs	4.09	6.90
322818	AW043782	Hs.293616	ESTs	1.20	1.63
322820	AI377755	Hs.120695	ESTs	0.21	1.93
322872	AA827228	Hs.126943	ESTs	2.04	1.63
322882	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	5.26	1.22
322887	AI986306	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.80	2.24
322913	AI733737	Hs.68837	ESTs	2.38	6.61
322926	AI825940	Hs.211192	ESTs	4.02	5.79
322929	AI365585	Hs.146246	ESTs	0.30	1.14
322958	AI905228	Hs.83484	SRY (sex determining region Y)-box 4	2.06	1.13
322971	C15953	Hs.212760	hypothetical protein FLJ13649	1.18	2.00
322981	AA493252	Hs.159577	ESTs	2.28	2.61

322988	C18727	Hs.171941	ESTs	0.39	2.00
323003	AI733859	Hs.149089	ESTs	3.28	1.00
323013	AA134042	Hs.191451	ESTs	3.38	5.68
323025	AL157565	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	0.06	1.10
323032	AW244073	Hs.145946	ESTs	10.18	21.27
323052	R21124	Hs.85573	Homo sapiens DC29 mRNA, complete cds	1.46	1.90
323064	AL119341	Hs.49359	Homo sapiens mRNA; cDNA DKFZp547E052 (fr	3.08	5.64
323098	AI700025	Hs.270471	ESTs	2.31	4.49
323102	AL119913	Hs.163615	ESTs	5.38	11.64
323155	AL135041		gb:DKFZp762K2310_r1 762 (synonym: hmel2)	2.38	5.56
323176	AW071648	Hs.82101	pleckstrin homology-like domain, family	1.06	1.41
323191	AA195600	Hs.301570	ESTs	0.73	1.24
323225	AA205654	Hs.24790	KIAA1573 protein	5.25	11.95
323232	AA148722	Hs.224680	ESTs	0.45	1.35
323266	AW003362	Hs.243886	nuclear autoantigenic sperm protein (his	1.71	1.83
323281	AI697556	Hs.292659	ESTs	1.24	3.21
323283	AA256014	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	12.68	15.05
323314	AA226310	Hs.191501	ESTs	4.42	9.61
323316	AL134620	Hs.280175	ESTs	2.98	5.93
323334	AI336501	Hs.77273	ras homolog gene family, member A	1.98	3.30
323338	R74219	Hs.23348	S-phase kinase-associated protein 2 (p45	1.62	1.00
323348	AA233056	Hs.191518	ESTs	1.00	1.07
323351	AA704103	Hs.24049	ESTs	1.43	1.68
323359	AA234172	Hs.137418	ESTs	0.34	1.18
323360	AA716061	Hs.161719	ESTs	3.01	3.71
323405	AW139550	Hs.115173	ESTs	1.90	8.81
323420	AI672386	Hs.263780	ESTs	0.29	1.01
323434	AW081455	Hs.120219	ESTs	2.27	1.92
323445	AA253103	Hs.135569	ESTs, Weakly similar to NEUROD [H.sapien	0.43	0.80
323449	AA282865	Hs.284153	Fanconi anemia, complementation group A	3.19	3.85
323492	H00978	Hs.20887	hypothetical protein FLJ10392	2.70	3.20
323501	AA182461	Hs.84520	ESTs	2.04	3.31
323505	AI652287		gb:EST382593 MAGE resequences, MAGK Homo	2.21	3.08
323515	AA282274	Hs.256083	ESTs	2.69	3.40
323541	AI185116	Hs.104613	RP42 homolog	1.20	1.09
323545	AI814405	Hs.224569	ESTs	1.25	1.55
323635	R63117	Hs.9691	Homo sapiens cDNA: FLJ23249 fis, clone C	0.27	0.72
323675	AA984759	Hs.272168	tumor differentially expressed 1	3.70	5.80
323678	AL042121	Hs.20880	ESTs	3.33	5.10
323691	AA317561	Hs.145599	ESTs	1.00	1.00
323693	AW297758	Hs.249721	ESTs	2.01	1.54
323746	AW298611	Hs.12808	MARK	4.11	5.53
323774	AA329806	Hs.321056	Homo sapiens mRNA; cDNA DKFZp586F1322 (f	2.06	3.70
323856	AA355264	Hs.267604	hypothetical protein FLJ10450	3.42	8.13
323857	T18988	Hs.293668	ESTs	5.97	12.51
323870	AA341774	Hs.129212	ESTs	3.17	4.52
323876	AL042492	Hs.147313	ESTs	0.36	1.00
323885	AA344308	Hs.128427	Homo sapiens BAC clone RP11-335J18 from	2.31	3.33
323911	AL043212	Hs.92550	ESTs	4.38	5.41
323919	AA862973	Hs.220704	ESTs	5.80	10.20
323972	AI869964	Hs.182906	ESTs	3.10	5.14
324005	AA610011	Hs.208021	ESTs	5.34	10.07
324036	AI472078	Hs.303662	ESTs	1.00	5.03
324055	AA528794	Hs.128644	ESTs	0.86	1.00
324063	AW292740	Hs.272813	dual oxidase 1	0.45	0.91
324072	AA381829		gb:EST94855 Activated T-cells I Homo sap	2.82	5.12
324092	AW269931	Hs.202473	Homo sapiens cDNA: FLJ22278 fis, clone H	2.40	2.52
324095	AW377983	Hs.298140	Homo sapiens cDNA: FLJ22502 fis, clone H	1.32	4.30
324129	AI381918	Hs.285833	Homo sapiens cDNA: FLJ22135 fis, clone H	1.40	1.77
324132	AW504860	Hs.288836	hypothetical protein FLJ12673	4.24	6.21
324214	AA412395	Hs.225740	ESTs	6.96	10.69
324227	AA295552	Hs.28631	Homo sapiens cDNA: FLJ22141 fis, clone H	0.81	0.53
324266	AL047634	Hs.231913	ESTs	2.42	4.05
324275	AA429088	Hs.98523	ESTs	3.62	5.38
324281	AL048026	Hs.124675	ESTs, Weakly similar to T14742 hypotheti	0.14	0.70
324290	AA432032	Hs.304420	ESTs	3.71	4.34
324303	AL118754		gb:DKFZp761P1910_r1 761 (synonym: hamy2)	0.95	0.91
324312	AI198841	Hs.128173	ESTs	4.06	5.91
324325	AL138153	Hs.300410	ESTs	5.88	8.25
324338	AL138357	Hs.145078	regulator of differentiation (in S. pomb	0.87	1.25
324341	AW197734	Hs.99807	ESTs, Weakly similar to unnamed protein	1.28	1.00
324343	AW452016	Hs.293232	ESTs	2.54	3.46
324371	AA452305	Hs.270319	ESTs	5.85	8.36
324382	AW502749	Hs.24724	MFH-amplified sequences with leucine-ric	0.76	1.64
324384	AA453396	Hs.127656	KIAA1349 protein	2.88	5.69
324385	F28212	Hs.284247	KIAA1491 protein	1.81	1.99
324388	AI924963	Hs.306206	hypothetical protein FLJ11215	1.00	1.00
324432	AA464510	Hs.152812	ESTs	2.73	2.17
324497	AW152624	Hs.136340	ESTs, Weakly similar to unnamed protein	0.71	1.90
324510	AI148353	Hs.287425	Homo sapiens cDNA FLJ11569 fis, clone HE	1.00	1.00
324580	AA492588		gb:ng99c08.s1 NCI_CGAP_Thy1 Homo sapiens	2.18	3.50
324582	AA506935	Hs.132036	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.96	11.36
324633	AA572994	Hs.325489	ESTs	2.92	4.22
324640	AW295832	Hs.134798	ESTs, Moderately similar to TTL MOUSE TU	5.48	11.74
324675	AW014734	Hs.157969	ESTs	0.39	0.73

324699	AW504732	Hs.21275	hypothetical protein FLJ11011	0.93	0.93
324747	AA603532	Hs.130807	ESTs	1.57	1.81
324748	AA657457	Hs.292385	ESTs	1.55	1.34
324801	AI819924	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	1.00	6.56
324804	AI692552		gb:wd73f12.x1 NCI_CGAP_Lu24 Homo sapiens	1.00	7.53
324828	AA843926	Hs.124434	ESTs	2.00	3.25
324855	AW152305	Hs.122364	ESTs	2.74	3.43
324866	AI541214	Hs.46320	Small proline-rich protein SPRK (human,	1.07	0.95
324871	AW297755	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	1.68	1.21
324886	AA806794	Hs.131511	ESTs	2.56	5.61
324889	D31010		gb:HUML12147 Human fetal lung Homo sapie	2.20	4.65
324948	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN A	5.28	7.05
324953	AI264628	Hs.125428	ESTs	3.37	5.51
324958	AA625076	Hs.132892	protocadherin 20	5.12	9.81
324988	T06997	Hs.121028	hypothetical protein FLJ10549	2.52	1.08
325024	F13254	Hs.78672	laminin, alpha 4	5.24	10.22
325105	H97109	Hs.105421	ESTs	1.00	1.00
325108	AA401863	Hs.22380	ESTs	1.99	2.14
325114	D83901	Hs.315562	ESTs	2.73	3.17
325146	AI064690	Hs.171176	ESTs	1.86	3.41
325149	D61117	Hs.187646	ESTs	0.42	0.93
325187	AI653682	Hs.197812	ESTs	6.50	11.31
325228				6.18	15.76
325235				2.64	4.12
325328				2.87	4.42
325340				0.29	0.33
325367				16.56	24.29
325373				0.63	1.22
325389				0.88	1.05
325436				5.75	14.14
325471				8.46	17.82
325498				3.32	6.42
325557				5.51	8.28
325559				7.48	21.40
325560				4.08	6.25
325569				4.20	5.24
325585				1.10	1.13
325587				1.00	1.00
325597				2.98	13.40
325639				0.78	0.78
325685				0.46	0.66
325686				0.95	1.55
325735				4.48	9.20
325739				0.59	0.88
325740				2.42	6.61
325792				7.88	9.83
325819				4.74	7.18
325883				2.02	2.64
325895				7.78	15.98
325925				2.04	10.60
325932				4.18	7.36
325941				3.66	9.03
325969				0.61	0.80
325971				4.88	7.42
326025				0.55	1.07
326046				7.21	14.72
326099				3.60	5.98
326108				1.27	1.06
326163				3.27	5.70
326165				0.45	1.11
326189				0.13	0.45
326204				5.60	9.00
326230				7.00	12.01
326274				1.00	8.09
326360				9.86	15.35
326393				0.52	0.77
326505				1.00	1.42
326515				1.24	5.84
326589				9.20	13.49
326592				2.77	4.01
326605				2.01	2.53
326692				1.00	1.00
326693				1.00	1.31
326720				0.19	0.65
326742				2.34	7.20
326770				0.25	0.83
326818				3.09	4.56
326936				2.08	3.45
326964				0.41	1.70
326983				2.02	3.80
326991				1.09	1.20
327036				1.00	8.04
327040				3.05	4.22
327053				3.55	6.31
327075				1.59	1.40

327085	2.50	12.57
327130	5.38	8.04
327156	3.74	6.58
327220	1.28	1.54
327224	6.56	12.91
327288	2.61	5.40
327321	2.42	3.11
327332	6.62	10.58
327361	2.69	4.41
327377	2.04	6.72
327396	2.61	4.50
327414	1.00	8.01
327442	5.91	9.65
327467	6.58	18.01
327473	3.79	7.48
327483	4.08	8.87
327562	0.68	2.86
327568	1.00	2.00
327606	2.06	3.61
327611	5.90	14.26
327642	4.06	8.74
327654	1.05	2.08
327734	1.00	1.00
327775	1.46	11.79
327796	3.47	5.65
327840	3.26	6.64
327940	5.84	15.58
327984	0.36	1.50
328004	1.87	1.42
328021	0.42	0.59
328068	2.83	4.68
328100	3.04	5.39
328101	3.54	5.20
328113	0.72	0.91
328157	5.58	5.16
328196	5.76	11.13
328197	5.98	10.58
328264	3.11	4.88
328299	2.20	3.06
328342	1.49	1.94
328365	1.00	1.00
328369	4.40	7.36
328381	1.86	4.93
328451	5.51	7.56
328481	0.13	0.72
328500	2.71	3.97
328530	5.41	7.62
328600	3.14	10.68
328608	4.56	8.17
328616	2.24	11.91
328623	3.04	5.46
328632	0.70	1.19
328664	3.48	6.80
328666	10.42	26.47
328698	9.68	14.56
328700	2.74	10.22
328708	0.15	0.57
328735	6.23	8.91
328743	3.62	6.54
328806	0.22	0.78
328861	3.68	10.54
328908	5.42	16.36
328933	2.02	5.29
328934	1.73	4.45
328949	3.34	5.41
329005	2.88	7.26
329011	2.52	3.72
329033	1.00	1.03
329037	5.07	8.16
329067	1.98	2.41
329134	2.24	3.25
329157	2.30	11.04
329178	2.64	5.02
329192	6.41	15.27
329194	0.31	0.79
329204	1.60	3.75
329224	2.99	6.11
329228	0.83	0.83
329288	0.63	1.01
329337	1.00	1.00
329541	0.76	1.68
329560	1.34	2.02
329588	1.68	2.22
329643	4.18	11.77
329703	1.00	1.00

329764				5.78	15.50
329816				2.09	5.44
329860				3.13	10.77
329993				7.83	14.21
330020				5.58	13.12
330036				3.32	5.57
330052				4.31	7.97
330085				1.34	1.76
330088				4.70	12.46
330093				0.44	1.06
330100				3.47	4.83
330106				2.14	3.61
330107				3.17	6.87
330120				5.61	11.89
330123				4.50	12.74
330208				1.55	7.62
330263				13.10	23.38
330300				2.81	4.98
330313				3.00	4.41
330366				0.67	0.76
330372				4.76	11.82
330385	AA449749	Hs.182971	karyopherin alpha 5 (importin alpha 6)	2.14	2.15
330397	D14659	Hs.154387	KIAA0103 gene product	0.40	1.15
330468	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	1.11	0.94
330472	L24203	Hs.82237	ataxia-telangiectasia group D-associated	1.67	1.17
330478	L38486	Hs.296049	microfibrillar-associated protein 4	0.46	1.07
330493	M27826	Hs.267319	endogenous retroviral protease	1.07	0.95
330495	M31328	Hs.71642	guanine nucleotide binding protein (G pr	0.97	0.96
330506	M61906	Hs.6241	phosphoinositide-3-kinase, regulatory su	0.17	3.66
330512	M80563	Hs.81256	S100 calcium-binding protein A4 (calcium	0.60	1.06
330537	U19765	Hs.2110	zinc finger protein 9 (a cellular retrov	2.81	2.07
330547	U32989	Hs.183671	tryptophan 2,3-dioxygenase	3.91	1.49
330551	U39840	Hs.299867	hepatocyte nuclear factor 3, alpha	1.15	1.03
330568	U56244		(NONE)	2.83	4.79
330599	U90437		gb:Human RP1 homolog mRNA, 3'UTR region	2.08	1.54
330601	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	0.89	1.35
330605	X02419	Hs.77274	plasminogen activator, urokinase	1.87	1.55
330609	X04741	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.83	1.30
330617	X53587	Hs.85266	integrin, beta 4	1.54	1.15
330630	X78669	Hs.79088	reticulocalbin 2, EF-hand calcium bindin	1.39	1.19
330644	Y07755	Hs.38991	S100 calcium-binding protein A2	3.83	1.13
330650	Z68228	Hs.2340	junction plakoglobin	1.25	0.95
330660	AA347868	Hs.139293	ESTs, Weakly similar to ALU7_HUMAN ALU S	15.50	29.07
330692	AA017045	Hs.6702	ESTs	1.00	1.00
330707	AA133891	Hs.293690	ESTs	0.20	1.35
330715	AA233707	Hs.11571	Homo sapiens cDNA FLJ11570 fis, clone HE	0.12	1.40
330717	AA233926	Hs.52620	integrin, beta 8	6.62	5.42
330722	AA243560	Hs.34382	ESTs	1.40	1.65
330740	AA297746	Hs.22654	Homo sapiens voltage-gated sodium channe	0.27	2.04
330742	AA400979	Hs.25691	receptor (calcitonin) activity modifying	0.44	0.90
330744	AA406142	Hs.12393	dTDP-D-glucose 4,6-dehydratase	0.71	3.23
330751	AA428286	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	1.66	1.52
330760	AA448663	Hs.30469	ESTs	0.52	0.90
330763	AA450200	Hs.274337	hypothetical protein FLJ20666	0.37	0.97
330786	D60374	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	0.78	0.84
330790	T48536	Hs.105807	ESTs	0.23	3.17
330814	AA015730	Hs.265398	ESTs, Weakly similar to transformation-r	0.37	2.07
330827	AA040332	Hs.12744	ESTs	1.60	1.00
330844	AA063037	Hs.66803	ESTs	0.93	1.16
330901	AA157818	Hs.267319	endogenous retroviral protease	1.02	1.03
330931	F01443	Hs.284256	hypothetical protein FLJ14033 similar to	0.24	0.88
330952	H02855	Hs.29567	ESTs	0.08	1.31
330961	H10998	Hs.7164	a disintegrin and metalloproteinase doma	1.29	1.26
330968	H16568	Hs.23748	ESTs	0.48	0.96
331014	H98597	Hs.30340	hypothetical protein KIAA1165	0.29	0.74
331046	N66563	Hs.191358	ESTs	0.99	8.56
331060	N75081	Hs.157148	Homo sapiens cDNA FLJ11883 fis, clone HE	1.24	1.00
331099	R36671	Hs.83937	hypothetical protein	0.75	1.03
331108	R41408	Hs.21983	ESTs	1.00	2.75
331131	R54797		gb:yg87b07.s1 Soares infant brain 1NIB H	6.04	10.68
331135	R61398	Hs.4197	ESTs	0.80	0.96
331170	T23461	Hs.159293	ESTs	2.63	4.29
331180	T32446	Hs.6640	Human DNA sequence from PAC 75N13 on chr	1.78	2.71
331183	T40769	Hs.8469	ESTs	1.00	3.01
331203	T82310		(NONE)	1.70	3.80
331271	AA059347	Hs.82226	glycoprotein (transmembrane) nmb	1.20	3.19
331306	AA252079	Hs.63931	dachshund (Drosophila) homolog	0.31	1.30
331327	AA281076	Hs.109221	ESTs	2.09	2.41
331341	AA303125	Hs.23240	Homo sapiens cDNA FLJ13496 fis, clone PL	0.72	2.43
331359	AA416979	Hs.46901	KIAA1462 protein	0.09	0.91
331363	AA421562	Hs.91011	anterior gradient 2 (Xenepus laevis) hom	1.02	0.87
331378	AA448881	Hs.49282	hypothetical protein FLJ11088	1.03	1.23
331384	AA456001	Hs.93847	NADPH oxidase 4	1.40	1.00
331402	AA505135	Hs.44037	ESTs	1.80	3.93
331422	F10802	Hs.163628	ESTs, Moderately similar to ALU7_HUMAN	1.65	1.89

331490	N32912	Hs.26813	CDA14	2.48	1.73
331531	N51343		gb:yz15g04.s1 Soares_multiple_sclerosis_	0.98	1.68
331547	N54811		gb:od74f04.s1 NCI_CGAP_Ov2 Homo sapiens	3.80	5.75
331578	N67960	Hs.249989	ESTs	0.11	0.67
331589	N71027	Hs.152618	ESTs	1.09	1.38
331608	N89861	Hs.112110	PTD007 protein	0.93	0.76
331614	N92293	Hs.240272	EST	0.17	1.34
331668	W69707	Hs.58030	EST	2.24	3.82
331671	W72033	Hs.194695	ras homolog gene family, member I	1.00	1.24
331676	W79834	Hs.58559	ESTs, Weakly similar to rhotekin [M.musc	0.08	1.07
331681	W85712	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	8.72	4.27
331692	W93592	Hs.152213	wingless-type MMTV integration site fami	0.94	0.54
331717	AA190888	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par	1.57	1.34
331718	AA191404	Hs.104072	ESTs	6.80	11.77
331811	AA404500	Hs.301570	ESTs	1.10	1.00
331820	AA405970	Hs.97996	transcription termination factor, mitoc	0.73	0.59
331831	AA412031	Hs.97901	EST	2.77	4.08
331852	AA418988	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	0.23	0.93
331943	AA453418	Hs.21275	hypothetical protein FLJ11011	0.36	1.88
331969	AA460702	Hs.82772	collagen, type XI, alpha 1	1.00	1.00
331990	AA478102	Hs.139631	ESTs	3.04	3.87
332002	AA482009	Hs.105104	ESTs	1.19	0.78
332027	AA489671	Hs.65641	hypothetical protein FLJ20073	1.27	1.03
332029	AA489697	Hs.145053	ESTs	0.30	1.62
332033	AA489840	Hs.251014	EST	2.30	3.70
332048	AA496019	Hs.201591	ESTs	0.17	0.52
332071	AA598594	Hs.205293	KIAA1211 protein	1.35	1.23
332074	AA599012		gb:ae41e11.s1 Gessler Wilms tumor Homo s	0.19	2.00
332083	AA600200	Hs.155546	KIAA1080 protein; Golgi-associated, gamm	0.31	1.18
332085	AA600353	Hs.173933	nuclear factor I/A	0.30	1.50
332125	AA609861	Hs.312447	ESTs	0.22	0.62
332177	F10812	Hs.101433	ESTs	8.21	18.03
332180	H03348	Hs.7327	claudin 1	2.27	1.57
332185	H10356	Hs.101689	ESTs	0.09	1.18
332203	H49388	Hs.317769	EST	8.05	5.02
332232	N48891	Hs.101915	Stargardt disease 3 (autosomal dominant)	0.78	0.85
332240	N54803	Hs.324267	ESTs, Weakly similar to putative p150 [	0.96	1.23
332261	N70294	Hs.269137	ESTs	2.40	3.74
332275	R08838	Hs.26530	serum deprivation response (phosphatidyl	0.27	0.75
332280	R38100	Hs.146381	RNA binding motif protein, X chromosome	0.39	1.88
332299	R69250	Hs.21201	nectin 3; DKFZP566B0846 protein	5.24	12.76
332304	R74041	Hs.101539	ESTs	1.44	3.18
332314	T25862	Hs.101774	hypothetical protein FLJ23045	0.68	1.32
332384	M11433	Hs.101850	retinol-binding protein 1, cellular	1.71	0.88
332434	N75542	Hs.289068	Homo sapiens cDNA FLJ11918 fis, clone HE	0.43	0.86
332445	T63781	Hs.11112	ESTs	0.68	1.00
332453	L00205	Hs.111758	keratin 6A	31.54	1.00
332458	M33493	Hs.250700	tryptase beta 1	0.51	1.00
332504	AA053917	Hs.15106	chromosome 14 open reading frame 1	0.79	1.24
332525	M17252	Hs.278430	cytochrome P450, subfamily XXIA (steroid	0.98	1.70
332530	M31682	Hs.1735	inhibin, beta B (activin AB beta polypep	0.88	0.66
332535	N20284	Hs.19280	cysteine-rich motor neuron 1	0.22	1.46
332539	AA412528	Hs.20183	ESTs, Weakly similar to AF164793 1 prote	0.93	1.49
332559	M13955	Hs.166189	cytokeratin 2	0.35	1.13
332563	N92924	Hs.274407	protease, serine, 16 (thymus)	1.00	1.00
332565	AA234896	Hs.25272	E1A binding protein p300	0.36	1.05
332594	AA279313	Hs.3239	methyl CpG binding protein 2 (Rett syndr	0.53	0.59
332634	S38953	Hs.283750	tenascin XA	0.38	1.16
332638	AA283034	Hs.50640	JAK binding protein	1.00	1.70
332640	AA417152	Hs.5101	protein regulator of cytokinesis 1	6.15	1.16
332654	AA001296	Hs.288217	hypothetical protein MGC2941	1.50	2.73
332665	AA223335	Hs.63788	propionyl Coenzyme A carboxylase, beta p	1.20	0.91
332692	AA496035	Hs.247926	gap junction protein, alpha 5, 40kD (con	0.17	1.12
332716	L00058	Hs.79070	v-myc avian myelocytomatosis viral oncog	1.00	1.44
332736	L13773	Hs.114765	myeloid/lymphoid or mixed-lineage leukem	1.00	1.81
332758	X93921	Hs.296938	dual specificity phosphatase 7	0.53	0.78
332781	AA233258	Hs.247112	hypothetical protein FLJ10902	1.44	1.56
332792				1.70	1.19
332816				1.85	2.47
332858				1.04	1.57
332906				3.48	8.04
332911				1.00	1.00
332912				1.06	4.40
332922				1.00	1.00
332956				0.42	0.88
332959				1.96	6.34
332982				0.56	0.99
332984				0.30	0.78
332998				1.47	2.01
333058				0.47	1.38
333097				2.14	3.19
333121				2.76	3.70
333122				1.92	1.21
333123				1.85	1.39
333138				0.47	0.52

333139	1.88	0.84
333140	0.21	0.64
333221	1.51	1.11
333260	0.75	1.01
333380	6.68	15.75
333387	4.56	12.61
333512	5.05	8.01
333524	2.28	3.98
333585	2.31	1.53
333603	2.23	1.17
333604	2.51	1.58
333618	0.52	0.98
333627	1.44	1.36
333628	1.90	1.90
333650	1.85	2.10
333678	1.85	2.35
333750	2.18	5.67
333763	1.99	2.60
333767	1.02	0.96
333768	1.78	1.65
333769	2.15	2.13
333772	1.46	2.53
333777	1.00	1.42
333846	2.99	4.50
333884	0.47	0.94
333887	0.50	1.00
333891	0.43	0.89
333892	0.51	0.91
333904	0.26	1.13
333906	0.55	0.98
333948	1.70	2.15
333954	0.37	1.09
333966	8.10	14.30
333968	0.63	1.38
334061	4.24	12.30
334094	1.30	12.03
334113	4.55	8.63
334161	0.82	1.59
334183	0.47	0.76
334187	1.36	3.70
334219	0.69	1.04
334222	1.88	1.70
334223	4.72	3.14
334239	0.79	0.62
334255	0.45	1.10
334333	1.00	3.56
334378	3.98	5.76
334382	1.50	1.31
334492	3.59	4.75
334562	5.94	15.40
334588	8.14	19.53
334616	1.55	1.56
334633	5.16	8.07
334648	0.59	2.13
334787	3.70	7.15
334866	8.13	10.60
334891	0.32	1.14
334933	1.00	3.84
334934	4.01	7.43
334945	1.04	2.96
334967	0.29	1.14
334990	1.50	1.39
335015	5.88	18.65
335093	0.55	1.75
335120	4.31	8.01
335125	0.38	1.97
335179	1.24	1.98
335188	0.46	1.47
335211	1.61	1.42
335288	0.73	0.97
335289	0.20	0.26
335361	2.18	1.58
335379	0.50	0.71
335414	3.64	14.94
335416	2.93	3.98
335496	0.96	0.91
335497	1.71	1.92
335548	1.15	2.40
335551	3.22	10.54
335558	3.42	4.89
335586	5.50	12.75
335619	2.99	3.07
335620	3.80	8.29
335621	0.28	0.57
335682	0.46	1.17

335686	2.55	3.81
335755	2.24	1.07
335784	0.20	0.97
335814	1.13	1.48
335815	2.45	3.51
335823	1.00	4.16
335835	0.49	1.70
335851	1.66	1.39
335868	2.98	6.43
335896	0.98	0.99
335936	12.10	21.93
335948	1.00	1.64
335983	1.00	4.21
335995	0.37	1.17
336021	1.04	0.84
336034	11.40	23.54
336038	1.19	1.21
336066	0.54	1.63
336107	0.95	0.70
336205	3.13	6.29
336275	3.20	10.10
336292	2.34	3.09
336331	1.00	1.00
336419	0.65	0.79
336632	2.33	2.16
336633	2.55	2.23
336634	2.19	2.03
336635	2.69	2.48
336636	2.13	1.83
336637	2.43	2.24
336638	2.31	2.03
336659	0.60	1.31
336675	0.31	1.18
336684	1.50	1.14
336694	4.74	7.10
336716	4.43	6.37
336721	2.20	0.74
336798	1.64	2.14
336900	6.14	12.73
336948	1.00	1.00
337028	1.30	2.09
337043	4.01	11.53
337046	1.67	1.84
337054	2.78	7.35
337128	7.20	16.14
337162	3.45	5.34
337183	5.72	11.41
337184	3.72	5.90
337192	1.27	1.06
337194	1.88	1.68
337229	0.22	1.03
337268	1.00	3.31
337299	3.23	5.14
337325	2.76	3.72
337389	5.80	10.42
337493	2.06	6.30
337497	7.88	20.29
337500	3.80	4.48
337549	1.66	2.31
337603	1.27	8.54
337605	5.76	7.16
337671	0.73	0.97
337755	1.54	0.92
337786	5.07	9.73
337809	6.18	12.87
337862	3.78	12.97
337871	2.66	8.16
337958	0.26	1.34
338008	1.48	1.12
338033	2.38	14.59
338083	0.65	2.16
338110	1.00	1.61
338112	5.86	8.25
338145	1.70	1.97
338148	8.07	18.19
338158	1.30	4.55
338161	2.58	3.57
338179	1.00	1.00
338182	3.32	4.63
338189	1.00	3.34
338197	0.99	1.69
338199	4.58	7.62
338215	6.01	15.85
338279	0.63	0.95
338316	20.58	38.66

338322	3.23	7.39
338357	4.10	11.39
338359	10.12	21.59
338366	0.69	1.02
338374	0.40	1.18
338414	0.47	1.06
338418	6.12	13.86
338469	3.09	5.11
338501	6.28	10.32
338506	6.97	12.41
338523	3.10	5.84
338549	1.70	2.70
338561	0.79	0.81
338662	1.72	1.46
338671	0.17	0.91
338676	2.10	15.86
338726	1.20	1.09
338779	0.12	0.57
338804	0.99	1.67
338836	1.00	1.00
338871	4.30	9.81
338872	5.02	12.81
338879	0.23	1.12
338937	6.55	12.26
338966	1.76	5.42
338993	1.00	2.40
339047	5.26	10.81
339100	5.10	6.88
339114	1.00	1.70
339121	1.00	3.75
339170	10.36	19.67
339229	4.08	13.48
339264	2.64	3.83
339293	1.73	1.94

TABLE 8B shows the accession numbers for those Pkeys in Table 8A lacking unigeneID's. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
322044	187363_1	AW340926 AA249063 N86075
322060	44320_1	AI341937 AW003063 U34725 AA904742
321430	42705_1	X57414 X57415
321467	43034_1	X13075 X13076
322125	46779_1	R93901 AF075073 R93902
322166	46861_1	H69434 AF085958 H69846
322173	46873_1	H52567 H52557 AF085970 H52164
322178	46882_1	H56535 AF085980 H56712
322179	46885_1	H92891 AF085982 H92777
321577	1615102_1	H84849 H84252 H84260 H86664 H85320
321587	1615333_1	H95531 H95521 H84529
313723	111953_1	AA070412 AA102346 AA081885
320997	627492_1	H22544 H46842 AI204929
322278	47271_1	W69304 AF086283 W69200
321687	218439_1	AA625149 AA313030 AA313052 H97463
313883	129439_1	AA665089 AA135130 AA484059 AA102419 AW877765
322320	47422_1	W79150 AF086419
322339	814584_1	AI668646 AI734214 W17348
314648	293660_1	AW979268 AA878419 AA431342 AA431628
300201	682222_1	AI308300 AI308296
306897	25196_-2	AI093967
323155	979809_1	AL120701 AL135041 AL121524
322527	38927_1	AF147359 T58511 T58560
322585	473768_2	W88919 W89125
300362	1574395_1	Z42308 H23514
322635	82296_1	AA005129 AA679084 AA694399
322664	85042_1	AA011522 AA702841 AA011691 AA330797
315454	380580_1	AI239464 AI239473 AA625812 AI208703
322687	37372_1	AF074666 AI110759 AF090902
314852	327472_1	AI903735 AA491283 AI694953 AW976903 AA761362
307783	697809_1	AI347274 AW844024
324072	269032_1	AA381722 AA381829 AW963906 AW963902 AA381242
300627	221345_1	AA488472 W27363 AA317053 BE082689 AW967036 BE079872
323505	196389_1	AW970512 AA280251 AI652287 BE466438 AI650725 AA551854 AA281574 AW571481
315791	403558_1	AA678177 AA677034
324303	233842_1	AL118754 AA333202 H38001
316519	442885_1	AA847835 AA768376
300926	333127_1	AA504860 AA504911

324580	328264_1	AA492588 AA492498 AA492571
301882	275087_1	T78054 T79888 AA398185
324804	398093_1	AI692552 AI393343 AI800510 AI377711 F24263 AA661876
324889	1515978_1	D31010 D30991 D31168 D31166 D31465
302697	43219_1	AJ001409 AJ001410
302711	45419_1	L08442 D51348
302742	458_39	L12061
318499	364430_1	T25451 AA585296 AA585305
310624	34624_4	U88896 U88898 AA916056 T03285 AI341594 AI359534 AI634031 U88897
302847	458_105	X98941 X98942 X98943 X98953 X98949
304122	77271_-5	H28966
303598	270283_1	AA382814 AA402411 AA412355
311409	837264_1	AI698839 AI909260 AI909259
312094	797889_1	Z78390 T97427
319312	1540116_1	Z45481 F12393 T74437
319407	1688823_1	R05329 R01555 R08276
319425	1689571_1	T82930 R02424 T85145
320007	229683_1	AA336314 T82938 AA327744 AW967388 AA639967 T10753
320018	1815987_1	T83263 T85731 T85730
319484	1691553_1	T91772 R07257 R07098
318865	1535937_1	H10818 F07831 Z43072
312220	1671607_1	N74613 T98756 T98589
319546	243305_1	R09692 R09414 AA346353
312389	902067_1	AI863140 W80703 R43474
319611	1566863_1	H14957 R56522 R11908
312437	291472_1	BE080180 AW827313 AW231970 AA995028 AA428584 AW872716 AW892508 AW854593 AA578441 AW975234 AA664937 AA984131 AA528743 AA552874 AA564758 AW063245 AI267534 AW070190 AW893483 AA770330 AA906928 AA906582 AA758746 AA551717 AW063311 AA429538
311896	579192_1	AW206447 AI248530 AI084433 AI400976 R16553
319834	112523_1	AA071267 T65940 T64515 AA071334
321102	80531_1	AA018306 H38925 AA001221
321158	410938_1	H79670 H47798 AA700289
321199	212379_1	N34524 AA305071 AW954803 AA502335 AI433430 AI203597 AW026670 AW265323 AW850787 AA317554 AW993643 AW835572 AW385512 AI334966 W32951 H62656 H53902 R88904 AW835732
305528	28832_-3	AA769156
321270	1662057_1	N59537 N78278 R83560
314126	177666_1	AA226431 AA226569 AA488748
320714	743644_1	R91883 AI445591
306442	AA976899	
306446	AA977348	
306458	AA978186	
306510	AA988546	
306557	AA994530	
306572	AA995686	
306582	AA996248	
306656	AI004024	
306686	AI015615	
306751	AI032589	
308011	AI439473	
306892	AI092465	
308106	AI476803	
308154	AI500600	
306956	AI125111	
306958	AI125152	
308213	AI557041	
308216	AI557135	
308219	AI557246	
308588	AI718299	
308599	AI719893	
308643	AI745040	
308673	AI760864	
308697	AI767143	
308778	AI811109	
308808	AI818289	
308875	AI832332	
308886	AI833240	
308898	AI858845	
308966	AI870704	
308979	AI873111	
303011	41689_1	AF090405 AF090407 AF090406
303077	44060_1	AF163305 AF163307 AF163303
305016	AA626876	
305034	AA630128	
305072	AA641012	
305148	AA654070	
305190	AA665955	
303978	AW513315	
303990	AW515465	
303998	AW516449	
303999	AW516611	
305235	AA670480	
305312	AA700201	
305413	AA724659	
305447	AA737856	
321244	29327_1	AF068654 AF068656 AF068655

305614	AA782866	
305637	AA806124	
305639	AA806138	
305650	AA807709	
305690	AA813477	
305728	AA828209	
305759	AA835353	
305792	AA845256	
307041	AI144243	
307091	AI167439	
307181	AI189251	
305901	AA872968	
305910	AA875981	
307415	AI242118	
307426	AI243364	
307517	AI275055	
307551	AI281556	
307561	AI282207	
307608	AI290295	
307691	AI318285	
307730	AI336092	
307760	AI342387	
307764	AI342731	
307796	AI350556	
309045	AI910902	
309051	AI911975	
307807	AI351799	
307808	AI351826	
307820	AI355761	
307852	AI365541	
309122	AI928178	
309164	AI937761	
309177	AI951118	
307902	AI380462	
309299	AW003478	
309303	AW004823	
309476	AW129368	
309532	AW151119	
309747	AW264889	
309769	AW272346	
309799	AW276964	
309866	AW299916	
302679	311853_1	H65022 AA186889
309923	AW340684	
309928	AW341418	
309931	AW341683	
309933	AW341936	
302705	31765_1	U09060 U09061
302789	34161_1	AJ245067 AJ245070
304006	AW517947	
304024	T03036	
304026	T03160	
304028	T03266	
304046	T54803	
304061	T61521	
304063	T62536	
302802	34487_1	Y08250 Y08245
304114	R78946	
304155	H68696	
304203	N56929	
304234	W81608	
304348	AA179868	
304430	AA347682	
304456	AA411240	
304521	AA464716	
304526	AA476427	
304607	AA513322	
304735	AA576453	
304760	AA580401	
306015	AA897116	
306063	AA906316	
306065	AA906725	
306104	AA910956	
306109	AA911861	
306242	AA932805	
306288	AA936900	
306396	AA970223	
330568	NOT_FOUND_entrez	U56244
330599	15323_-12	U90437
331131	genbank_R54797	R54797
331203	NOT_FOUND_entrez	T82310
331531	genbank_N51343	N51343
331547	467396_1	AA828597 N54811
332074	genbank_AA599012	AA599012

TABLE 8C shows the genomic position for those Pkeys in Table 8A lacking unigene ID's and accession numbers. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
332792	Dunham, I. et.al.	Plus	73381-73768
332816	Dunham, I. et.al.	Plus	359844-360030
332906	Dunham, I. et.al.	Plus	1923101-1923205
332911	Dunham, I. et.al.	Plus	1961767-1961858
332912	Dunham, I. et.al.	Plus	1962120-1962246
332922	Dunham, I. et.al.	Plus	2009620-2009738
332956	Dunham, I. et.al.	Plus	2510528-2510658
332959	Dunham, I. et.al.	Plus	2518145-2518213
333138	Dunham, I. et.al.	Plus	3369205-3369323
333139	Dunham, I. et.al.	Plus	3369495-3369571
333221	Dunham, I. et.al.	Plus	3978070-3978187
333380	Dunham, I. et.al.	Plus	4904775-4904846
333387	Dunham, I. et.al.	Plus	4910935-4910997
333512	Dunham, I. et.al.	Plus	5560510-5560564
333524	Dunham, I. et.al.	Plus	5612620-5612780
333585	Dunham, I. et.al.	Plus	6234778-6234894
333618	Dunham, I. et.al.	Plus	6562391-6562566
333627	Dunham, I. et.al.	Plus	6620584-6620903
333628	Dunham, I. et.al.	Plus	6629004-6629233
333650	Dunham, I. et.al.	Plus	6796852-6797128
333678	Dunham, I. et.al.	Plus	7068223-7068288
333750	Dunham, I. et.al.	Plus	7608165-7608234
333763	Dunham, I. et.al.	Plus	7692491-7692630
333767	Dunham, I. et.al.	Plus	7694407-7694623
333768	Dunham, I. et.al.	Plus	7695440-7695697
333769	Dunham, I. et.al.	Plus	7696625-7696707
333772	Dunham, I. et.al.	Plus	7706773-7706902
333777	Dunham, I. et.al.	Plus	7746805-7746916
333846	Dunham, I. et.al.	Plus	8008623-8008757
333884	Dunham, I. et.al.	Plus	8153960-8154161
333887	Dunham, I. et.al.	Plus	8154882-8155025
333891	Dunham, I. et.al.	Plus	8156437-8156709
333892	Dunham, I. et.al.	Plus	8156825-8157001
333948	Dunham, I. et.al.	Plus	8583497-8583627
333954	Dunham, I. et.al.	Plus	6563186-6563335
333966	Dunham, I. et.al.	Plus	8655643-8655826
333968	Dunham, I. et.al.	Plus	8681004-8681241
334061	Dunham, I. et.al.	Plus	9686941-9687077
334094	Dunham, I. et.al.	Plus	9889953-9890105
334113	Dunham, I. et.al.	Plus	10282459-10282597
334161	Dunham, I. et.al.	Plus	10599033-10599180
334219	Dunham, I. et.al.	Plus	12716160-12716384
334239	Dunham, I. et.al.	Plus	13056569-13056693
334333	Dunham, I. et.al.	Plus	13603544-13603657
334378	Dunham, I. et.al.	Plus	13907239-13907370
334382	Dunham, I. et.al.	Plus	13915866-13916036
334562	Dunham, I. et.al.	Plus	14987847-14987940
334588	Dunham, I. et.al.	Plus	15032740-15032817
334616	Dunham, I. et.al.	Plus	15176123-15176470
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334891	Dunham, I. et.al.	Plus	19299770-19299944
334934	Dunham, I. et.al.	Plus	20103970-20104058
335015	Dunham, I. et.al.	Plus	20682792-20682945
335120	Dunham, I. et.al.	Plus	21436286-21436384
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335416	Dunham, I. et.al.	Plus	23237354-23237465
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336637	Dunham, I. et.al.	Plus	989276-990813
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337183	Dunham, I. et.al.	Plus	23943606-23943696
337184	Dunham, I. et.al.	Plus	23973949-23974016
337268	Dunham, I. et.al.	Plus	28011979-28012034
337299	Dunham, I. et.al.	Plus	29022656-29022775
337389	Dunham, I. et.al.	Plus	31401509-31401579
337493	Dunham, I. et.al.	Plus	33330760-33330981
337549	Dunham, I. et.al.	Plus	34474472-34474531
337755	Dunham, I. et.al.	Plus	3971764-3971900
337809	Dunham, I. et.al.	Plus	4449069-4449193
337871	Dunham, I. et.al.	Plus	5443027-5443101
337958	Dunham, I. et.al.	Plus	6969162-6969270
338008	Dunham, I. et.al.	Plus	7697068-7697236
338033	Dunham, I. et.al.	Plus	8092128-8092271
338110	Dunham, I. et.al.	Plus	10384481-10384621
338112	Dunham, I. et.al.	Plus	10391398-10391600
338145	Dunham, I. et.al.	Plus	11386629-11386692
338148	Dunham, I. et.al.	Plus	11448985-11449085
338179	Dunham, I. et.al.	Plus	12808775-12808833
338197	Dunham, I. et.al.	Plus	13638107-13638181
338279	Dunham, I. et.al.	Plus	16168944-16169091
338316	Dunham, I. et.al.	Plus	17089711-17089988
338322	Dunham, I. et.al.	Plus	17132477-17132547
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338937	Dunham, I. et.al.	Plus	29160655-29160725
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339170	Dunham, I. et.al.	Plus	32216399-32216527
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332998	Dunham, I. et.al.	Minus	2711704-2711565
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333097	Dunham, I. et.al.	Minus	3204124-3204036
333121	Dunham, I. et.al.	Minus	3308446-3308358
333122	Dunham, I. et.al.	Minus	3309596-3309531
333123	Dunham, I. et.al.	Minus	3310817-3310749
333140	Dunham, I. et.al.	Minus	3377220-3376309
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333603	Dunham, I. et.al.	Minus	6466335-6465727
333604	Dunham, I. et.al.	Minus	6467090-6466768
333904	Dunham, I. et.al.	Minus	8217374-8217261
333906	Dunham, I. et.al.	Minus	8218238-8218063
334183	Dunham, I. et.al.	Minus	11832582-11832508
334187	Dunham, I. et.al.	Minus	11921456-11921205
334222	Dunham, I. et.al.	Minus	12732417-12732289
334223	Dunham, I. et.al.	Minus	12734365-12734269
334255	Dunham, I. et.al.	Minus	13200776-13200692
334492	Dunham, I. et.al.	Minus	14478333-14478172
334648	Dunham, I. et.al.	Minus	15363301-15363222
334787	Dunham, I. et.al.	Minus	16299093-16298937
334933	Dunham, I. et.al.	Minus	20078117-20077991

334945	Dunham, I. et.al.	Minus	20138885-20138837
334967	Dunham, I. et.al.	Minus	20173311-20173218
334990	Dunham, I. et.al.	Minus	20341159-20341087
335093	Dunham, I. et.al.	Minus	21297367-21297214
335288	Dunham, I. et.al.	Minus	22304275-22303770
335289	Dunham, I. et.al.	Minus	22305950-22305708
335548	Dunham, I. et.al.	Minus	24662773-24662673
335551	Dunham, I. et.al.	Minus	24679828-24678961
335619	Dunham, I. et.al.	Minus	25082677-25082498
335620	Dunham, I. et.al.	Minus	25092561-25092434
335621	Dunham, I. et.al.	Minus	25098878-25098767
335682	Dunham, I. et.al.	Minus	25421215-25421093
335755	Dunham, I. et.al.	Minus	25763806-25763747
335814	Dunham, I. et.al.	Minus	26320043-26319845
335815	Dunham, I. et.al.	Minus	26320518-26320421
335835	Dunham, I. et.al.	Minus	26393311-26393245
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335868	Dunham, I. et.al.	Minus	26711437-26711300
335896	Dunham, I. et.al.	Minus	26977639-26977558
335936	Dunham, I. et.al.	Minus	27360474-27360400
335948	Dunham, I. et.al.	Minus	27555924-27555788
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336275	Dunham, I. et.al.	Minus	32086675-32086536
336292	Dunham, I. et.al.	Minus	32818035-32817927
336331	Dunham, I. et.al.	Minus	33594527-33594371
336419	Dunham, I. et.al.	Minus	34052568-34052445
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336684	Dunham, I. et.al.	Minus	2158060-2157993
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336798	Dunham, I. et.al.	Minus	5888954-5888757
337043	Dunham, I. et.al.	Minus	17407330-17407251
337046	Dunham, I. et.al.	Minus	17610892-17610821
337128	Dunham, I. et.al.	Minus	22215251-22215034
337192	Dunham, I. et.al.	Minus	24591853-24591771
337194	Dunham, I. et.al.	Minus	24610510-24610359
337229	Dunham, I. et.al.	Minus	26716579-26716481
337325	Dunham, I. et.al.	Minus	30015948-30015800
337497	Dunham, I. et.al.	Minus	33371317-33371258
337500	Dunham, I. et.al.	Minus	33376212-33376158
337603	Dunham, I. et.al.	Minus	1299296-1299194
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337671	Dunham, I. et.al.	Minus	3260634-3260547
337786	Dunham, I. et.al.	Minus	4133203-4133081
337862	Dunham, I. et.al.	Minus	5347658-5347550
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338215	Dunham, I. et.al.	Minus	14055447-14055355
338469	Dunham, I. et.al.	Minus	20520387-20520242
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338561	Dunham, I. et.al.	Minus	22311966-22311856
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338726	Dunham, I. et.al.	Minus	25926206-25925618
338779	Dunham, I. et.al.	Minus	27030151-27029795
338871	Dunham, I. et.al.	Minus	28301708-28301611
338872	Dunham, I. et.al.	Minus	28300921-28300790
338966	Dunham, I. et.al.	Minus	29614876-29614749
339229	Dunham, I. et.al.	Minus	32722330-32722199
339264	Dunham, I. et.al.	Minus	32975145-32975053
325228	6381940	Plus	2630-2694
325235	6381943	Minus	162154-162264
329588	3962484	Plus	1169-1619
329560	3962491	Plus	2095-2990
329541	3983503	Minus	2765-3059
325328	5866875	Plus	86780-86854
325340	6017033	Minus	166656-166819
325373	5866920	Minus	1136686-1136777
325367	5866920	Minus	922881-922958
325389	5866921	Plus	239672-239759
325436	5866939	Minus	29778-29907
325498	5866967	Plus	173372-173930
325471	6017034	Minus	289268-289342
325557	6056302	Plus	50921-51050
325559	6249595	Minus	118590-119172
325560	6249595	Minus	133794-133981
325569	6249599	Plus	79927-80217
325587	6682462	Plus	126724-126967
325585	6682462	Plus	73476-73574
325597	5866992	Plus	1065020-1065089
325639	5867002	Plus	253525-253608

325739	5867038	Minus	205138-205269
325740	5867038	Minus	207533-207690
325792	6469828	Minus	1018-1176
325735	6552447	Minus	269122-269190
325685	6682468	Plus	117397-117483
325686	6682468	Plus	118337-118439
325819	6682490	Minus	130314-130370
329764	6048195	Minus	109733-109968
329703	6065793	Minus	139994-140138
329643	6448539	Plus	53403-53537
329816	6624888	Minus	70296-70423
329860	6687260	Minus	163474-163605
325883	5867087	Plus	22498-22663
325895	5867097	Plus	358317-358476
325925	5867124	Plus	115749-115962
325932	5867127	Plus	7369-7441
325941	5867133	Minus	64228-64402
325969	5867153	Plus	101911-102081
325971	5867153	Plus	105841-106035
329993	4567166	Minus	101307-101434
330020	6671887	Plus	172397-172491
326163	5867168	Minus	7831-8035
326274	5867171	Minus	410289-410404
326025	5867176	Plus	70854-70915
326046	5867182	Minus	62668-62825
326099	5867186	Minus	661381-661510
326108	5867187	Minus	23784-23903
326165	5867208	Minus	62787-62929
326189	5867212	Plus	69288-69413
326204	5867218	Minus	148088-148200
326230	5867230	Minus	301868-301972
330052	4567182	Plus	352560-352963
330036	6042048	Plus	117120-117216
326360	5867293	Plus	13627-13844
326589	5867320	Plus	22760-22919
326393	5867341	Plus	41702-41841
326505	5867435	Minus	8818-8949
326515	5867439	Plus	36683-36809
326592	6138928	Plus	23689-23828
330107	6015249	Minus	100091-100282
330106	6015249	Minus	99443-99778
330100	6015253	Plus	21166-21301
330093	6015278	Plus	1043-1199
330088	6015293	Plus	37517-37638
330085	6015302	Minus	59613-59770
330120	6671864	Minus	127553-127656
330123	6671869	Minus	35311-35406
326742	5867611	Minus	95187-95248
326605	5867637	Plus	24656-24749
326818	6117831	Minus	15199-15309
326720	6552456	Plus	84525-84677
326770	6598307	Minus	513603-513668
326692	6682502	Plus	117697-117899
326693	6682502	Minus	335002-335095
326983	5867657	Minus	16023-16581
326991	5867660	Plus	18147-18339
326936	6004446	Minus	10217-10357
326964	6469836	Plus	75340-75456
327040	6531965	Plus	783670-783817
327053	6531965	Plus	2247267-2247437
327075	6531965	Plus	4041318-4041431
327085	6531965	Plus	4734947-4735069
327036	6531965	Plus	319951-320040
327130	6531976	Plus	20247-22343
327156	5866841	Minus	2462-2620
327288	5867481	Plus	48583-48773
327332	5867516	Minus	56361-56532
327220	5867525	Minus	65701-65781
327224	5867534	Plus	188468-188544
327321	6249562	Minus	99745-99836
327361	6552412	Minus	61013-62130
327396	5867743	Plus	8702-8820
327414	5867750	Plus	102461-102586
327442	5867759	Plus	111483-111618
327467	5867772	Plus	88030-88151
327473	5867775	Plus	75101-75181
327483	5867783	Plus	181573-181662
327377	5867793	Minus	37610-37676
327562	5867804	Minus	343989-344474
327568	5867811	Minus	46152-46287
327606	6004463	Plus	200262-200495
327611	5867868	Minus	175063-175392
327642	5867891	Minus	2513-2743
327654	5867910	Minus	97564-97710
327734	5867940	Minus	31003-31583

327775	5867964	Minus	130791-130871
327796	5867982	Plus	85267-85405
327840	6249578	Minus	73065-73206
330208	6013599	Plus	66517-66931
330263	6671884	Minus	101503-101634
328004	5867993	Minus	157407-157887
328101	5868020	Plus	289920-290014
328100	5868020	Minus	263545-263635
328113	5868024	Minus	80378-80491
328157	5868064	Plus	73326-73615
328196	5868080	Minus	16551-16729
328197	5868081	Minus	42133-42438
327940	5868197	Minus	95240-95428
327984	5868216	Plus	66611-66677
328021	5902482	Plus	713478-714590
328068	6117819	Plus	253903-254022
328264	6381912	Plus	55086-55404
330300	2905862	Minus	3246-3302
328608	5868222	Minus	87770-87953
328600	5868229	Minus	38889-40010
328616	5868239	Plus	293920-294224
328623	5868246	Minus	120020-120126
328632	5868247	Plus	76734-76853
328666	5868254	Minus	778-901
328698	5868264	Minus	625555-625633
328700	5868264	Plus	764089-764203
328708	5868271	Minus	68114-68854
328735	5868289	Plus	89389-89455
328743	5868289	Plus	274638-274726
328806	5868324	Plus	29408-29684
328299	5868366	Minus	149708-149889
328342	5868383	Plus	59955-60094
328365	5868387	Minus	270724-270798
328369	5868388	Plus	75371-75583
328381	5868392	Plus	662758-662848
328451	5868425	Minus	217275-217336
328481	5868449	Minus	8987-9180
328500	5868464	Plus	59098-59481
328530	5868482	Plus	334973-335406
328664	6004473	Plus	1193739-1193866
328861	6381928	Minus	108317-108403
328908	5868493	Plus	117002-117059
328933	5868500	Plus	771755-771889
328934	5868500	Plus	846342-846448
328949	6456765	Minus	43552-43619
330313	6042030	Minus	33642-33775
329005	5868542	Plus	85470-85673
330366	2944106	Plus	151837-151914
330372	6580495	Minus	317461-317688
329033	5868561	Minus	5390-5479
329037	5868562	Minus	32466-32562
329067	5868591	Minus	146417-147652
329134	5868679	Plus	29959-30018
329157	5868687	Minus	145940-146155
329178	5868704	Plus	179177-179463
329192	5868716	Plus	166936-167020
329194	5868716	Minus	304450-304559
329204	5868720	Minus	3050-3190
329224	5868728	Plus	27422-27664
329228	5868728	Minus	50118-50287
329288	5868771	Plus	25554-26299
329337	5868806	Minus	467155-467222
329011	6682532	Plus	48658-48741

TABLE 9A: Potential Therapeutic, Diagnostic and Prognostic targets for Therapy of Lung Cancer

Table 9A shows about 1312 genes up-regulated in lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) relative to normal body tissues. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 9B show the accession numbers for those Pkey's lacking UnigeneID's for table 9A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 9C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 9A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
400195			NM_007057*:Homo sapiens ZW10 interactor	1.00	1.00
400205			NM_006265*:Homo sapiens RAD21 (S. pombe)	15.80	396.00
400220			Eos Control	2.28	2.84
400277			Eos Control	7.68	9.72
400285			Eos Control	1.00	1.00
400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	1.04	2.24
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	132.45	4.00
400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	43.86	74.00
400301	X03635	Hs.1657	estrogen receptor 1	1.00	1.00
400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	1.75	1.65
400328	X87344	Hs.180062	transporter 2, ATP-binding cassette, sub	0.87	1.80
400419	AF084545		Target	156.55	253.00
400512			NM_030878*:Homo sapiens cytochrome P450,	1.00	2.00
400517	AF242388		lengsin	3.67	87.00
400560			NM_030878*:Homo sapiens cytochrome P450,	1.00	1.00
400664			NM_002425:Homo sapiens matrix metallopro	20.26	45.00
400665			NM_002425:Homo sapiens matrix metallopro	1.36	1.07
400666			NM_002425:Homo sapiens matrix metallopro	3.26	3.22
400749			NM_003105*:Homo sapiens sortilin-related	1.00	91.00
400763			Target Exon	7.63	24.00
401027			Target Exon	1.00	1.00
401093			C12000586*:gi|6330167|dbj|BAA86477.1| (A	1.00	155.00
401203			Target Exon	1.00	86.00
401212			C12000457*:gi|7512178|pir||T30337 polypr	1.00	400.00
401411			ENSP00000247172*:HYPOTHETICAL 126.2 kDa	1.00	72.00
401435			C14000397*:gi|7499898|pir||T33295 hypoth	1.00	64.00
401464	AF039241		histone deacetylase 5	3.82	49.00
401714			ENSP00000241802*:CDNA FLJ11007 FIS, CLON	2.02	40.00
401747			Homo sapiens keratin 17 (KRT17)	128.43	68.00
401760			Target Exon	1.74	35.00
401780			NM_005557*:Homo sapiens keratin 16 (foca	26.47	10.50
401781			Target Exon	10.33	4.61
401785			NM_002275*:Homo sapiens keratin 15 (KRT1	4.13	2.70
401797			Target Exon	1.44	2.10
401961			NM_021626:Homo sapiens serine carboxypep	1.41	1.86
401985	AF053004		class I cytokine receptor	1.00	177.00
401994			Target Exon	61.84	47.00
402075			ENSP00000251056*:Plasma membrane calcium	1.00	1.00
402260			NM_001436*:Homo sapiens fibrillarin (FBL	1.58	1.39
402265			Target Exon	2.09	35.00
402297			Target Exon	1.00	92.00
402408			NM_030920*:Homo sapiens hypothetical pro	28.87	13.00
402420			C1000823*:gi|10432400|emb|CAC10290.1| (A	1.00	1.44
402674			Target Exon	7.44	243.00
402802			NM_001397:Homo sapiens endothelin conver	1.00	70.00
402994			NM_002463*:Homo sapiens myxovirus (influ	1.37	1.43
403137			NM_005381*:Homo sapiens nucleolin (NCL),	1.00	19.00
403306	NM_006825		transmembrane protein (63kD), endoplasmi	1.00	43.00
403329			Target Exon	1.00	61.00
403381			ENSP00000231844*:Ecotropic virus integra	1.00	119.00
403478			NM_022342:Homo sapiens kinesin protein 9	28.13	136.00
403485			C3001813*:gi|12737279|ref|XP_012163.1| k	20.23	76.00
403627			Target Exon	6.30	29.33
403715			Target Exon	1.30	35.00
404044			ENSP00000237855*:DJ398G3.2 (NOVEL PROTEI	1.00	54.00
404076			NM_016020*:Homo sapiens CGI-75 protein (	14.29	91.00
404101			C8000950:gi|423560|pir||A47318 RNA-bindi	1.00	1.00
404140			NM_006510:Homo sapiens ret finger protei	1.42	1.44
404165			ENSP00000244562:NRH dehydrogenase [quino	1.00	54.00
404185			Target Exon	1.00	117.00
404210			NM_005936:Homo sapiens myeloid/lymphoid	5.93	13.77
404253			NM_021058*:Homo sapiens H2B histone fami	1.00	1.00

404287			C6001909:gi|704441|dbj|BAA18909.1| (D298	29.71	42.00
404298			C6001238*:gi|121715|sp|P26697|GTA3_CHICK	1.30	1.00
404347			Target Exon	1.00	1.00
404440			NM_021048:Homo sapiens melanoma antigen,	1.00	15.00
404721			NM_005596*:Homo sapiens nuclear factor I	1.00	60.00
404794	NM_000078		cholesteryl ester transfer protein, plas	1.07	1.38
404854			Target Exon	1.61	2.01
404877			NM_005365:Homo sapiens melanoma antigen,	1.00	1.00
404927			Target Exon	1.00	1.00
404996			Target Exon	1.00	1.00
405449			CY000047*:gi|11427234|ref|XP_009399.1| z	1.00	1.00
405568			NM_031413*:Homo sapiens cat eye syndrome	1.00	78.00
405572			Target Exon	0.76	1.14
405646			C12000200:gi|4557225|ref|NP_000005.1| al	1.01	1.28
405676	BE336714		cytochrome c-1	1.13	2.89
405770			NM_002362:Homo sapiens melanoma antigen,	45.52	37.00
405932			C15000305:gi|3806122|gb|AAC69198.1| (AF0	1.99	1.99
406137			NM_000179*:Homo sapiens mutS (E. coli) h	2.77	2.38
406360			Target Exon	1.00	35.00
406399			NM_003122*:Homo sapiens serine protease	1.00	39.00
406467			Target Exon	1.00	1.00
406621	X57809	Hs.181125	immunoglobulin lambda locus	1.41	1.74
406642	AJ245210		gb:Homo sapiens mRNA for immunoglobulin	2.16	3.91
406663	U24683	Hs.293441	immunoglobulin heavy constant mu	2.07	2.93
406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	15.00	51.00
406673	M34996	Hs.198253	major histocompatibility complex, class	0.98	3.09
406676	X58399	Hs.81221	Human L2-9 transcript of unrearranged im,	1.30	1.53
406678	U77534		gb:Human clone 1A11 immunoglobulin varia	1.33	1.45
406685	M18728		gb:Human nonspecific crossreacting antig	1.46	2.85
406687	M31126	Hs.272822	pregnancy specific beta-1-glycoprotein 9	8.61	8.50
406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	226.37	350.00
406698	X03068	Hs.73931	major histocompatibility complex, class	1.01	2.52
406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transferas	20.25	32.00
406851	AA609784		major histocompatibility complex, class	0.75	1.91
406964	M21305		gb:Human alpha satellite and satellite 3	38.15	1114.00
406967	M24349		gb:Human parathyroid hormone-like protei	1.00	1.00
406974	M57293		gb:Human parathyroid hormone-related pep	1.00	1.00
407103	AA424881	Hs.256301	hypothetical protein MGC13170	1.77	1.10
407128	R83312	Hs.237260	EST	1.00	1.00
407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	142.70	135.00
407168	R45175	Hs.117183	ESTs	2.16	18.00
407239	AA076350	Hs.67846	leukocyte immunoglobulin-like receptor,	1.10	1.57
407242	M18728		gb:Human nonspecific crossreacting antig	1.12	2.85
407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	3.24	15.38
407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MA	3.53	3.68
407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	19.74	73.00
407366	AF026942	Hs.271530	gb:Homo sapiens cig33 mRNA, partial sequ	0.06	8.25
407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	1.00	26.00
407430	AF169351		gb:Homo sapiens protein tyrosine phospha	1.00	25.00
407453	AJ132087		gb:Homo sapiens mRNA for axonemal dynein	1.00	75.00
407577	AW131324	Hs.246759	hypothetical protein MGC12538	1.00	1.00
407634	AW016569	Hs.136414	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	111.20	228.00
407710	AW022727	Hs.23616	ESTs	1.00	28.00
407720	AB037776	Hs.38002	KIAA1355 protein	1.89	1.31
407746	AK001962		hypothetical protein FLJ11100	1.00	1.00
407756	AA116021	Hs.38260	ubiquitin specific protease 18	4.51	5.00
407758	D50915	Hs.38365	KIAA0125 gene product	1.00	28.00
407782	AA608956	Hs.112619	ESTs, Moderately similar to PURKINJE CEL	0.97	1.14
407788	BE514982	Hs.38991	S100 calcium-binding protein A2	7.88	3.83
407790	AI027274	Hs.288941	Homo sapiens cDNA FLJ14866 fis, clone PL	3.63	42.00
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	89.96	109.00
407839	AA045144	Hs.161566	ESTs	173.91	108.00
407944	R34008	Hs.239727	desmocollin 2	111.30	70.00
408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	151.17	8.00
408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT	9.91	93.00
408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	195.78	231.00
408070	AW148852		gb:xf05d05.x1 NCI_CGAP_Brn35 Homo sapien	1.00	1.00
408101	AW968504	Hs.123073	CDC2-related protein kinase 7	37.84	61.00
408122	AI432652	Hs.42824	hypothetical protein FLJ10718	0.85	1.71
408212	AA297567	Hs.43728	hypothetical protein	5.88	7.91
408243	Y00787	Hs.624	interleukin 8	4.27	9.98
408349	BE546947	Hs.44276	homeo box C10	3.79	3.46
408353	BE439838	Hs.44298	mitochondrial ribosomal protein S17	1.88	1.65
408354	AI382803	Hs.159235	ESTs	1.00	73.00
408369	R38438	Hs.182575	solute carrier family 15 (H??? transport	1.41	16.50
408380	AF123050	Hs.44532	diubiquitin	15.19	37.22
408482	NM_000676	Hs.45743	adenosine A2b receptor	1.65	1.19
408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	1.98	1.24
408536	AW381532	Hs.135188	ESTs	1.55	1.50
408545	AW235405	Hs.253690	ESTs	1.00	1.00
408572	AA055611	Hs.226568	ESTs, Moderately similar to ALU4_HUMAN A	1.00	44.00
408633	AW963372	Hs.46677	PRO2000 protein	107.16	56.00
408660	AA525775		ESTs, Moderately similar to PC4259 ferri	1.00	1.00
408761	AA057264	Hs.238936	ESTs, Weakly similar to (define not ava	52.24	141.00
408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	3.05	109.00

408783	AF192522	Hs.47701	NPC1 (Niemann-Pick disease, type C1, gen	1.02	1.07
408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	41.19	61.00
408805	H69912	Hs.48269	vaccinia related kinase 1	24.67	45.00
408841	AW438865	Hs.256862	ESTs	1.00	58.00
408873	AL046017	Hs.182278	calmodulin 2 (phosphorylase kinase, delt	1.00	89.00
408908	BE296227	Hs.250822	serine/threonine kinase 15	7.76	1.00
408992	AA059325	Hs.71642	guanine nucleotide binding protein (G pr	1.00	1.00
408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	3.71	5.50
409015	BE389387	Hs.49767	NM_004553:Homo sapiens NADH dehydrogenas	1.44	1.24
409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	4.28	5.32
409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	112.42	195.00
409077	AA401369	Hs.190721	ESTs	1.00	17.00
409093	BE243834	Hs.50441	CGI-04 protein	2.02	1.93
409103	AF251237	Hs.112208	XAGE-1 protein	80.44	40.00
409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	14.87	6.00
409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	1.00	1.00
409228	AI654298	Hs.271695	ESTs, Weakly similar to 2109260A B cell	1.22	1.00
409234	AI879419	Hs.27206	ESTs	1.00	1.00
409268	AA625304	Hs.187579	ESTs	11.90	23.00
409269	AA576953	Hs.22972	hypothetical protein FLJ13352	1.00	1.00
409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	168.91	35.00
409404	BE220053	Hs.129056	ESTs	1.00	1.00
409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	79.74	96.00
409430	R21945	Hs.346735	splicing factor, arginine/serine-rich 5	1.45	2.10
409446	AI561173	Hs.67688	ESTs	1.00	4.00
409506	NM_006153	Hs.54589	NCK adaptor protein 1	3.97	28.00
409522	AA075382		gb:zm87b03.s1 Stratagene ovarian cancer	15.98	141.00
409582	AA401369	Hs.190721	ESTs	1.00	17.00
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	292.12	79.00
409705	M37762	Hs.56023	brain-derived neurotrophic factor	1.00	82.00
409719	AI769160	Hs.108681	Homo sapiens brain tumor associated prot	1.00	1.00
409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	0.12	18.12
409744	AW675258	Hs.56265	Homo sapiens mRNA; cDNA DKFZp586P2321 (f	20.75	51.00
409757	NM_001898	Hs.123114	cystatin SN	22.46	15.80
409866	AW502152		gb:UI-HF-BR0p-ajr-f-11-0-UI.r1 NIH_MGC_5	1.00	1.00
409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	1.50	1.09
409902	AI337658	Hs.156351	ESTs	25.92	50.00
409935	AW511413	Hs.278025	ESTs	2.63	2.11
409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	2.17	4.01
409958	NM_001523	Hs.57697	hyaluronan synthase 1	0.91	2.07
410001	AB041036	Hs.57771	kallikrein 11	1.04	2.28
410032	BE065985		gb:RC3-BT0319-120200-014-a09 BT0319 Homo	1.00	58.00
410037	AB020725	Hs.58009	KIAA0918 protein	1.00	34.00
410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	1.00	1.00
410048	W76467	Hs.58218	proline oxidase homolog	1.03	1.44
410076	T05387	Hs.7991	ESTs	1.12	1.50
410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	9.89	1.00
410153	BE311926	Hs.15830	hypothetical protein FLJ12691	1.00	1.00
410166	AK001376	Hs.59346	hypothetical protein FLJ10514	1.00	1.00
410193	AJ132592	Hs.59757	zinc finger protein 281	42.01	51.00
410274	AA381807	Hs.61762	hypoxia-inducible protein 2	1.72	1.32
410309	BE043077	Hs.278153	ESTs	1.00	2.00
410340	AW182833	Hs.112188	hypothetical protein FLJ13149	32.08	75.00
410348	AW182663	Hs.95469	ESTs	1.00	1.00
410407	X66839	Hs.63287	carbonic anhydrase IX	1.40	1.11
410418	D31382	Hs.63325	transmembrane protease, serine 4	4.30	2.03
410438	AB037756	Hs.45207	hypothetical protein KIAA1335	1.00	18.00
410553	AW016824	Hs.255527	hypothetical protein MGC14128	1.34	1.04
410555	W27235	Hs.64311	a disintegrin and metalloproteinase doma	23.99	1.41
410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	10.04	1.00
410681	AW246890	Hs.65425	calbindin 1, (28kD)	10.88	18.92
410781	AI375672	Hs.165028	ESTs	1.00	57.00
411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	1.62	3.78
411074	X60435	Hs.68137	adenylate cyclase activating polypeptide	1.00	1.15
411089	AA456454		cell division cycle 2-like 1 (PITSLRE pr	1.56	1.58
411152	BE069199		gb:QV3-BT0379-010300-105-g03 BT0379 Homo	1.00	84.00
411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HE	1.82	1.45
411252	AB018549	Hs.69328	MD-2 protein	7.32	12.74
411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	3.44	2.55
411365	M76477	Hs.289082	GM2 ganglioside activator protein	1.35	2.02
411402	BE297855	Hs.69855	NRAS-related gene	1.00	46.00
411573	AB029000	Hs.70823	KIAA1077 protein	11.40	11.35
411579	AC005258	Hs.70830	U6 snRNA-associated Sm-like protein LSm7	1.08	1.90
411617	AA247994	Hs.90063	neurocalcin delta	1.74	2.57
411732	AA059325	Hs.71642	guanine nucleotide binding protein (G pr	1.02	1.00
411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	1.34	2.19
411789	AF245505	Hs.72157	Adlican	2.19	2.79
411800	N39342	Hs.103042	microtubule-associated protein 1B	23.34	34.00
411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	1.00	8.00
412115	AK001763	Hs.73239	hypothetical protein FLJ10901	2.07	1.64
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	118.48	92.00
412276	BE262621	Hs.73798	macrophage migration inhibitory factor (	1.98	1.49
412464	T78141	Hs.22826	ESTs, Weakly similar to I55214 salivary	1.16	1.34
412530	AA766268	Hs.266273	hypothetical protein FLJ13346	41.52	84.00
412537	AL031778		nuclear transcription factor Y, alpha	17.90	55.00

412659	AW753865	Hs.74376	olfactomedin related ER localized protei	14.65	47.00
412719	AW016610	Hs.816	ESTs	382.46	128.00
412723	AA648459	Hs.335951	hypothetical protein AF301222	54.90	1.00
412811	H06382		ESTs	1.00	11.00
412817	AL037159	Hs.74619	proteasome (prosome, macropain) 26S subu	1.63	1.42
412863	AA121673	Hs.59757	zinc finger protein 281	17.63	56.00
412924	BE018422	Hs.75258	H2A histone family, member Y	1.00	22.00
413004	T35901	Hs.75117	interleukin enhancer binding factor 2, 4	2.19	2.05
413011	AW068115	Hs.821	biglycan	1.22	1.88
413048	M93221	Hs.75182	mannose receptor, C type 1	0.30	6.23
413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	3.43	8.71
413129	AF292100	Hs.104613	RP42 homolog	4.67	4.77
413142	M81740	Hs.75212	ornithine decarboxylase 1	1.92	2.59
413223	AI732182	Hs.191866	ESTs	5.73	27.00
413248	T64858	Hs.21433	hypothetical protein DKFZp547J036	0.99	1.06
413273	U75679	Hs.75257	stem-loop (histone) binding protein	1.00	18.00
413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.10	1.09
413281	AA861271	Hs.222024	transcription factor BMAL2	95.94	69.00
413364	BE536218	Hs.137516	fidgetin-like 1	1.00	1.00
413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	0.95	2.09
413409	AI638418	Hs.1440	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.00	1.00
413453	AA129640	Hs.128065	ESTs	1.00	31.00
413527	BE250788	Hs.179882	hypothetical protein FLJ12443	1.08	1.46
413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	79.15	114.00
413573	AI733859	Hs.149089	ESTs	1.00	1.00
413582	AW295647	Hs.71331	hypothetical protein MGC5350	8.80	10.00
413597	AW302885	Hs.117183	ESTs	1.00	1.00
413690	BE157489		gb:RC1-HT0375-120200-011-e06 HT0375 Homo	1.00	1.00
413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	3.16	2.32
413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	2.88	9.52
413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	144.10	108.00
413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	1.00	17.00
413833	Z15005	Hs.75573	centromere protein E (312kD)	1.00	1.00
413882	AA132973	Hs.184492	ESTs	64.24	148.00
413926	AA133338	Hs.54310	ESTs	1.00	67.00
413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	43.42	42.00
413995	BE048146	Hs.75671	syntaxin 1A (brain)	1.23	1.11
414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibito	2.02	2.51
414142	AW368397	Hs.334485	Homo sapiens cDNA FLJ14438 fis, clone HE	1.00	102.00
414180	AI863304	Hs.120905	Homo sapiens cDNA FLJ11448 fis, clone HE	6.92	77.00
414245	BE148072	Hs.75850	WAS protein family, member 1	1.00	1.00
414275	AW970254	Hs.889	Charot-Leyden crystal protein	1.00	59.00
414317	BE263280	Hs.75888	phosphogluconate dehydrogenase	1.52	1.73
414334	AA824298	Hs.21331	hypothetical protein FLJ10036	1.78	1.72
414341	D80004	Hs.75909	KIAA0182 protein	33.90	151.00
414368	W70171	Hs.75939	uridine monophosphate kinase	171.60	97.00
414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.32	1.85
414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	226.15	66.00
414570	Y00285	Hs.76473	insulin-like growth factor 2 receptor	1.64	1.98
414618	AI204600	Hs.96978	hypothetical protein MGC10764	1.87	72.00
414675	R79015	Hs.296281	interleukin enhancer binding factor 1	1.51	1.39
414683	S78296	Hs.76888	hypothetical protein MGC12702	43.61	64.00
414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	28.63	71.00
414711	AI310440	Hs.288735	Homo sapiens cDNA FLJ13522 fis, clone PL	14.86	42.00
414718	H95348	Hs.107987	ESTs	1.00	5.00
414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	1.64	1.44
414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosin	65.01	74.00
414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	130.35	121.00
414774	X02419	Hs.77274	plasminogen activator, urokinase	2.24	2.19
414806	D14694	Hs.77329	phosphatidylserine synthase 1	1.63	1.53
414809	AI434699	Hs.77356	transferrin receptor (p90, CD71)	1.97	2.60
414812	X72755	Hs.77367	monokine induced by gamma interferon	3.48	10.60
414825	X06370	Hs.77432	epidermal growth factor receptor (avian	103.22	143.00
414839	X63692	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	1.80	1.69
414883	AA926960		CDC28 protein kinase 1	14.29	10.06
414907	X90725	Hs.77597	polo (Drosophia)-like kinase	1.95	2.20
414914	U49844	Hs.77613	ataxia telangiectasia and Rad3 related	3.00	2.90
414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	1.02	1.21
414972	BE263782	Hs.77695	KIAA0008 gene product	1.00	1.00
415014	AW954064	Hs.24951	ESTs	1.42	2.84
415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.00	30.00
415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	34.72	107.00
415227	AW821113	Hs.72402	ESTs	1.87	49.00
415238	R37780	Hs.21422	ESTs	1.00	1.00
415263	AA948033	Hs.130853	ESTs	1.00	1.00
415295	R41450	Hs.6546	ESTs	1.00	1.00
415339	NM_015156	Hs.78398	KIAA0071 protein	51.18	166.00
415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	30.84	63.00
415674	BE394784	Hs.78596	proteasome (prosome, macropain) subunit,	1.48	1.39
415709	AA649850	Hs.278558	ESTs	1.00	1.00
415735	AA704162	Hs.120811	ESTs, Weakly similar to I38022 hypotheti	1.00	72.00
415799	AA653718	Hs.225841	DKFZP434D193 protein	6.23	31.00
415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	24.30	1.00
415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	32.51	35.00
415989	AI267700		ESTs	78.89	1.00

416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin t	1.00	1.00
416065	BE267931	Hs.78996	proliferating cell nuclear antigen	3.35	2.32
416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	39.03	3.00
416177	AA174069	Hs.187607	ESTs	1.00	9.00
416178	AI808527	Hs.192822	serologically defined breast cancer anti	3.83	3.76
416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.67	1.00
416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	9.70	1.00
416239	AL038450	Hs.48948	ESTs	83.87	129.00
416250	AA581386	Hs.73452	hypothetical protein MGC10791	1.96	2.12
416322	BE019494	Hs.79217	pyrroline-5-carboxylate reductase 1	2.08	1.73
416423	H54375	Hs.268921	ESTs	1.00	89.00
416448	L13210	Hs.79339	lectin, galactoside-binding, soluble, 3	1.28	1.54
416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	27.29	67.00
416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	53.29	51.00
416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	9.96	5.00
416722	AA354604	Hs.122546	hypothetical protein FLJ23017	3.68	33.00
416819	U77735	Hs.80205	pim-2 oncogene	1.59	1.84
416936	N21352	Hs.42987	ESTs, Weakly similar to S21348 probable	1.00	1.00
417034	NM_006183	Hs.80962	neurotensin	1.00	1.00
417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	32.95	156.00
417079	U65590	Hs.81134	interleukin 1 receptor antagonist	3.91	4.93
417218	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	1.00	51.00
417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	3.38	2.05
417308	H60720	Hs.81892	KIAA0101 gene product	82.94	25.36
417315	AI080042	Hs.180450	ribosomal protein S24	106.61	121.00
417324	AW265494		ESTs	1.20	1.28
417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	8.97	3.27
417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	2.59	1.82
417428	N87579	Hs.278871	gb:LL2030F Human fetal heart, Lambda ZAP	1.00	52.00
417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	304.75	173.00
417466	AI681547	Hs.59457	hypothetical protein FLJ22127	1.24	1.34
417512	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	2.14	5.50
417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	2.66	1.68
417542	J04129	Hs.82269	progestagen-associated endometrial prote	1.28	1.35
417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	42.76	51.00
417715	AW969587	Hs.86366	ESTs	6.35	2.75
417720	AA205625	Hs.208067	ESTs	113.31	56.00
417791	AW965339	Hs.111471	ESTs	39.98	16.00
417830	AW504786	Hs.122579	hypothetical protein FLJ10461	2.61	31.00
417866	AW067903	Hs.82772	collagen, type XI, alpha 1	2.35	2.44
417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	1.52	1.11
417933	X02308	Hs.82962	thymidylate synthetase	4.74	2.55
417944	AU077196	Hs.82985	collagen, type V, alpha 2	3.61	5.21
417975	AA641836	Hs.30085	hypothetical protein FLJ23186	12.49	38.00
417991	AA731452	Hs.190008	ESTs	1.00	26.00
418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	3.02	2.12
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	187.59	1.00
418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.85	2.63
418057	NM_012151	Hs.83363	coagulation factor VIII-associated (intr	1.54	1.69
418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	6.82	5.22
418140	BE613836	Hs.83551	microfibrillar-associated protein 2	1.26	1.46
418203	X54942	Hs.83758	CDC28 protein kinase 2	134.19	144.00
418207	C14685	Hs.34772	ESTs	1.00	1.00
418216	AA662240	Hs.283099	AF15q14 protein	64.66	61.00
418236	AW994005	Hs.337534	ESTs	18.53	147.00
418249	H89226	Hs.34892	KIAA1323 protein	30.53	106.00
418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	1.00	3.00
418283	S79895	Hs.83942	cathepsin K (pycnodysostosis)	3.96	5.16
418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	3.18	2.91
418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	11.96	6.68
418327	U70370	Hs.84136	paired-like homeodomain transcription fa	9.23	2.22
418345	AJ001696	Hs.241407	serine (or cysteine) proteinase inhibito	1.00	1.00
418379	AA218940	Hs.137516	fidgetin-like 1	21.68	44.00
418397	NM_001269	Hs.84746	chromosome condensation 1	1.00	8.00
418403	D86978	Hs.84790	KIAA0225 protein	16.91	18.98
418462	BE001596	Hs.85266	integrin, beta 4	1.56	1.16
418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.22	2.38
418506	AA084248	Hs.85339	G protein-coupled receptor 39	2.66	2.22
418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	2.04	2.21
418538	BE244323	Hs.85951	exportin, tRNA (nuclear export receptor	1.33	37.00
418543	NM_005329	Hs.85962	hyaluronan synthase 3	1.04	1.23
418574	N28754		M-phase phosphoprotein 9	48.60	85.00
418592	X99226	Hs.284153	Fanconi anemia, complementation group A	18.24	26.00
418641	BE243136	Hs.86947	a disintegrin and metalloproteinase doma	1.19	1.41
418661	NM_001949	Hs.1189	E2F transcription factor 3	29.05	43.00
418663	AK001100	Hs.41690	desmocollin 3	112.17	19.00
418678	NM_001327	Hs.87225	cancer/testis antigen	1.18	1.10
418686	Z36830	Hs.87268	annexin A8	1.54	1.98
418689	AI360883	Hs.274448	hypothetical protein FLJ11029	1.19	1.04
418712	Z42183		gb:HSC0BF041 normalized infant brain cDN	1.00	12.00
418727	AA227609	Hs.94834	ESTs	1.00	49.00
418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	49.85	1.00
418819	AA228776	Hs.191721	ESTs	1.00	140.00
418830	BE513731	Hs.88959	hypothetical protein MGC4816	20.97	23.00
418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	57.09	35.00

418971	AA360392	Hs.87113	ESTs	1.00	12.00
418973	AA233056	Hs.191518	ESTs	4.89	28.00
419078	M93119	Hs.89584	insulinoma-associated 1	1.00	10.00
419079	AW014836	Hs.18844	ESTs	1.09	1.98
419080	AW150835	Hs.18878	hypothetical protein FLJ21620	2.06	1.68
419088	AI538323	Hs.52620	integrin, beta 8	15.60	51.00
419092	J05581	Hs.89603	mucin 1, transmembrane	1.11	1.83
419121	AA374372	Hs.89626	parathyroid hormone-like hormone	1.00	1.00
419171	NM_002846	Hs.89655	protein tyrosine phosphatase, receptor t	1.10	1.14
419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	1.00	1.00
419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	3.18	2.43
419288	AA256106	Hs.87507	ESTs	1.00	34.00
419335	AW960146	Hs.284137	hypothetical protein FLJ12888	1.00	8.00
419354	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	22.63	54.00
419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	2.50	1.98
419423	D26488	Hs.90315	KIAA0007 protein	1.00	7.00
419443	D62703		gb:HUM316G10B Clontech human aorta polyA	1.00	12.00
419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	1.64	1.84
419474	AW968619	Hs.155849	ESTs	13.63	62.00
419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	4.27	2.26
419488	AA316241	Hs.90691	nucleophosmin/nucleoplasmin 3	3.66	3.63
419502	AU076704		fibrinogen, A alpha polypeptide	13.05	115.00
419539	AF070590	Hs.90869	Homo sapiens clones 24622 and 24623 mRNA	74.60	117.00
419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	1.47	4.98
419569	AI971651	Hs.91143	jagged 1 (Alagille syndrome)	1.00	4.00
419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	94.30	94.00
419703	AI793257	Hs.128151	ESTs	15.26	50.00
419721	NM_001650	Hs.288650	aquaporin 4	1.00	191.00
419729	AA586442	Hs.21411	gb:no53a03.s1 NCI_CGAP_SS1 Homo sapiens	1.00	59.00
419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.02	1.08
419745	AF042001	Hs.93005	slug (chicken homolog), zinc finger prot	1.00	1.00
419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	29.87	77.00
419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	50.99	214.00
419936	AI792788		gb:ot91d05.y5 NCI_CGAP_Kid5 Homo sapiens	1.00	1.00
419937	AB040959	Hs.93836	DKFZP434N014 protein	1.64	2.47
419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	15.72	94.00
420005	AW271106	Hs.133294	ESTs	3.15	1.43
420047	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	12.45	39.00
420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT	1.00	117.00
420162	BE378432	Hs.95577	cyclin-dependent kinase 4	1.43	1.21
420251	AW374968	Hs.348112	Human DNA sequence from clone RP5-1103G7	2.35	3.23
420259	AF004884	Hs.96253	calcium channel, voltage-dependent, P/Q	0.77	1.15
420281	AI623693	Hs.323494	ESTs	45.04	54.00
420309	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU S	49.22	31.00
420332	NM_001756	Hs.1305	serine (or cysteine) proteinase inhibito	0.05	2.82
420380	AA640891	Hs.102406	ESTs	0.99	2.74
420462	AF050147	Hs.97932	chondromodulin I precursor	1.00	1.00
420520	AK001978	Hs.98510	similar to rab11-binding protein	49.74	133.00
420552	AK000492	Hs.98806	hypothetical protein	94.65	88.00
420560	AW207748	Hs.59115	ESTs	1.00	17.00
420610	AI683183	Hs.99348	distal-less homeo box 5	1.00	13.00
420689	H79979	Hs.88678	ESTs	50.09	95.00
420721	AA927802	Hs.159471	ZAP3 protein	1.00	31.00
420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	1.00	48.00
420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	3.04	1.25
420900	AL045633	Hs.44269	ESTs	2.24	7.00
420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	1.00	8.00
421002	AF116030	Hs.100932	transcription factor 17	1.00	27.00
421027	AA761198	Hs.55254	ESTs	2.87	38.00
421037	AI684808	Hs.197653	ESTs	1.00	46.00
421041	N36914	Hs.14691	ESTs, Moderately similar to I38022 hypot	1.00	98.00
421073	NM_004689	Hs.101448	metastasis associated 1	1.34	1.46
421110	AJ250717	Hs.1355	cathepsin E	119.47	427.00
421133	AA401369	Hs.190721	ESTs	1.10	17.00
421150	AI913562	Hs.189902	ESTs	1.45	1.63
421155	H87879	Hs.102267	lysyl oxidase	1.00	15.00
421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	1.37	1.10
421316	AA287203	Hs.324728	SMA5	1.00	21.00
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	1.92	3.94
421451	AA291377	Hs.50831	ESTs	5.89	14.00
421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	1.46	1.76
421506	BE302796	Hs.105097	thymidine kinase 1, soluble	1.56	1.08
421508	NM_004833	Hs.105115	absent in melanoma 2	5.11	5.23
421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, l	1.00	3.00
421524	AA312082	Hs.105445	GDNF family receptor alpha 1	2.63	10.58
421526	AL080121	Hs.105460	DKFZP564O0823 protein	1.46	1.88
421552	AF026692	Hs.105700	secreted frizzled-related protein 4	30.21	50.32
421574	AJ000152	Hs.105924	defensin, beta 2	1.67	1.74
421582	AI910275		trefoil factor 1 (breast cancer, estroge	1.23	1.00
421633	AF121860	Hs.106260	sorting nexin 10	1.00	116.00
421659	NM_014459	Hs.106511	protocadherin 17	0.05	6.33
421677	H64092	Hs.38282	ESTs	1.31	1.42
421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	1.41	1.20
421773	W69233	Hs.112457	ESTs	1.12	1.14
421777	BE562088	Hs.108196	HSPC037 protein	1.97	1.29

421800	AA298151	Hs.222969	ESTs	1.03	1.30
421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.88	1.59
421896	N62293	Hs.45107	ESTs	11.84	22.80
421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	45.89	90.00
421931	NM_000814	Hs.1440	gamma-aminobutyric acid (GABA) A recepto	1.13	1.49
421948	L42583	Hs.334309	keratin 6A	51.83	20.25
421975	AW961017	Hs.6459	hypothetical protein FLJ11856	1.17	1.15
422026	U80736	Hs.110826	trinucleotide repeat containing 9	1.00	52.00
422094	AF129535	Hs.272027	F-box only protein 5	67.61	62.00
422095	AI868872	Hs.282804	hypothetical protein FLJ22704	4.37	2.34
422109	S73265	Hs.1473	gastrin-releasing peptide	4.18	95.50
422128	AW881145		gb:QV0-OT0033-010400-182-a07 OT0033 Homo	40.89	71.00
422129	AU076635	Hs.1478	serine (or cysteine) proteinase inhibito	1.13	1.38
422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	41.59	96.00
422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.37	1.10
422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	3.29	1.68
422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	4.93	5.73
422282	AF019225	Hs.114309	apolipoprotein L	1.49	1.71
422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	25.99	10.91
422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS, polypept	1.54	1.41
422311	AF073515	Hs.114948	cytokine receptor-like factor 1	1.15	1.78
422330	D30783	Hs.115263	epiregulin	1.00	112.00
422364	AF067800	Hs.115515	C-type (calcium dependent, carbohydrate-	9.39	60.00
422406	AF025441	Hs.116206	Opa-interacting protein 5	18.33	53.00
422424	AI186431	Hs.296638	prostate differentiation factor	1.71	3.21
422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	47.53	32.00
422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	73.68	35.54
422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	173.97	26.00
422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	4.68	2.92
422656	AI870435	Hs.1569	LIM homeobox protein 2	1.00	1.00
422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	3.89	4.55
422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	1.05	1.46
422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	3.88	1.53
422809	AK001379	Hs.121028	hypothetical protein FLJ10549	99.56	53.00
422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.69	3.17
422938	NM_001809	Hs.1594	centromere protein A (17kD)	70.46	61.00
422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	77.74	3.00
422960	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	5.88	8.55
422963	AA401369	Hs.190721	ESTs	171.41	17.00
422976	AU076657	Hs.1600	chaperonin containing TCP1, subunit 5 (e	2.12	1.62
422981	AF026445	Hs.122752	TATA box binding protein (TBP)-associate	10.49	35.00
422986	AA319777	Hs.221974	ESTs	12.40	32.47
423034	AL119930		gb:DKFZp761A092_r1 761 (synonym: hamy2)	16.41	60.00
423049	X59373	Hs.188023	ESTs, Moderately similar to HXDA_HUMAN H	1.00	1.00
423081	AF262992	Hs.123159	sperm associated antigen 4	1.82	2.96
423184	NM_004428	Hs.1624	ephrin-A1	1.14	1.53
423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.14	1.69
423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	7.18	14.00
423309	BE006775	Hs.126782	sushi-repeat protein	21.90	64.00
423361	AW170055	Hs.47628	ESTs	1.00	1.00
423453	AW450737	Hs.128791	CGI-09 protein	55.52	66.00
423511	AF036329	Hs.129715	gonadotropin-releasing hormone 2	0.88	1.17
423516	AB007933	Hs.129729	ligand of neuronal nitric oxide synthase	1.76	5.40
423551	AA327598	Hs.233785	ESTs	3.54	4.33
423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	1.00	50.00
423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	38.88	70.00
423624	AI807408	Hs.166368	ESTs	1.00	67.00
423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	76.02	1.00
423642	AW452650	Hs.157148	hypothetical protein MGC13204	19.14	58.00
423662	AA642452	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	3.61	13.57
423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	240.73	40.00
423698	AA329796	Hs.1098	DKFZp434J1813 protein	1.00	59.00
423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.20	1.00
423761	NM_006194	Hs.132576	paired box gene 9	1.00	1.00
423787	AJ295745	Hs.236204	nuclear pore complex protein	7.18	6.64
423816	AF151064		hypothetical protein	1.00	44.00
423826	U20325	Hs.1707	cocaine- and amphetamine-regulated trans	1.00	1.00
423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	1.00	1.00
423887	AL080207	Hs.134585	DKFZP434G232 protein	1.00	1.00
423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription f	31.33	31.00
423954	AW753164	Hs.288604	KIAA1632 protein	5.81	10.87
423961	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin	3.55	3.30
424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	233.42	68.00
424016	AW163729	Hs.6140	hypothetical protein MGC15730	0.93	1.01
424028	AF055084	Hs.153692	Homo sapiens cDNA FLJ14354 fis, clone Y7	21.30	52.00
424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	1.00	1.00
424086	AI351010	Hs.102267	lysyl oxidase	21.91	70.00
424098	AF077374	Hs.139322	small proline-rich protein 3	137.82	54.00
424120	T80579	Hs.290270	ESTs	1.00	1.00
424165	AW582904	Hs.142255	islet amyloid polypeptide	1.00	34.00
424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	13.06	48.00
424279	L29306	Hs.171814	tryptophan hydroxylase (tryptophan 5-mon	1.00	1.00
424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	164.58	87.00
424326	NM_014479	Hs.145296	disintegrin protease	53.72	302.00
424340	AA339036	Hs.7033	ESTs	0.88	1.15

424351	BE622117	Hs.145567	hypothetical protein	0.93	1.03
424364	AW383226	Hs.201189	ESTs, Weakly similar to G01763 atrophin-	7.02	3.24
424381	AA285249	Hs.146329	protein kinase Chk2	95.55	92.00
424411	NM_005209	Hs.146549	crystallin, beta A2	1.63	3.25
424420	BE614743	Hs.146688	prostaglandin E synthase	1.63	1.33
424441	X14850	Hs.147097	H2A histone family, member X	1.82	1.29
424502	AF242388	Hs.149585	langsin	1.00	1.00
424503	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	1.02	2.24
424513	BE385864	Hs.149894	mitochondrial translational initiation f	1.00	17.00
424539	L02911	Hs.150402	Activin A receptor, type I (ACVR1) (ALK	32.46	108.00
424568	AF005418	Hs.150595	cytochrome P450, subfamily XXVIA, polype	3.40	2.58
424602	AK002055	Hs.151046	hypothetical protein FLJ11193	31.87	25.00
424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.58	2.37
424645	NM_014682	Hs.151449	KIAA0535 gene product	1.00	1.00
424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.12	2.23
424717	AW992292	Hs.152213	wingless-type MMTV integration site fami	1.00	1.00
424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	56.19	12.00
424840	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	2.65	1.30
424867	AI024860	Hs.153591	Not56 (D. melanogaster)-like protein	1.23	1.05
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	21.35	1.00
424979	D87989	Hs.154073	UDP-galactose transporter related	1.36	1.35
424999	AW953120		gb:EST365190 MAGE resequences, MAGB Homo	1.24	1.41
425048	H05468	Hs.164502	ESTs	1.00	11.00
425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	7.46	87.00
425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	2.52	3.82
425118	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	4.84	4.03
425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	3.62	2.73
425202	AW962282	Hs.152049	ESTs, Weakly similar to I38022 hypotheti	1.00	53.00
425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	100.77	44.00
425236	AW067800	Hs.155223	stanniocalcin 2	3.30	2.90
425245	AI751768	Hs.155314	KIAA0095 gene product	1.91	2.32
425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	1.41	1.49
425266	J00077	Hs.155421	alpha-fetoprotein	1.00	68.00
425274	BE281191	Hs.155462	minichromosome maintenance deficient (mi	1.97	1.63
425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	141.49	123.00
425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	1.00	84.00
425371	D49441	Hs.155981	mesothelin	0.87	1.59
425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	14.90	5.76
425420	BE536911	Hs.234545	hypothetical protein NUF2R	1.00	1.00
425424	NM_004954	Hs.157199	ELKL motif kinase	10.58	9.74
425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolo	1.74	1.40
425566	AW162943	Hs.250618	UL16 binding protein 2	1.49	1.14
425580	L11144	Hs.1907	galanin	53.29	233.00
425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	33.45	1.00
425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	1.00	55.00
425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-recept	1.00	10.00
425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	1.00	41.00
425776	U25128	Hs.159499	parathyroid hormone receptor 2	1.00	48.00
425810	AI923627	Hs.31903	ESTs	27.39	98.00
425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.99	1.58
425849	AI077288	Hs.296323	serum/glucocorticoid regulated kinase	71.16	3.42
425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	1.35	1.34
426067	AA401369	Hs.190721	ESTs	1.01	17.00
426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	26.26	47.00
426215	AW067800	Hs.155223	stanniocalcin 2	1.91	2.90
426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	22.40	25.00
426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	1.00	1.00
426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	91.39	229.00
426329	AL389951	Hs.271623	nucleoporin 50kD	4.34	4.08
426427	M86699	Hs.169840	TTK protein kinase	7.02	1.00
426432	AF001601	Hs.169857	paraoxonase 2	1.16	1.68
426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	2.59	1.71
426459	AF151812	Hs.169992	hypothetical 43.2 Kd protein	1.56	1.66
426471	M22440	Hs.170009	transforming growth factor, alpha	20.60	26.00
426496	D31765	Hs.170114	KIAA0061 protein	9.81	22.00
426501	AA401369	Hs.190721	ESTs	19.23	17.00
426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	103.74	41.00
426536	AI949749	Hs.44441	ESTs	4.65	23.00
426572	AB037783	Hs.170623	hypothetical protein FLJ11183	1.00	43.00
426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	160.06	8.00
426691	NM_006201	Hs.171834	PCTAIRE protein kinase 1	1.51	1.35
426746	J03626	Hs.2057	uridine monophosphate synthetase (orotat	2.13	1.68
426752	X69490	Hs.172004	titin	0.02	5.14
426784	U03749	Hs.172216	chromogranin A (parathyroid secretory pr	1.72	1.71
426807	AA385315	Hs.156682	ESTs	1.30	1.64
426812	AF105365	Hs.172613	solute carrier family 12 (potassium/chlo	1.47	1.53
426814	AF036943	Hs.172619	myelin transcription factor 1-like	1.00	1.00
426831	BE296216	Hs.172673	S-adenosylhomocysteine hydrolase	1.51	1.25
426897	AA401369	Hs.190721	ESTs	141.56	17.00
426925	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	32.61	38.00
426935	NM_000088	Hs.172928	collagen, type I, alpha 1	2.65	3.16
426964	AA393739	Hs.287416	Homo sapiens cDNA FLJ11439 fis, clone HE	1.97	3.49
426966	AI493134		sclerostin	1.00	1.00
426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.39	2.28
427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.24	17.00

427239	BE270447	Hs.174070	ubiquitin carrier protein	1.58	1.05
427260	AA663848		gb:ae70b06.s1 Stratagene schizo brain S1	1.34	1.60
427281	AA906147	Hs.102869	ESTs	1.00	66.00
427335	AA448542	Hs.251677	G antigen 7B	51.83	4.00
427354	T57896	Hs.191095	ESTs	1.17	1.95
427356	AW023482	Hs.97849	ESTs	7.31	41.00
427376	AA401533	Hs.19440	ESTs	1.00	57.00
427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	0.42	1.32
427427	AF077345	Hs.177936	lectin, superfamily member 1 (cartilage-	1.00	20.00
427441	AA412605	Hs.343879	SPANX family, member C	1.00	1.00
427445	X80818	Hs.178078	glutamate receptor, metabotropic 4	0.97	1.03
427505	AA361562	Hs.178761	26S proteasome-associated pad1 homolog	4.60	4.04
427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	22.00	45.00
427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	97.45	92.00
427546	AA188763	Hs.36793	hypothetical protein FLJ23188	1.50	3.24
427562	R56424	Hs.26534	ESTs	6.81	40.00
427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	69.91	62.00
427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	2.70	49.00
427666	AI791495	Hs.180142	calmodulin-like skin protein	1.37	1.88
427668	AA298760	Hs.180191	hypothetical protein FLJ14904	29.55	67.00
427677	NM_007045	Hs.180296	FGFR1 oncogene partner	3.52	2.63
427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	7.41	34.00
427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	15.84	70.00
427719	AI393122	Hs.134726	ESTs	7.03	4.52
427722	AK000123	Hs.180479	hypothetical protein FLJ20116	2.92	1.74
427747	AW411425	Hs.180655	serine/threonine kinase 12	1.76	1.26
427912	AL022310	Hs.181097	tumor necrosis factor (ligand) superfami	9.63	59.00
427961	AW293165	Hs.143134	ESTs	41.97	118.00
428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	23.82	1.00
428023	AL038843		Homo sapiens cDNA: FLJ23602 fis, clone L	1.40	1.33
428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	96.28	167.00
428093	AW594506	Hs.104830	ESTs	1.25	1.29
428098	AU077258	Hs.182429	protein disulfide isomerase-related prot	1.86	1.60
428129	AI244311	Hs.26912	ESTs	1.00	42.00
428169	AI928984	Hs.182793	golgi phosphoprotein 2	2.76	2.11
428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00	1.00
428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	85.59	181.00
428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	8.57	21.64
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	7.77	15.90
428434	AI909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	0.58	1.43
428450	NM_014791	Hs.184339	KIAA0175 gene product	237.53	204.00
428471	X57348	Hs.184510	stratifin	6.00	4.60
428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	56.54	16.00
428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.53	2.15
428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	1.00	1.00
428532	AF157326	Hs.184786	TBP-interacting protein	1.00	58.00
428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	1.00	16.00
428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	1.00	1.00
428698	AA852773	Hs.334838	KIAA1866 protein	187.37	255.00
428728	NM_016625	Hs.191381	hypothetical protein	47.24	80.00
428748	AW593206	Hs.98785	Ksp37 protein	1.00	87.00
428758	AA433988	Hs.98502	hypothetical protein FLJ14303	1.06	1.13
428771	AB028992	Hs.193143	KIAA1069 protein	1.98	92.00
428801	AW277121	Hs.254881	ESTs	1.67	6.15
428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible, hep	1.03	1.27
428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	124.17	43.00
428845	AL157579	Hs.153610	KIAA0751 gene product	1.00	1.00
428959	AF100779	Hs.194680	WNT1 inducible signaling pathway protein	15.16	27.00
428969	AF120274	Hs.194689	artemin	1.36	1.24
429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like	0.97	3.31
429065	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	6.82	16.47
429164	AI688663	Hs.116586	ESTs	19.08	67.00
429170	NM_001394	Hs.2359	dual specificity phosphatase 4	16.18	105.00
429183	AB014604	Hs.197955	KIAA0704 protein	79.72	104.00
429201	X03178	Hs.198246	group-specific component (vitamin D bind	1.00	1.00
429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	1.33	1.09
429220	AW207206		ESTs	1.00	7.00
429228	AI553633	Hs.326447	ESTs	39.47	29.25
429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.01	1.18
429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	1.07	1.00
429276	AF056085	Hs.198612	G protein-coupled receptor 51	3.70	142.00
429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	1.30	1.94
429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	94.09	86.00
429413	NM_014058	Hs.201877	DESC1 protein	41.91	10.00
429486	AF155827	Hs.203963	hypothetical protein FLJ10339	12.19	1.00
429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	1.61	1.08
429538	BE182592	Hs.11261	small proline-rich protein 2A	4.43	2.90
429547	AA401369	Hs.190721	ESTs	1.06	17.00
429551	AW450624	Hs.220931	ESTs	2.89	65.00
429563	BE619413	Hs.2437	eukaryotic translation initiation factor	1.49	1.37
429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	61.86	100.00
429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.59	1.69
429612	AF062649	Hs.252587	pituitary tumor-transforming 1	2.78	1.74
429616	AI982722	Hs.120845	ESTs	1.00	1.00
429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	1.00	4.00

429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	69.95	104.00
429736	AF125304	Hs.212680	tumor necrosis factor receptor superfami	1.25	1.21
429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	1.00	7.00
429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	11.80	1.00
429918	AW873986	Hs.119383	ESTs	1.00	78.00
429978	AA249027		ribosomal protein S6	1.98	3.09
429986	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	1.00	48.00
430044	AA464510	Hs.152812	ESTs	69.27	59.00
430114	AA847744	Hs.99640	ESTs	1.00	1.00
430134	BE380149	Hs.105223	ESTs, Weakly similar to T33188 hypotheti	1.00	51.00
430147	R60704	Hs.234434	hairy/enhancer-of-split related with YRP	1.10	2.22
430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	1.00	127.00
430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	3.80	1.47
430300	U60805	Hs.238648	oncostatin M receptor	1.00	35.00
430315	NM_004293	Hs.239147	guanine deaminase	92.31	28.00
430337	M36707	Hs.239600	calmodulin-like 3	1.18	1.08
430378	Z29572	Hs.2556	tumor necrosis factor receptor superfami	5.28	66.00
430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	16.76	38.00
430393	BE185030	Hs.241305	estrogen-responsive B box protein	1.63	1.50
430439	AL133561		DKFZP434B061 protein	1.00	1.00
430451	AA836472	Hs.297939	cathepsin B	1.64	2.12
430454	AW469011	Hs.105635	ESTs	63.35	44.00
430466	AF052573	Hs.241517	polymerase (DNA directed), theta	2.47	1.91
430481	AA479678	Hs.203269	ESTs, Moderately similar to ALU8_HUMAN A	1.00	31.00
430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	12.28	41.00
430508	AI015435	Hs.104637	ESTs	4.75	7.27
430533	AA480895	Hs.57749	ESTs, Weakly similar to T17288 hypotheti	1.00	1.00
430563	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.00	1.59
430677	Z26317	Hs.94560	desmoglein 2	1.72	1.30
430678	AA401369	Hs.190721	ESTs	0.90	17.00
430686	NM_001942	Hs.2633	desmoglein 1	1.00	1.00
430788	AI742925	Hs.7179	ESTs, Weakly similar to 2004399A chromos	1.62	1.84
430890	X54232	Hs.2699	glypican 1	1.58	1.40
430935	AW072916		zinc finger protein 131 (clone pHZ-10)	90.28	132.00
430985	AA490232	Hs.27323	ESTs, Weakly similar to I78885 serine/th	0.94	1.28
431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	60.25	28.00
431089	BE041395		ESTs, Weakly similar to unknown protein	23.32	941.00
431092	AI332764	Hs.125757	ESTs	13.46	63.00
431124	AF284221	Hs.59506	doublesex and mab-3 related transcriptio	49.43	62.00
431164	AA493650	Hs.94367	Homo sapiens cDNA: FLJ23494 fis, clone L	0.44	2.20
431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	182.26	101.00
431221	AW207837	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	4.15	13.97
431277	AA501806	Hs.345824	ESTs	1.00	86.00
431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	40.55	200.00
431342	AW971018	Hs.21659	ESTs	1.00	53.00
431384	BE158000	Hs.285026	gb:MR2-HT0377-150200-202-e03 HT0377 Homo	0.94	1.14
431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	1.30	1.25
431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	3.90	26.00
431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	1.41	1.87
431548	AI834273	Hs.9711	novel protein	5.66	15.00
431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	0.99	1.44
431745	AW972448	Hs.163425	ESTs	0.99	3.51
431770	BE221880	Hs.268555	5'-3' exoribonuclease 2	67.12	91.00
431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	3.36	4.71
431846	BE019924	Hs.271580	uroplakin 1B	4.49	2.51
431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	2.20	3.32
431934	AB031481	Hs.272214	STG protein	1.01	1.04
431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	51.17	46.35
432006	AL137382	Hs.272320	Homo sapiens mRNA; cDNA DKFZp434L1226 (f	0.94	1.65
432023	R43020	Hs.236223	EST	0.94	47.00
432201	AI538613	Hs.298241	Transmembrane protease, serine 3	1.10	2.24
432210	AI567421	Hs.273330	Homo sapiens, clone IMAGE:3544662, mRNA,	1.42	1.45
432226	AW182766	Hs.273558	phosphate cytidylyltransferase 1, cholin	1.00	1.00
432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	18.67	1.00
432265	BE382679	Hs.285753	SCG10-like-protein	1.09	1.21
432281	AK001239	Hs.274263	hypothetical protein FLJ10377	40.98	58.00
432365	AK001106	Hs.274419	hypothetical protein FLJ10244	1.00	214.00
432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	157.34	37.00
432375	BE536069	Hs.2962	S100 calcium-binding protein P	1.65	1.06
432407	AA221036		gb:zr03f12.r1 Stratagene NT2 neuronal pr	73.71	75.00
432441	AW292425	Hs.163484	ESTs	56.35	72.00
432489	AI804855	Hs.207530	ESTs	1.00	24.00
432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	137.72	98.00
432552	AI537170	Hs.173725	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.00	31.00
432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	0.27	35.18
432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	2.87	6.22
432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	26.63	56.00
432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	1.92	5.29
432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.00	48.00
432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	45.13	31.00
432753	NM_014075	Hs.336938	Homo sapiens PRO0593 mRNA, complete cds	1.00	68.00
432788	AA521091	Hs.178499	Homo sapiens cDNA: FLJ23117 fis, clone L	2.69	3.67
432842	AW674093	Hs.334822	hypothetical protein MGC4485	1.22	1.34
432867	AW016936	Hs.233364	ESTs	1.00	1.00
432917	NM_014125	Hs.241517	PRO0327 protein	10.25	6.62

432920	U37689	Hs.3128	polymerase (RNA) II (DNA directed) polyp	1.44	1.30
433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	154.79	85.64
433023	AW864793	Hs.87409	thrombospondin 1	20.96	100.00
433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	1.00	10.00
433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.20	1.09
433159	AB035898	Hs.150587	kinesin-like protein 2	13.82	39.00
433183	AF231338	Hs.222024	transcription factor BMAL2	1.00	69.00
433258	AA622788	Hs.203613	ESTs, Weakly similar to ALUB_HUMAN !!!!	1.00	1.25
433409	AI278802	Hs.25661	ESTs	44.81	117.00
433437	U20536	Hs.3280	caspase 6, apoptosis-related cysteine pr	70.39	105.00
433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2	11.55	2.00
433537	AI733692	Hs.112488	ESTs	8.66	55.00
433547	W04978	Hs.303023	beta tubulin 1, class VI	25.16	83.00
433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	1.00	19.00
433647	AA603367	Hs.222294	ESTs	20.30	49.00
433658	L03678	Hs.156110	immunoglobulin kappa constant	5.92	10.03
433800	AI094221	Hs.135150	lung type-I cell membrane-associated gly	2.29	2.22
433819	AW511097	Hs.112765	ESTs	3.71	8.00
433862	D86960	Hs.3610	KIAA0205 gene product	62.08	104.00
433980	AA137152	Hs.286049	phosphoserine aminotransferase	108.91	47.00
434088	AF116677	Hs.249270	hypothetical protein PRO1966	1.00	1.00
434094	AA305599	Hs.238205	hypothetical protein PRO2013	121.27	87.00
434105	AW952124	Hs.13094	presenilins associated rhomboid-like pro	1.22	1.23
434217	AW014795	Hs.23349	ESTs	14.11	57.00
434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	2.10	2.56
434360	AA401369	Hs.190721	ESTs	40.98	17.00
434414	AI798376		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens	1.48	1.56
434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	1.00	64.00
434467	BE552368	Hs.231853	Homo sapiens cDNA FLJ13445 fis, clone PL	54.91	85.00
434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	2.46	2.00
434627	AI221894	Hs.39311	ESTs	1.00	1.00
434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	1.00	23.00
434769	AA648884	Hs.134278	Homo sapiens cDNA FLJ12676 fis, clone NT	7.08	56.00
434792	AA649253	Hs.132458	ESTs	8.52	44.00
434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	11.33	1.00
434828	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced	1.00	1.00
434876	AF160477	Hs.61460	Ig superfamily receptor LNIR	1.25	1.29
434891	AA814309	Hs.123583	ESTs	1.00	6.00
434928	AW015595	Hs.4267	Homo sapiens clones 24714 and 24715 mRNA	1.00	1.00
435013	H91923	Hs.110024	Target CAT	1.26	1.10
435066	BE261750	Hs.4747	dyskeratosis congenita 1, dyskerin	1.69	1.37
435087	AW975241	Hs.23567	ESTs	1.00	1.00
435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.90	1.93
435159	AA668879	Hs.116649	ESTs	1.00	1.00
435205	X54136	Hs.181125	immunoglobulin lambda locus	1.02	1.46
435232	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1	2.04	2.70
435304	H10709	Hs.269524	ESTs	27.58	139.00
435313	AI769400	Hs.189729	ESTs	1.00	14.00
435505	AF200492	Hs.211238	interleukin-1 homolog 1	1.00	38.00
435509	AI458679	Hs.181915	ESTs	1.00	1.00
435525	AI831297	Hs.123310	ESTs	1.00	56.00
435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	1.00	2.00
435550	AI224456	Hs.324507	H.sapiens polyA site DNA	3.42	3.92
435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	3.95	1.80
435766	R11673	Hs.186498	ESTs	1.00	28.00
435793	AB037734	Hs.4993	KIAA1313 protein	23.68	42.00
436069	AI056879	Hs.263209	ESTs	1.00	58.00
436170	AW450381	Hs.14529	ESTs	1.00	18.00
436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	5.84	22.00
436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	1.42	1.27
436217	T53925	Hs.107	fibrinogen-like 1	57.97	31.00
436238	AK002163	Hs.301724	hypothetical protein FLJ11301	2.51	1.71
436251	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	2.33	1.64
436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	108.99	52.00
436302	AL355841	Hs.99330	hypothetical protein FLJ23588	0.75	2.81
436396	AW992292	Hs.152213	wingless-type MMTV integration site faml	60.01	1.00
436414	BE264633	Hs.143638	WD repeat domain 4	2.50	2.19
436419	AI948626	Hs.171356	ESTs	0.95	1.33
436443	AW138211	Hs.128746	ESTs	1.12	9.26
436474	AJ270693	Hs.199887	ESTs	1.00	1.00
436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.28	1.56
436486	AA742221	Hs.120633	ESTs	1.00	19.00
436511	AA721252	Hs.291502	ESTs	16.76	14.00
436553	X57809	Hs.181125	immunoglobulin lambda locus	1.08	1.74
436557	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	19.20	9.75
436608	AA628980		down syndrome critical region protein DS	33.92	25.00
436667	AW025183	Hs.127680	ESTs	0.89	1.19
436771	AW975687	Hs.292979	ESTs	1.00	10.00
436839	AA401369	Hs.190721	ESTs	1.00	17.00
436887	AW953157	Hs.193235	hypothetical protein DKFZp547D155	1.06	1.15
436944	AW268614	Hs.5840	ESTs	1.00	1.00
436961	AW375974	Hs.156704	ESTs	25.13	25.00
436972	AA284679	Hs.25640	claudin 3	1.59	1.46
437016	AU076916	Hs.5398	guanine monphosphate synthetase	2.35	1.78
437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 g	1.34	1.13

437181	AI306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	1.00	17.00
437204	AL110216	Hs.22826	ESTs, Weakly similar to I55214 salivary	40.55	82.00
437205	AL110232	Hs.279243	Homo sapiens mRNA; cDNA DKFZp564D2071 (f	1.00	112.00
437259	AI377755	Hs.120695	ESTs	1.00	205.00
437270	R18087	Hs.323769	cisplatin resistance related protein CRR	1.56	1.54
437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFZp566O134 (fr	113.25	125.00
437370	AL359567	Hs.161962	Homo sapiens mRNA; cDNA DKFZp547D023 (fr	1.82	4.57
437390	AI125859	Hs.112607	ESTs	1.35	1.75
437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	3.58	3.20
437435	AI306152	Hs.27027	hypothetical protein DKFZp762H1311	3.03	1.08
437444	H46008	Hs.31518	ESTs	1.00	39.00
437568	AI954795	Hs.156135	ESTs	1.00	19.00
437623	D63880	Hs.5719	chromosome condensation-related SMC-asso	1.95	1.57
437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	1.00	3.00
437814	AI088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	1.00	45.00
437840	AA884836	Hs.292014	ESTs	1.07	1.78
437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.sa	1.68	3.26
437879	BE262082	Hs.5894	hypothetical protein FLJ10305	1.87	2.52
437915	AI637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	74.05	35.00
437916	BE566249	Hs.20999	hypothetical protein FLJ23142	23.15	89.00
437937	AI917222	Hs.121655	ESTs	1.00	1.00
437942	AI888256	Hs.307526	ESTs	12.28	31.00
438091	AW373062		nuclear receptor subfamily 1, group I, m	1.53	10.85
438113	AI467908	Hs.8882	ESTs	1.80	2.39
438119	AW963217	Hs.203961	ESTs, Moderately similar to AF116721 89	22.67	36.90
438274	AI918906	Hs.55080	ESTs	1.00	1.00
438378	AW970529	Hs.86434	hypothetical protein FLJ21816	38.92	38.00
438403	AA806607	Hs.292206	ESTs	1.00	1.00
438494	AA908678	Hs.130183	ESTs	2.05	80.00
438546	AW297204	Hs.125811	ESTs	1.00	131.00
438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	1.43	1.45
438702	AI879064	Hs.54618	ESTs	1.00	34.00
438724	AW612553	Hs.114670	Human DNA sequence from clone RP11-16L21	1.33	1.10
438746	AI885815	Hs.184727	Human melanoma-associated antigen p97 (m	2.42	1.59
438779	NM_003787	Hs.6414	nucleolar protein 4	1.00	18.00
438821	AA826425	Hs.192375	ESTs	2.03	2.57
438885	AI886558	Hs.184987	ESTs	6.42	88.00
438898	AA401369	Hs.190721	ESTs	22.41	17.00
438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.00	1.00
438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9	2.20	1.88
439000	AW979121		gb:EST391231 MAGE resequences, MAGP Homo	2.78	4.81
439023	AA745978	Hs.28273	ESTs	1.17	1.31
439024	R96696	Hs.35598	ESTs	1.00	28.00
439128	AI949371	Hs.153089	ESTs	1.00	67.00
439146	AW138909	Hs.156110	immunoglobulin kappa constant	1.38	1.41
439223	AW238299	Hs.250618	UL16 binding protein 2	1.93	1.64
439285	AL133916		hypothetical protein FLJ20093	46.23	139.00
439318	AW837046	Hs.6527	G protein-coupled receptor 56	2.00	2.20
439343	AF086161	Hs.114611	hypothetical protein FLJ11808	6.10	7.37
439394	AA401369	Hs.190721	ESTs	3.39	17.00
439410	AA632012	Hs.188746	ESTs	1.83	3.07
439451	AF086270	Hs.278554	heterochromatin-like protein 1	23.28	52.00
439452	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	18.76	122.00
439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	2.78	1.58
439477	W69813	Hs.58042	ESTs, Moderately similar to GFR3_HUMAN G	1.22	1.44
439492	AF086310	Hs.103159	ESTs	7.46	39.00
439523	W72348	Hs.185029	ESTs	1.00	1.19
439592	AF086413	Hs.58399	ESTs	1.00	1.00
439606	W79123	Hs.58561	G protein-coupled receptor 87	33.61	1.00
439670	AF088076	Hs.59507	ESTs, Weakly similar to AC004858 3 U1 sm	1.00	1.00
439702	AW085525	Hs.134182	ESTs	4.30	10.00
439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	86.55	11.00
439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	2.36	1.88
439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	2.02	6.08
439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	1.00	21.00
439780	AL109688		gb:Homo sapiens mRNA full length insert	7.27	25.00
439840	AW449211	Hs.105445	GDNF family receptor alpha 1	1.00	1.00
439926	AW014875	Hs.137007	ESTs	32.58	71.00
439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	21.28	9.55
439979	AW600291	Hs.6823	hypothetical protein FLJ10430	68.83	61.00
440006	AK000517	Hs.6844	hypothetical protein FLJ20510	1.83	4.02
440028	AW473675	Hs.125843	ESTs, Weakly similar to T17227 hypotheti	1.42	2.54
440106	AA864968	Hs.127699	KIAA1603 protein	1.00	54.00
440138	AB033023	Hs.318127	hypothetical protein FLJ10201	24.18	52.00
440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	3.21	4.72
440289	AW450991	Hs.192071	ESTs	38.63	113.00
440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	62.88	147.00
440492	R39127	Hs.21433	hypothetical protein DKFZp547J036	2.35	3.62
440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	10.84	57.00
440659	AF134160	Hs.7327	claudin 1	3.18	2.37
440704	M69241	Hs.162	insulin-like growth factor binding prote	2.89	2.09
440943	AW082298	Hs.146161	hypothetical protein MGC2408	2.02	1.41
440994	AI160011	Hs.272068	ESTs	1.29	1.14
441020	AA401369	Hs.190721	ESTs	142.99	17.00
441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	1.41	99.00

441128	AA570256		ESTs, Weakly similar to T23273 hypotheti	4.13	3.50
441290	W27501	Hs.89605	cholinergic receptor, nicotinic, alpha p	1.00	1.00
441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	130.23	43.00
441377	BE218239	Hs.202656	ESTs	22.03	1.00
441390	AI692560	Hs.131175	ESTs	3.65	7.70
441497	R51064	Hs.23172	ESTs	1.00	1.00
441525	AW241867	Hs.127728	ESTs	1.53	1.42
441553	AA281219	Hs.121296	ESTs	1.89	1.57
441607	NM_005010	Hs.7912	neuronal cell adhesion molecule	1.47	2.11
441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	216.22	363.00
441636	AA081846	Hs.7921	Homo sapiens mRNA; cDNA DKFZp566E183 (fr	2.31	2.05
441737	X79449	Hs.7957	adenosine deaminase, RNA-specific	1.30	1.49
441790	AA401369	Hs.190721	ESTs	44.15	17.00
441801	AW242799	Hs.86366	ESTs	1.00	1.00
441919	AI553802	Hs.128121	ESTs	1.00	122.00
441937	R41782	Hs.22279	ESTs	0.86	1.37
441954	AI744935	Hs.8047	Fanconi anemia, complementation group G	1.48	1.39
442025	AW887434	Hs.11810	CDA11 protein	1.00	46.00
442029	AW956698	Hs.14456	neural precursor cell expressed, develop	9.92	45.00
442072	AI740832	Hs.12311	Homo sapiens clone 23570 mRNA sequence	25.05	77.00
442108	AW452649	Hs.166314	ESTs	3.61	3.14
442117	AW664964	Hs.128899	ESTs	3.00	5.49
442137	AA977235	Hs.128830	ESTs, Weakly similar to Z192_HUMAN ZINC	1.00	1.00
442159	AW163390	Hs.278554	heterochromatin-like protein 1	1.92	1.66
442179	AA983842	Hs.333555	chromosome 2 open reading frame 2	27.22	50.00
442328	AI952430	Hs.150614	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.00	3.42
442432	BE093589	Hs.38178	hypothetical protein FLJ23468	181.59	76.00
442530	AI580830	Hs.176508	Homo sapiens cDNA FLJ14712 fis, clone NT	10.59	144.00
442547	AA306997	Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU S	109.23	98.00
442556	AL137761	Hs.8379	Homo sapiens mRNA; cDNA DKFZp586L2424 (f	1.00	53.00
442619	AA447492	Hs.20183	ESTs, Weakly similar to AF164793 1 prote	29.02	50.00
442710	AI015631	Hs.23210	ESTs	1.00	19.00
442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	1.00	5.00
442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	22.85	50.00
442914	AW188551	Hs.99519	hypothetical protein FLJ14007	25.33	82.00
442932	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	3.18	4.41
442942	AW167087	Hs.131562	ESTs	8.45	64.00
443068	AI188710		ESTs	1.00	27.00
443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	1.00	24.00
443211	AI128388	Hs.143655	ESTs	12.42	2.00
443247	BE614387	Hs.333893	c-Myc target JPO1	128.84	96.00
443324	R44013	Hs.164225	ESTs	0.02	4.59
443383	AI792453	Hs.166507	ESTs	1.00	47.00
443400	R28424	Hs.250648	ESTs	18.52	61.00
443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	4.02	1.75
443572	AA025610	Hs.9605	cleavage and polyadenylation specific fa	2.98	2.57
443575	AI078022	Hs.269636	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.00	29.00
443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	1.00	16.00
443633	AL031290	Hs.9654	similar to pregnancy-associated plasma p	1.00	39.00
443648	AI085377	Hs.143610	ESTs	39.81	70.00
443715	AI583187	Hs.9700	cyclin E1	48.74	7.00
443723	AI144442	Hs.157144	syntaxin 6	1.29	1.30
443802	AW504924	Hs.9805	KIAA1291 protein	1.75	1.61
443859	NM_013409	Hs.9914	follistatin	1.35	1.13
443892	AA401369	Hs.190721	ESTs	1.00	17.00
443947	W24187		gb:zb47f09.r1 Soares_fetal_lung_NbHL19W	1.33	1.64
443991	NM_002250	Hs.10082	potassium intermediate/small conductance	5.71	6.87
444006	BE395085	Hs.10086	type I transmembrane protein Fn14	1.47	1.92
444009	AI380792	Hs.135104	ESTs	1.00	77.00
444017	U04840	Hs.214	neuro-oncological ventral antigen 1	1.00	1.00
444127	N63620	Hs.13281	ESTs	1.00	29.00
444129	AW294292	Hs.256212	ESTs	1.00	1.00
444279	U62432	Hs.89605	cholinergic receptor, nicotinic, alpha p	0.60	7.80
444371	BE540274	Hs.239	forkhead box M1	2.91	1.14
444378	R41339	Hs.12569	ESTs	1.00	1.00
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	469.00	556.00
444461	R53734	Hs.25978	ESTs, Weakly similar to 2109260A B cell	12.88	105.00
444471	AB020684	Hs.11217	KIAA0877 protein	24.91	90.00
444489	AI151010	Hs.157774	ESTs	1.00	111.00
444619	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-lin	1.00	70.00
444665	BE613126	Hs.47783	B aggressive lymphoma gene	30.56	139.00
444707	AI188613	Hs.41690	desmocollin 3	1.00	1.00
444735	BE019923	Hs.243122	hypothetical protein FLJ13057 similar to	77.02	90.00
444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	1.57	1.31
444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	77.55	2.00
445236	AK001676	Hs.12457	hypothetical protein FLJ10814	1.00	27.00
445258	AI635931	Hs.147613	ESTs	1.00	73.00
445413	AA151342	Hs.12677	CGI-147 protein	28.14	50.00
445417	AK001058	Hs.12680	Homo sapiens cDNA FLJ10196 fis, clone HE	1.81	2.62
445443	AV653838	Hs.322971	ESTs	1.00	1.00
445462	AA378776	Hs.288649	hypothetical protein MGC3077	2.09	1.70
445517	AF208855	Hs.12830	hypothetical protein	1.87	70.00
445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	1.71	2.72
445580	AF167572	Hs.12912	skb1 (S. pombe) homolog	1.52	1.34
445654	X91247	Hs.13046	thioredoxin reductase 1	1.51	1.52

445669	AI570830	Hs.174870	ESTs	10.95	11.45
445818	BE045321	Hs.136017	ESTs	1.00	1.00
445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	49.42	54.00
445885	AI734009	Hs.127699	KIAA1603 protein	1.00	132.00
445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	1.00	1.00
445903	AI347487	Hs.132781	class I cytokine receptor	1.00	36.00
445932	BE046441	Hs.333555	Homo sapiens clone 24859 mRNA sequence	2.41	2.88
445982	BE410233	Hs.13501	pescadillo (zebrafish) homolog 1, contai	1.60	1.35
446078	AI339982	Hs.156061	ESTs	1.00	42.00
446102	AW168067	Hs.317694	ESTs	1.00	1.00
446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	1.70	1.53
446269	AW263155	Hs.14559	hypothetical protein FLJ10540	73.01	48.00
446292	AF081497	Hs.279682	Rh type C glycoprotein	1.55	1.26
446293	AI420213	Hs.149722	ESTs	1.00	2.00
446423	AW139655	Hs.150120	ESTs	1.10	4.19
446428	AW082270	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	0.53	3.26
446432	AI377320	Hs.150058	ESTs	1.00	5.00
446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	1.36	1.31
446574	AI310135	Hs.335933	ESTs	3.89	72.00
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	32.03	20.23
446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonin	4.19	5.07
446783	AW138343	Hs.141867	ESTs	2.82	9.47
446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	110.28	28.00
446849	AU076617	Hs.16251	cleavage and polyadenylation specific fa	3.26	2.94
446856	AI814373	Hs.164175	ESTs	6.38	11.30
446872	X97058	Hs.16362	pyrimidinergic receptor P2Y, G-protein c	1.98	2.03
446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	94.90	113.00
446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	1.67	3.90
446989	AK001898	Hs.16740	hypothetical protein FLJ11036	2.82	3.12
447022	AW291223	Hs.157573	ESTs	1.00	170.00
447033	AI357412	Hs.157601	ESTs	7.15	107.00
447078	AW885727	Hs.9914	ESTs	47.24	24.00
447081	Y13896	Hs.17287	potassium inwardly-rectifying channel, s	0.12	17.88
447131	NM_004585	Hs.17466	retinoic acid receptor responder (tazaro	0.97	1.48
447149	BE299857	Hs.326	TAR (HIV) RNA-binding protein 2	1.24	1.28
447153	AA805202	Hs.315562	ESTs	1.00	54.00
447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	1.00	67.00
447178	AW594641	Hs.192417	ESTs	3.42	50.00
447250	AI878909	Hs.17883	protein phosphatase 1G (formerly 2C), ma	1.60	1.52
447289	AW247017	Hs.36978	melanoma antigen, family A, 3	1.00	1.00
447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	28.63	1.00
447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	146.62	51.00
447350	AI375572	Hs.172634	ESTs	1.00	12.00
447377	N27687	Hs.334334	transcription factor AP-2 alpha (activat	2.55	63.00
447415	AW937335	Hs.28149	ESTs, Weakly similar to KF3B_HUMAN KINES	0.91	1.13
447425	AI963747	Hs.18573	acylphosphatase 1, erythrocyte (common)	1.00	35.00
447519	U46258	Hs.339665	ESTs	59.89	49.00
447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.23	1.63
447534	AA401369	Hs.190721	ESTs	1.00	17.00
447636	Y10043		high-mobility group (nonhistone chromoso	1.41	1.11
447688	N87079	Hs.19236	Target CAT	1.00	39.00
447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast, h	1.17	1.12
447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	6.47	5.95
447802	AW593432	Hs.161455	ESTs	0.73	2.34
447850	AB018298	Hs.19822	SEC24 (S. cerevisiae) related gene famil	86.45	116.00
447924	AI817226	Hs.313413	ESTs, Weakly similar to T23110 hypotheti	1.00	1.00
447973	AB011169	Hs.20141	similar to S. cerevisiae SSM4	3.50	4.27
448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	4.13	142.00
448105	AI538613	Hs.298241	Transmembrane protease, serine 3	1.15	2.24
448243	AW369771	Hs.52620	integrin, beta 8	15.84	1.00
448278	W07369	Hs.11782	ESTs	0.97	1.90
448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	1.00	1.00
448296	BE622756	Hs.10949	Homo sapiens cDNA FLJ14162 fis, clone NT	2.42	2.17
448357	BE274396	Hs.108923	RAB38, member RAS oncogene family	1.44	1.08
448390	AL035414	Hs.21068	hypothetical protein	1.00	43.00
448469	AW504732	Hs.21275	hypothetical protein FLJ11011	2.63	2.49
448569	BE382657	Hs.21486	signal transducer and activator of trans	1.84	2.53
448663	BE614599	Hs.106823	hypothetical protein MGC14797	3.29	46.00
448672	AI955511	Hs.225106	ESTs	1.00	21.00
448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	1.82	1.08
448741	BE614567	Hs.19574	hypothetical protein MGC5469	2.48	1.92
448757	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	23.53	20.00
448775	AB025237	Hs.388	nudix (nucleoside diphosphate linked moi	2.34	1.97
448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	74.07	62.67
448830	AL031658	Hs.22181	hypothetical protein dJ310O13.3	1.37	1.31
448844	AI581519	Hs.177164	ESTs	1.00	31.00
448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.84	1.95
448993	AI471630		KIAA0144 gene product	1.63	1.49
449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	1.00	1.00
449029	N28989	Hs.22891	solute carrier family 7 (cationic amino	1.97	2.26
449040	AF040704	Hs.149443	putative tumor suppressor	0.97	1.56
449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	27.13	90.00
449053	AI625777	Hs.344766	ESTs	8.33	44.00
449054	AF148848	Hs.22934	myoneurin	73.85	104.00
449101	AA205847	Hs.23016	G protein-coupled receptor	2.58	27.00

449167	T05095	Hs.19597	KIAA1694 protein	1.61	2.36
449207	AL044222	Hs.23255	nucleoporin 155kD	2.36	1.56
449228	AJ403107	Hs.148590	protein related with psoriasis	1.15	1.15
449230	BE613348	Hs.211579	melanoma cell adhesion molecule	206.65	151.00
449305	AI638293		gb:ti09b07.x1 NCI_CGAP_GC6 Homo sapiens	17.28	45.00
449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	26.39	35.00
449448	D60730	Hs.57471	ESTs	1.00	1.00
449467	AW205006	Hs.197042	ESTs	1.00	1.00
449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	56.80	216.86
449722	BE280074	Hs.23960	cyclin B1	150.03	1.00
449976	H05350	Hs.135056	Human DNA sequence from clone RP5-850E9	2.16	2.85
450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte	1.17	1.45
450098	W27249	Hs.8109	hypothetical protein FLJ21080	1.79	2.38
450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	1.00	69.00
450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	1.00	1.00
450193	AI916071	Hs.15607	Homo sapiens Fanconi anemia complementat	29.85	34.00
450221	AA328102	Hs.24641	cytoskeleton associated protein 2	1.00	1.00
450372	BE218107	Hs.202436	ESTs	1.00	1.00
450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	51.26	93.00
450447	AF212223	Hs.25010	hypothetical protein P15-2	123.20	181.00
450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	1.00	19.00
450589	AI701505	Hs.202526	ESTs	1.00	23.00
450684	AA872605	Hs.25333	interleukin 1 receptor, type II	1.00	100.00
450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	1.89	1.55
450705	U90304	Hs.25351	iroquois homeobox protein 2A (IRX-2A) (	1.00	45.00
450832	AA401369	Hs.190721	ESTs	25.17	17.00
450937	R49131	Hs.26267	ATP-dependant interferon response protei	90.92	90.00
450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	3.33	1.70
451105	AI761324		gb:wi60b11.x1 NCI_CGAP_Co16 Homo sapiens	15.02	124.00
451110	AI955040	Hs.265398	ESTs, Weakly similar to transformation-r	1.00	143.00
451253	H48299	Hs.26126	claudin 10	3.02	2.29
451291	R39288	Hs.6702	ESTs	1.00	1.00
451320	AW498974		diacylglycerol kinase, zeta (104kD)	2.92	18.00
451380	H09280	Hs.13234	ESTs	6.90	6.67
451386	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant	35.75	72.00
451437	H24143	Hs.31945	hypothetical protein FLJ11071	1.00	69.00
451462	AK000367	Hs.26434	hypothetical protein FLJ20360	1.83	2.10
451524	AK001466	Hs.26516	hypothetical protein FLJ10604	1.13	1.07
451541	BE279383	Hs.26557	plakophilin 3	1.88	1.33
451592	AI805416	Hs.213897	ESTs	1.00	1.00
451635	AA018899	Hs.127179	cryptic gene	1.52	1.92
451743	AA401369	Hs.190721	ESTs	4.95	17.00
451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	13.55	31.00
451807	W52854		hypothetical protein FLJ23293 similar to	1.55	35.00
451871	AI821005	Hs.118599	ESTs	1.81	2.53
451952	AL120173	Hs.301663	ESTs	1.00	22.00
452012	AA307703	Hs.279766	kinesin family member 4A	3.43	2.26
452046	AB018345	Hs.27657	KIAA0802 protein	56.59	19.00
452194	AI694413	Hs.332649	olfactory receptor, family 2, subfamily	1.67	4.09
452206	AW340281	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	9.31	53.00
452240	AA401369	Hs.190721	ESTs	13.42	17.00
452256	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	39.03	94.00
452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	153.01	340.00
452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	1.95	23.00
452295	BE379936	Hs.28866	programmed cell death 10	42.33	61.00
452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	1.17	2.14
452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	1.00	13.00
452349	AB028944	Hs.29189	ATPase, Class VI, type 11A	1.09	1.42
452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	54.49	53.00
452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	1.00	32.00
452410	AL133619		Homo sapiens mRNA; cDNA DKFZp434E2321 (f	1.26	1.99
452461	N78223	Hs.108106	transcription factor	24.47	35.00
452571	W31518	Hs.34665	ESTs	54.61	102.00
452613	AA461599	Hs.23459	ESTs	1.39	1.32
452699	AW295390	Hs.213062	ESTs	1.00	26.00
452705	H49805	Hs.246005	ESTs	1.00	1.00
452747	AF160477	Hs.61460	Ig superfamily receptor LNIR	112.87	1.29
452787	AW294022	Hs.222707	KIAA1718 protein	1.00	1.00
452795	AW392555	Hs.18878	hypothetical protein FLJ21620	1.00	1.00
452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	7.91	75.00
452833	BE559681	Hs.30736	KIAA0124 protein	3.16	1.92
452838	U65011	Hs.30743	preferentially expressed antigen in mela	174.35	1.00
452862	AA401369	Hs.190721	ESTs	98.26	17.00
452865	AW173720	Hs.345805	ESTs, Weakly similar to A47582 B-cell gr	1.55	1.00
452934	AA581322	Hs.4213	hypothetical protein MGC16207	1.73	1.19
452946	X95425	Hs.31092	EphA5	1.00	1.00
452976	R44214	Hs.101189	ESTs	1.58	1.98
453028	AB006532	Hs.31442	RecQ protein-like 4	1.80	1.60
453095	AW295660	Hs.252756	ESTs	0.77	1.50
453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	1.00	1.00
453103	AI301052	Hs.153444	ESTs	1.00	1.00
453120	AA292891	Hs.31773	pregnancy-induced growth inhibitor	1.23	1.20
453153	N53893	Hs.24360	ESTs	1.00	83.00
453160	AI263307	Hs.239884	H2B histone family, member L	1.00	30.00
453197	AI916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU S	1.00	134.00

453210	AL133161	Hs.32360	hypothetical protein FLJ10867	1.69	1.93
453240	AI969564	Hs.166254	hypothetical protein DKFZp566I133	1.00	1.00
453317	NM_002277	Hs.41696	keratin, hair, acidic, 1	1.19	1.27
453323	AF034102	Hs.32951	solute carrier family 29 (nucleoside tra	4.90	4.11
453331	AI240665	Hs.8850	ESTs	199.42	340.00
453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	1.00	16.00
453431	AF094754	Hs.32973	glycine receptor, beta	1.00	1.00
453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	3.44	5.17
453459	BE047032	Hs.257789	ESTs	2.84	5.58
453563	AW608906.comp	Hs.181163	hypothetical protein MGC5629	4.58	90.00
453633	AA357001	Hs.34045	hypothetical protein FLJ20764	1.74	1.60
453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	19.49	1.00
453830	AA534296	Hs.20953	ESTs	24.92	25.00
453857	AL080235	Hs.35861	DKFZP586E1621 protein	167.59	66.00
453867	AI929383	Hs.33032	hypothetical protein DKFZp434N185	1.00	39.00
453883	AI638516	Hs.347524	cofactor required for Sp1 transcriptiona	1.97	1.58
453884	AA355925	Hs.36232	KIAA0186 gene product	63.89	20.00
453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	20.41	16.00
453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	7.09	22.00
453941	U39817	Hs.36820	Bloom syndrome	29.75	19.00
453964	AI961486	Hs.12744	ESTs	1.00	1.00
453968	AA847843	Hs.62711	Homo sapiens, clone IMAGE:3351295, mRNA	2.06	1.81
453976	BE463830	Hs.163714	ESTs	3.02	131.00
454024	AA993527	Hs.293907	hypothetical protein FLJ23403	1.00	131.00
454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	1.23	1.02
454042	T19228	Hs.172572	hypothetical protein FLJ20093	30.63	171.00
454059	NM_003154	Hs.37048	statherin	1.00	1.00
454066	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	1.01	1.45
454098	W27953	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.26	1.11
454241	BE144666		gb:CM2-HT0176-041099-017-c02 HT0176 Homo	6.33	5.04
454417	AI244459	Hs.110826	trinucleotide repeat containing 9	4.30	7.82
454439	AW819152	Hs.154320	DKFZP566O1646 protein	1.00	1.00
455175	AW993247		gb:RC2-BN0033-180200-014-h09 BN0033 Homo	13.75	103.00
455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	206.11	1.00
456237	AA203682		gb:zx52e07.r1 Soares_fetal_liver_spleen_	1.00	1.00
456321	NM_001327	Hs.87225	cancer/testis antigen	1.14	1.10
456475	NM_000144	Hs.95998	Friedreich ataxia	1.00	48.00
456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	162.25	189.00
456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	2.12	1.80
456736	AW248217	Hs.1619	achaete-scute complex (Drosophila) homol	1.15	1.94
456759	BE259150	Hs.127792	delta (Drosophila)-like 3	1.00	1.00
456990	NM_004504	Hs.171545	HIV-1 Rev binding protein	16.42	84.00
457200	U33749	Hs.197764	thyroid transcription factor 1	0.57	1.76
457234	AW968360	Hs.14355	Homo sapiens cDNA FLJ13207 fis, clone NT	2.71	4.15
457465	AW301344	Hs.122908	DNA replication factor	46.37	47.00
457489	AI693815	Hs.127179	cryptic gene	1.12	1.35
457646	AA725650	Hs.112948	ESTs	1.55	2.51
457733	AW974812	Hs.291971	ESTs	1.00	55.00
457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein	4.36	3.18
458092	BE545684	Hs.343566	KIAA0251 protein	1.00	1.32
458098	BE550224		metallothionein 1E (functional)	1.00	22.00
458207	T28472	Hs.7655	U2 small nuclear ribonucleoprotein auxil	2.06	1.88
458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone H	1.00	1.00
458247	R14439	Hs.209194	ESTs	7.00	9.85
458679	AW975460	Hs.142913	ESTs	1.00	3.00
458778	AW451034	Hs.326525	arylsulfatase D	1.31	2.01
458933	AI638429	Hs.24763	RAN binding protein 1	1.98	1.71
459352	AW810383	Hs.206828	ESTs	12.60	63.00
459670	F01020	Hs.172004	titin	1.00	1.00
459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	1.00	237.00

TABLE 9B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
407746	10125_1	AK001962 R69415 BE464605 AA418699 AA053293 AA149075 AA058396 AW338226 AW272659 AA454607 AI139535 AW469852 AI275461 AW271982 AA730033 AA576507 AA991217 AA782067 AI985851 AA805864 AA505598 AW469857 R69546 AA988279 AW001647 N63320 D82661 T27343 AA306950 AA360989 R58778
408070	1036688_1	AW148852 BE350895
408660	107294_1	AA525775 AA056342 AI538978 AW975281 AA664986
409522	113735_1	AA075382 AA075431
409866	1156522_1	AW502152 H41202 H29772
410032	1170435_1	BE065985 BE065944 BE066008 BE066083 BE066093
411089	123172_1	AA456454 AA713730 AA091294 AA584921 N86077 AW836781 AA601031 AA579876 AA551106 AA633188 AW905577 AI955808 AI679386 AI679895 AA514764 AA454562 AI082382 AA595822 AA551351 AA586369 AA666384 AA188934 AA666398 AA551297 AA565188
411152	1234028_1	BE069199 AW936012 AW877466 AW819782 AW935798 AW835546 AW936042 BE069121 AW835625 AW877536 AW935885 BE069202 AW820019 AW935937 BE160180 AW935946 BE069101 BE069125 AW877527 BE160316 BE160398 AW935794 AW835701 AW935784
412537	1304_1	AL031778 X59711 NM_002505 M59079 AI870439 AI494259 AW664010 AA405063 AA436132 BE174516 AA412691 AI400314 AA436024 T29403 BE079412 BE079428 N90322 AI631202 AI141758 AI016793 AI167566 AI862075 AI375230 AI208445 AW235763 AL044113 AA382556 AW953918 AA927051 AA889823 BE003094 AW390155 AW360805 AW360823 AW360810 AA425472 AI694282 AL044114 AI684577 AI809865

		AI478773 AI160445 AI674630 N69088 AW665529 N49278 AI129239 AI457890 AI621264 AW297152 AI268215 AA907787 AI286170 AI017982 AI963541 AI469807 AI969353 BE552356 N66509 AA736741 AA382555 AW075811 AW292026
412811	132943_1	H06382 AW957730 AA352014 R13591 AA121201 D60420 BE263253 BE047862 Z41952 AI424991 AI693507 AI863108 AA599060 AI091148 AA598689 R39887 AA813482 AW016452 H06383 R41807 AI354268 AA620528 AI241940 AW089149 AW090733 AW088875 Z38240 AA121202 R17734
413690	1383256_1	BE157489 BE157560
414883	15024_1	AA926960 AA926959 W76521 W24270 W21526 AA037172 BE267636 H83186 AA469909 N86396 AA001348 BE535736 AA081745 BE566245 AA082436 H72525 H77575 N49786 W80565 H78746 BE569085 W04339 R98127 T55938 BE279271 AW960304 T29812 AA476873 BE297387 AA292753 AA177048 NM_001826 X54941 BE314366 AA908783 AI719075 BE270172 BE269819 AA889955 AI204630 W25243 AI935150 AA872039 W72395 T99630 AI422691 H98460 N31428 BE255916 H03265 AI857576 AA776920 AA910644 AA459522 AA293140 AW514667 R75953 AW662396 AA662522 AI865147 AI423153 AW262230 AA584410 AA583187 AW024595 AW069734 AI828996 AA282997 AA876046 AW613002 AA527373 AW972459 AI831360 AA621337 AA100926 AA772418 AA594628 AI033892 W95096 AI034317 AA398727 AI085031 N95210 AI459432 AI041437 AA932124 AA627684 AA935829 AI004827 AI423513 AI094597 H42079 R54703 AI630359 AA617681 AA978045 AA643280 W44561 AI991988 AI537692 AI090262 AA740817 AI312104 AI911822 AA416871 AI185409 AA129784 AA701623 AI075239 AI139549 AA633648 AI339996 AI336880 AA399239 AI078708 AI085351 AI362835 AI346618 AI146955 AI989380 AI348243 N92892 AA765850 AI494230 AI278887 AA962596 AI492600 W80435 AA001979 R97424 AI129015 N24127 AA157451 AA235549 AA459292 AA037114 AA129785 AI494211 AW059601 AW886710 R92790 N59755 AI361128 AW589407 H47725 H97534 H48076 H48450 T99631 AW300758 H03431 R76789 AA954344 H77576 R96823 AI457100 N92845 N49682 H42038 BE220698 BE220715 H99552 AA701624 N74173 R54704 H79520 H72923 H03266 BE261919 AA769633 AA480310 AA507454 AA910586 AI203723 AW104725 W25611 W25071 T88980 H03513 T77589 R99156 W95095 R97470 AA702275 T77551 AA911952 H82956 N83673 AA283672
415989	156454_1	AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086
417324	166714_1	AW265494 AA455904 AA195677 AW265432 AW991605 AA456370
418574	17690_1	N28754 N28747 AI568146 AI979339 AA322671 AA322672 AW955043 AI990326 AA776406 AI016250 AA843678 AW451882 N23137 N23129 W70051 AI038748 AA831327 AI925845 AW945895
418712	1784125_1	Z42183 T31621 T97478
419443	184788_1	D62703 AA242966 D79798
419502	18535_1	AU076704 T74854 T74860 T72098 T73265 T73873 T69180 T74658 T58786 T60385 T73410 T68781 T67845 T67593 T73952 T67864 T60630 T68367 T68401 T53959 T72360 T72099 T60377 T58961 T71712 T72821 T64738 T74645 T72037 T68688 T72063 T73258 T72826 T64242 T68220 T74673 T71800 T68355 T61227 T62738 T69317 T53850 T64692 T73768 T73962 T73382 T68914 T70975 T73400 T60631 T73277 T73203 T70498 T61409 T58925 NM_000508 M64982 T68301 T73729 T69445 T60424 T67922 T67736 T68716 T67755 T74765 T73819 T58719 T74756 T60477 T74863 T61109 T68329 T58850 T71857 T73425 T53736 T68607 T58898 T64309 T72031 T72079 T64305 T71908 T68107 T71916 T73787 T56035 T64425 T71870 T60476 T61376 T67820 T71895 T41006 T69441 T68170 T74617 T71958 T69440 T61875 R06796 H48353 T71914 T53939 T64121 AA693996 T72525 T67779 T68078 AA011465 AA345378 AV654847 AV654272 AV656001 AI064740 T82897 N33594 AA344542 AW805054 AI207457 T61743 AA026737 H94389 AA382695 AA918409 T68044 S82092 T39959 AI017721 AA312395 AA312919 T40156 H66239 AV652989 H38728 R98521 AV655200 R95790 W03250 W00913 AA344136 AV660126 R97923 AA343596 AW470774 AV651256 N54417 AA812862 AW182929 AI111192 H61463 H72060 AA344503 H38639 AI277511 AV661108 AI207625 T47810 AA235252 T27853 T47778 R95746 H70620 AA701463 AW827166 R98475 C20925 AV657287 T71959 T71313 T73920 T73333 T61618 T69293 T69283 T73931 T72178 T72456 AV645639 AV653476 T72957 T72300 T58906 T71457 T70494 T72956 T70495 T68267 T74407 T85778 AA344726 T27854 T74485 T74101 T73868 T71518 T72304 AA343853 T73909 T68070 T72065 H72149 T73493 T73495 AV645993 R02293 T70475 T64751 AA344441 AA343657 AA345732 AA344328 AI110639 AA344603 AF063513 T64696 T68516 T72223 T60507 T67633 R29500 T72517 R02292 T60599 T69206 T70452 T74677 R29366 T61277 T74914 T60352 R29675 T74843 AV645792 AA344408 T69197 T72057 T69368 T69358 T68258 AV650429 T73341 T61702 T74598 T40095 K02272 T40106 AA343045 AA341908 AA341907 AA342807 AA341964 T53747 T72042 T62764 AI064899 AA343060 T67832 T72440 T71770 T68091 T69108 T72449 T69167 T71289 T68251 AV654844 T64375 AA345234 T67598 AA011414 T68036 H48262 AI207557 T68219 W86031 T69081 T64232 R93196 T62136 AV650539 H67459 T72978 AA344583 T60362 H58121 T95711 T72803 T68055 T71715 R29036 T72793 T69122 T64595 T62888 T69139 T68291 T64652 T67971 T46862 AA693592 AI248502 R29454 T64764 T57001 T73052 T71429 T51176 T58866 AV655414 H90426 AA342489 T73666 T67848 T72512 T53835 T67837 T73317 T74273 T69420 T68245 T74380 T67862 T74474 T56068
419936	189181_1	AI792788 BE142230 AA252019
421582	2041_1	AI910275 X00474 X52003 X05030 NM_003225 AA314326 AA308400 AA506787 AA314825 AI571948 AA507595 AA614579 AA587613 R83818 AA568312 AA614409 AA307578 AI925552 AW950155 AI910083 M12075 BE074052 AW004668 AA578674 AA582084 BE074053 BE074126 BE074140 AA514776 AA588034 BE074051 BE074068 AW009769 AW050690 AA858276 R55389 AI001051 AW050700 AW750216 AA614539 BE074045 AI307407 AW602303 BE073575 AI202532 AA524242 AI970839 AI909751 BE076078 AI909749 R55292
422128	211994_1	AW881145 AA490718 M85637 AA304575 T06067 AA331991
423034	224122_1	AL119930 AA320696 AW752565
423816	23234_1	AL031985 AL137241 AI792386 AI733664 AI857654 AI049911
424200	236595_1	AA337221 AA336756 AW966196
424999	245835_1	AW953120 R56325 AA349562
426966	273896_1	AI493134 AI498691 AW771508 AI498457 AI768408 AI783624 AI383985 AI580267 D79813 AA393768
426991	27415_1	AK001536 AA191092 AW510354 AI554256 AL353968 AA134266
427260	276598_1	AA663848 AA400100 AA401424
428023	28589_2	AL038843 AA161338 BE268213 AA425597 N87306 AA092969 BE566038 AA247451 N47392 AI928802 AW182584 AW027872 AI819831 AI936994 W56258 AI653448 AI278611 AI283557 AI824306 AW338658 AW150899 AA687514 N47393 N29885 AA973469 AI038904 AI292064 AI034339 AW674593 N72156 AI079733 AI038683 AI291616 AA491599 AA993675 AA837380 BE006554 BE006473 AI087090 T33044 AA652043 AI203503 AA583959 W35283 AI129926 Z41844 AW020925 AW575848 AI684603 AA493297 AI140689 AI277175 AA425444 AI932767 W02632 BE396786 R37261
429220	301384_1	AW207206 AW341473 AA448195 AI951341
429978	31150_1	AA249027 AL038984 AK001993 AL080066 AV652725 BE566226 AA345557 AA315222 AA090585 AA375688 AA301092 AA298454 W05762 AW607939 H51658 D83880 N84323 BE296821 AW947007 D61461 AW079261 AA329482 AW901780 AI354442 AA772275 R31663 AI354441 AI767525 H92431 AI916735 H93575 AI394255 AW014741 AI573090 C06195 AW612857 AW265195 AI339558 AI377532 AI308821 AI919424 AI589705 AW055215 AI336532 AI338051 AA806547 C75509 C00618 AW071172 AW769904 AA630381 AI678018 AI863985 D79662 BE221049 AW265018 AI589700 AW196655 N76573 AI370908 BE042393 N75017 AI698870 AW960115
430439	31808_1	AL133561 AL041090 AL117481 AL122069 AW439292 AI968826
430935	325772_1	AW072916 AI184913 AA489195 AW466994 AW469044 N59350 AI819642 AI280239 AI220572 AA789302 AI473611 AW841126 D60937
431089	327825_1	BE041395 AA491826 AA621946 AA715980 AA666102
431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188
432407	34624_1	AA221036 R87170 BE537068 BE544757 C18935 AW812058 T92565 AA227415 AA233942 AA223237 AA668403 AA601627 AW869639 BE061833 BE000620 AW961170 AW847519 AA308542 AW821833 AW945688 C04699 AA205504 AA377241 AW821667 AA055720 AW817981 AW856468 AA155719 AA179928 T03007 AW754298 AA227407 AA113928 AA307904 C16859
434414	38585_1	AI798376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231 AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139 AA149776 AA699829 AW879188 AW813567 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730 AA157715 AA053524 AW849581 AW854566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824 AI829309 AW991957 N66951 AA527374 H66215 AA045564 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659 BE081531 H59570
436608	42361_3	AA628980 AI126603 BE504035

438091	44964_1	AW373062 T55662 AI299190 BE174210 AW579001 H01811 W40186 R67100 AI923886 AW952164 AA628440 AW898607 AW898616 AA709126 AW898628 AW898544 AA947932 AW898625 AW898622 AI276125 AI185720 AW510698 AA987230 T52522 BE467708 AW243400 AW043642 AI288245 AI186932 D52654 D55017 D52715 D52477 D53933 D54679 AI298739 AI146984 AI922204 N98343 BE174213 AA845571 AI813854 AI214518 AI635262 AI139455 AI707807 AI698085 AW884528 AI024768 AI004723 AW087420 AI565133 N94964 AI268939 AW513280 AI061126 AI435818 AI859106 AI360506 AI024767 AA513019 AA757598 X56196 AA902959 AI334784 AI860794 AA010207 AW890091 AW513771 AI951391 AI337671 T52499 AA890205 AI640908 H75966 AA463487 AA358688 AI961767 AI866295 AA780994 AI985913 BE174196 AA029094 AW592159 T55581 N79072 AI611201 AA910812 AI220713 AW149306 AI758412 AA045713 R79750 N76096
439000	467716_1	AW979121 AA847986 AA829098
439285	47065_1	AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AI346341 AI867454 N54784 AI655270 AI421279 AW014882 AA775552 N62351 N59253 AA626243 AI341407 BE175639 AA456968 AI358918 AA457077
439780	47673_1	AL109688 R23665 R26578
441128	51021_2	AA570256 AW014761 AA573721 AI473237 AI022165 AA554071 AA127551 N90525 AW973623 AA447991 AA243852 BE328850 AI148171 AI359627 AI005068 AI356567 AA232991 AW016855 AA906902 AA233101 AA127550 BE512923
443068	558874_1	AI188710 AI032142 AW078833 N30308 AW675632 AI219028 AI341201 N22181 H95390
443947	586160_1	W24187 W24194 R17789
447636	7301_1	Y10043 NM_005342 L05085 AL034450 BE614226 AW749053 AA379173 AA248230 BE514634 AA334622 R70656 AA367593 AA214649 AA369318 AW957081 R05760 AA039903 AI886597 AW630122 AA906264 AA041527 R01145 AI088688 BE463637 AA398795 AI354883 AI768938 AI569996 AI452952 AI168582 AI189869 AI086670 AW262560 AW613854 AA862839 AA435840 AA670197 AI024032 AI990659 AI990089 N81095 AA847919 AW960150 AA211075 AA044704 AA367594 AW582587 AW858854 AW818630 AW818281 AW818433 AW582595 AA096002 N83992
448993	79225_1	AI471630 BE540637 BE265481 AW407710 BE513882 BE546739 AA053597 BE140503 BE218514 AW956702 AI656234 AI636283 AI567265 AW340858 BE207794 AA053085 R69173 AA292343 AA454908 AA293504 AI659741 AI927478 AA399460 AI760441 AA346416 BE047245 AA730380 AA394063 AA454833 AI982791 AI567270 AI813332 AI767858 AA427705 D20284 AI221458 BE048537 AI263048 AA346417 AA911497 BE537702
449305	804424_1	AI638293 AW813561
451105	859083_1	AI761324 AW880941 AW880937
451320	86576_1	AW118072 AI631982 T15734 AA224195 AI701458 W20198 F26326 AA890570 N90552 AW071907 AI671352 AI375892 T03517 R88265 AI124088 AA224388 AI084316 AI354686 T33652 AI140719 AI720211 T03490 AI372637 T15415 AW205836 AA630384 T03515 T33230 AA017131 AA443303 T33623 AI222556 T33511 T33785 AI419606 D55612
451807	8865_1	W52854 AL117600 BE208116 BE208432 BE206239 BE082291 AW953423 AA351619 BE180648 BE140560 W60080 AA865478 N90291 AW450652 AW449519 AA993634 AI806539 AA351618 AW449522 AI827626 AA904788 AA380381 AA886045 AA774409 BE003229 Z41756
452410	9163_1	AL133619 AA468118 AA383064 AI476447 T09430 AI673758 AA524895 AI581345 AI300820 AW498812 AA256162 AI559724 AI685732 AA602400 AA905453 AI204595 AW166541 AA157456 AA156269 AA383652 AA431072 AW592707 AI435410 AW272464 AI215594 AA622747 R74039 N35031 AI804128 AW513621 AA868351 AI026826 AI493388 AA614641 W81604 AI567080 AI214351 AA730140 AI125754 AI200813 AI269603 AI565082 AI807095 AI476629 AA505909 AI368449 AI686077 AI582930 AW085038 AA757863 AA730154 AI767072 AA468316 AI734130 AI734138 AA426284 AA433997 AI741241 AW043563 AI732741 AI732734 AA437369 AA425820 AA664048 R74130
454241	1067807_1	BE144666 BE184942 AW238414 BE184946
455175	1257335_1	AW993247 AW861464
456237	168730_1	AA203682 R11958
458098	47395_1	BE550224 AA832519 N45402 AW885857 N29245 BE465409 W07677 AW970089 AI299731 AA482971 BE503548 H18151 W79223 AF086393 AA461301 W74510 R34182 AI090689 N46003 BE071550 R28075 AW134982 AI240204 AI138906 AW026179 AI572316 BE466182 AI206395 AI276154 AI273269 AI422817 AI371014 AI421274 AI188525 AA939164 BE549810 AW137865 AI694996 BE503841 AA459718 BE327407 BE467534 BE218421 BE467767 AA989054 BE467063 AI797130 BE327781

TABLE 9C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400512	9796593	Minus	1439-1615
400517	9796686	Minus	49996-50346
400560	9843598	Plus	94182-94323,97056-97243,101095-101236,102824-103005
400664	8118496	Plus	13558-13721,13942-14090,14554-14679
400665	8118496	Plus	16879-17023
400666	8118496	Plus	17982-18115,20297-20456
400749	7331445	Minus	9162-9293
400763	8131616	Minus	35537-35784
401027	7230983	Minus	70407-70554,71060-71160
401093	8516137	Minus	22335-23166
401203	9743387	Minus	172961-173056,173868-173928
401212	9858408	Plus	87839-88028
401411	7799787	Minus	144144-144329
401435	8217934	Minus	54508-55233
401464	6682291	Minus	170688-170834
401714	6715702	Plus	96484-96681
401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
401760	9929699	Plus	83126-83250,85320-85540,94719-95287
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
401797	6730720	Plus	6973-7118
401961	4581193	Minus	124054-124209
401985	2580474	Plus	61542-61750
401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
402260	3399665	Minus	113765-113910,115653-115765,116808-116940
402265	3287673	Plus	21059-21168
402297	6598824	Plus	35279-35405,35573-35659
402408	9796239	Minus	110326-110491

402420	9796339	Plus	129750-129919
402674	8077108	Minus	39290-39502
402802	3287156	Minus	53242-53432
402994	2996643	Minus	4727-4969
403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
403306	8099945	Plus	127100-127251
403329	8516120	Plus	96450-96598
403381	9438267	Minus	26009-26178
403478	9958258	Plus	116458-116564
403485	9966528	Plus	2888-3001,3198-3532,3655-4117
403627	8569879	Minus	23868-24342
403715	7239669	Plus	85128-85292
404044	9558573	Minus	225757-225939
404076	9931752	Minus	3848-3967
404101	8076925	Minus	125742-125997
404140	9843520	Plus	37761-38147
404165	9926489	Minus	69025-69128
404185	4572584	Minus	129171-129327
404210	5006246	Plus	169926-170121
404253	9367202	Minus	55675-56055
404287	2326514	Plus	53134-53281
404298	9944263	Minus	73591-73723
404347	9838195	Plus	74493-74829
404440	7528051	Plus	80430-81581
404721	9856648	Minus	173763-174294
404794	4826439	Plus	101619-101898
404854	7143420	Plus	14260-14537
404877	1519284	Plus	1095-2107
404927	7342002	Plus	68690-69563
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
405449	7622497	Plus	42236-42570
405568	6006906	Plus	35912-36065
405572	3800891	Plus	85230-85938
405646	4914350	Plus	741-969
405676	4557087	Plus	73195-73917
405770	2735037	Plus	61057-62075
405932	7767812	Minus	123525-123713
406137	9166422	Minus	30487-31058
406360	9256107	Minus	7513-7673
406399	9256288	Minus	63448-63554
406467	9795551	Plus	182212-182958

TABLE 10A: Potential Therapeutic, Diagnostic and Prognostic targets for Therapy of Lung Cancer and Non-malignant Lung Disease
Table 2A shows about 307 genes up-regulated in non-malignant lung disease relative to lung tumors and normal body tissues and/or down-regulated in lung tumors relative to normal lung and non-malignant lung disease. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 10B show the accession numbers for those Pkey's lacking UnigeneID's for table 10A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 10C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 10A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
404394			ENSP00000241075:TRRAP PROTEIN.	0.79	3.10
404916			Target Exon	1.00	159.00
405257			Target Exon	1.00	422.00
407228	M25079	Hs.155376	hemoglobin, beta	0.47	2.33
407568	AA740964	Hs.62699	ESTs	1.00	123.00
408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	1.00	230.00
409031	AA376836	Hs.76728	ESTs	1.00	128.00
410434	AF051152	Hs.63668	toll-like receptor 2	39.65	149.00
410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	1.00	109.00
410808	T40326	Hs.167793	ESTs	1.14	13.14
412351	AL135960	Hs.73828	T-cell acute lymphocytic leukemia 1	0.37	2.27
412372	R65998	Hs.285243	hypothetical protein FLJ22029	1.00	173.00
413795	AL040178	Hs.142003	ESTs	0.10	11.90
414154	AW205314	Hs.323060	ESTs	0.62	2.09
414214	D49958	Hs.75819	glycoprotein M6A	0.03	4.55
414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	0.64	2.97
415122	D60708	Hs.22245	ESTs	0.07	8.97
415765	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and	0.67	1.65
415775	H00747	Hs.29792	ESTs, Weakly similar to I38022 hypotheti	0.29	2.64
415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	1.00	145.00

416319	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i	15.32	237.00
416402	NM_000715	Hs.1012	complement component 4-binding protein,	0.64	4.00
417355	D13168	Hs.82002	endothelin receptor type B	0.01	3.90
417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	36.30	357.00
417511	AL049176	Hs.82223	chordin-like	1.00	179.00
418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	0.02	6.00
418726	BE241812	Hs.87860	protein tyrosine phosphatase, non-recept	1.00	113.00
418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	0.44	1.90
418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	0.96	2.04
419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	0.62	2.74
419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	0.03	6.90
419235	AW470411	Hs.288433	neurotrimin	1.48	5.13
419407	AW410377	Hs.41502	hypothetical protein FLJ21276	37.55	336.00
420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	0.80	3.65
420656	AA279098	Hs.187636	ESTs	1.65	8.07
420729	AW964897	Hs.290825	ESTs	2.99	25.82
421177	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f	0.46	1.95
422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.00	156.00
422426	W79117	Hs.58559	ESTs	0.03	7.44
422652	AW967969	Hs.118958	syntaxin 11	0.14	3.62
423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	0.01	3.16
424433	H04607	Hs.9218	ESTs	0.75	141.75
424585	AA464840	Hs.131987	ESTs	1.00	167.00
424711	NM_005795	Hs.152175	calcitonin receptor-like	0.43	3.01
424973	X92521	Hs.154057	matrix metalloproteinase 19	0.37	19.45
425023	AW956889	Hs.154210	endothelial differentiation, sphingolipi	0.14	3.35
425664	AJ006276	Hs.159003	transient receptor potential channel 6	1.00	94.00
425998	AU076629	Hs.165950	fibroblast growth factor receptor 4	0.68	1.42
426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	0.03	3.74
426753	T89832	Hs.170278	ESTs	1.00	141.00
427558	D49493	Hs.2171	growth differentiation factor 10	1.00	117.00
427983	M17706	Hs.2233	colony stimulating factor 3 (granulocyte	0.75	2.20
428467	AK002121	Hs.184465	hypothetical protein FLJ11259	0.76	2.25
428927	AA441837	Hs.90250	ESTs	0.01	3.62
429496	AA453800	Hs.192793	ESTs	1.00	138.00
430468	NM_004673	Hs.241519	angiopoietin-like 1	1.00	132.00
431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	1.00	157.00
431728	NM_007351	Hs.268107	multimerin	1.00	157.00
431848	AI378857	Hs.126758	ESTs, Highly similar to AF175283 1 zinc	0.34	2.24
432128	AA127221	Hs.117037	ESTs	0.00	1.15
432519	AI221311	Hs.130704	ESTs, Weakly similar to BCHUIA S-100 pro	0.01	2.06
433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	1.00	267.00
433803	AI823593	Hs.27688	ESTs	1.00	105.00
434730	AA644669	Hs.193042	ESTs	1.05	3.15
435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	0.83	1.94
436532	AA721522		gb:nv54h12.r1 NCI_CGAP_Ew1 Homo sapiens	1.00	218.00
437119	AI379921	Hs.177043	ESTs	1.00	133.00
437140	AA312799	Hs.283689	activator of CREM in testis	0.67	122.67
437211	AA382207	Hs.5509	ecotropic viral integration site 2B	1.00	142.00
437960	AI669586	Hs.222194	ESTs	1.00	147.00
438202	AW169287	Hs.22588	ESTs	1.00	141.00
438873	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	0.71	3.66
438875	AA827640	Hs.189059	ESTs	23.32	370.00
441048	AA913488	Hs.192102	ESTs	0.77	8.50
441188	AW292830	Hs.255609	ESTs	3.43	16.36
441499	AW298235	Hs.101689	ESTs	1.00	167.00
444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	1.00	151.00
444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	46.47	153.00
444561	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	0.01	3.08
445279	R41900	Hs.22245	ESTs	0.60	141.00
446017	N98238	Hs.55185	ESTs	0.18	2.39
446984	AB020722	Hs.16714	Rho guanine exchange factor (GEF) 15	0.10	2.16
446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	0.01	2.53
447357	AI375922	Hs.159367	ESTs	0.46	2.64
448106	AI800470	Hs.171941	ESTs	18.05	296.00
448253	H25899	Hs.201591	ESTs	1.00	141.00
449275	AW450848	Hs.205457	periaxin	0.56	1.38
450400	AI694722	Hs.279744	ESTs	0.88	4.33
450696	AI654223	Hs.16026	hypothetical protein FLJ23191	0.52	2.08
450726	AW204600	Hs.250505	retinoic acid receptor, alpha	0.79	2.01
451497	H83294	Hs.284122	Wnt inhibitory factor-1	0.35	2.03
451533	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	0.13	2.25
453636	R67837	Hs.169872	ESTs	1.00	116.00
458332	AI000341	Hs.220491	ESTs	1.00	192.00
459580	AA022888	Hs.176065	ESTs	0.20	2.98
400269			Eos Control	0.40	2.40
403421			NM_016369*:Homo sapiens claudin 18 (CLDN	0.53	1.77
407570	Z19002	Hs.37096	zinc finger protein 145 (Kruppel-like, e	0.01	3.18
412295	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1	0.56	1.74
414517	M24461	Hs.76305	surfactant, pulmonary-associated protein	0.64	1.50
417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	0.33	1.16
418307	U70867	Hs.83974	solute carrier family 21 (prostaglandin	0.53	1.55
418935	T28499	Hs.89485	carbonic anhydrase IV	0.20	1.28
421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospha	0.78	1.90
421798	N74880	Hs.29877	N-acylsphingosine amidohydrolase (acid c	0.59	1.54

423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	0.59	1.55
423738	AB002134	Hs.132195	airway trypsin-like protease	10.14	51.00
425211	M18667	Hs.1867	progastricsin (pepsinogen C)	0.35	1.62
425438	T62216	Hs.270840	ESTs	0.23	9.45
426828	NM_000020	Hs.172670	activin A receptor type II-like 1	0.03	1.71
427019	AA001732	Hs.173233	hypothetical protein FLJ10970	0.01	1.49
428043	T92248	Hs.2240	uteroglobin	0.42	1.26
430280	AA361258	Hs.237868	interleukin 7 receptor	0.46	2.43
431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	0.57	1.59
431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	0.29	1.80
432985	T92363	Hs.178703	ESTs	0.32	2.27
441835	AB036432	Hs.184	advanced glycosylation end product-speci	0.31	1.51
442275	AW449467	Hs.54795	ESTs	0.55	1.78
443709	AI082692	Hs.134662	ESTs	0.00	3.02
444325	AW152618	Hs.16757	ESTs	0.32	2.49
450954	AI904740	Hs.25691	receptor (calcitonin) activity modifying	0.46	1.74
451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	0.52	1.87
453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	0.00	3.30
456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Dr	0.01	2.31
444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	0.66	2.20
400754			Target Exon	1.00	297.00
401045			C11001883*:gi|6753278|ref|NP_033938.1| c	1.00	109.00
401083			NM_016582*:Homo sapiens peptide transpor	0.89	1.39
402474			NM_004079:Homo sapiens cathepsin S (CTSS	1.45	4.47
402808			ENSP00000235229:SEMB.	1.00	1.87
403021			C21000030:gi|9955960|ref|NP_063957.1| AT	1.00	149.00
403438			NM_031419*:Homo sapiens molecule possess	1.06	2.96
403687			NM_007037*:Homo sapiens a disintegrin-li	0.04	4.89
403764			NM_005463:Homo sapiens heterogeneous nuc	1.00	225.00
404277			NM_019111*:Homo sapiens major histocompa	0.97	1.93
404288			NM_002944*:Homo sapiens v-ros avian UR2	1.00	68.00
404518	AI815601		CD83 antigen (activated B lymphocytes, i	0.02	1.83
405106			C11001637*:gi|5032241|ref|NP_005732.1| z	1.00	235.00
405381			Target Exon	1.00	93.00
406387			Target Exon	1.37	6.02
406646	M33600		major histocompatibility complex, class	0.86	2.46
406714	AI219304	Hs.266959	hemoglobin, gamma G	0.01	3.19
406753	AA505665	Hs.217493	annexin A2	1.00	147.00
406973	M34996	Hs.198253	major histocompatibility complex, class	1.03	2.04
407248	U82275	Hs.94498	leukocyte immunoglobulin-like receptor,	1.00	64.00
407510	U96191		gb:Human trophoblast hypoxia-regulated f	1.00	90.00
407731	NM_000066	Hs.38069	complement component 8, beta polypeptide	1.00	67.00
407830	NM_001086	Hs.587	arylacetamide deacetylase (esterase)	1.00	102.00
408045	AW138959	Hs.245123	ESTs	1.00	70.00
408074	R20723		ESTs	1.00	112.00
408374	AW025430	Hs.155591	forkhead box F1	0.07	10.17
409064	AA062954	Hs.141883	ESTs	0.39	2.31
409083	AF050083	Hs.673	interleukin 12A (natural killer cell sti	1.00	95.00
409153	W03754	Hs.50813	hypothetical protein FLJ20022	0.01	4.55
409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	0.01	3.72
409238	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr	1.00	79.00
409389	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	0.14	27.35
409718	D86640	Hs.56045	src homology three (SH3) and cysteine ri	1.00	113.00
410798	BE178622	Hs.16291	gb:PM3-HT0605-270200-001-a02 HT0605 Homo	0.64	2.47
411020	NM_006770	Hs.67726	macrophage receptor with collagenous str	0.55	2.40
411667	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	1.00	111.00
412000	AW576555	Hs.15780	ATP-binding cassette, sub-family A (ABC1	1.00	95.00
412358	BE047490	Hs.24172	ESTs	1.00	87.00
412420	AL035668	Hs.73853	bone morphogenetic protein 2	1.43	8.07
412564	X83703	Hs.31432	cardiac ankyrin repeat protein	0.02	3.07
412869	AA290712	Hs.82407	CXC chemokine ligand 16	0.93	1.72
412870	N22788	Hs.82407	CXC chemokine ligand 16	0.97	1.51
413529	U11874	Hs.846	interleukin 8 receptor, beta	0.02	2.42
413533	BE146973		gb:QV4-HT0222-011199-019-e05 HT0222 Homo	0.65	1.50
413689	BE157286	Hs.20631	zinc finger protein, subfamily 1A, 5 (Pe	20.87	232.00
413724	AA131466	Hs.23767	hypothetical protein FLJ12666	1.00	80.00
413800	AI129238	Hs.192235	ESTs	1.00	85.00
413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	1.00	213.00
413829	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)	0.02	3.93
414376	BE393856	Hs.66915	ESTs, Weakly similar to 16.7Kd protein [	1.00	115.00
414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	0.49	1.94
414700	H63202	Hs.38163	ESTs	0.03	3.75
415078	AA311223	Hs.283091	found in inflammatory zone 3	0.86	1.95
415120	N64464	Hs.34950	ESTs	1.00	120.00
415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	0.60	2.48
415335	AA847758	Hs.111030	ESTs	1.00	95.00
415582	W92445	Hs.165195	Homo sapiens cDNA FLJ14237 fis, clone NT	1.00	136.00
416030	H15261	Hs.21948	ESTs	0.02	8.07
416427	BE244050	Hs.79307	Rac/Cdc42 guanine exchange factor (GEF)	1.00	73.00
416464	NM_000132	Hs.79345	coagulation factor VIII, procoagulant co	0.70	3.36
416585	X54162	Hs.79386	leiomodin 1 (smooth muscle)	0.06	6.56
416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	0.70	3.66
417148	AA359896	Hs.293885	hypothetical protein FLJ14902	1.00	114.00
417370	T28651	Hs.82030	tryptophanyl-tRNA synthetase	0.85	1.30
417673	T87281	Hs.16355	ESTs	0.16	15.54

418067	AI127958	Hs.83393	cystatin E/M	0.81	1.74
418296	C01566	Hs.86671	ESTs	1.00	99.00
418643	J03798	Hs.86948	small nuclear ribonucleoprotein D1 polyp	1.00	60.00
418832	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro	2.40	14.74
418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	0.67	3.16
419261	X07876	Hs.89791	wingless-type MMTV integration site fami	1.00	73.00
419564	U08989	Hs.91139	solute carrier family 1 (neuronal/epithe	1.00	192.00
419574	AK001989	Hs.91165	hypothetical protein	1.00	94.00
419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	61.16	500.00
420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	0.52	1.70
420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	1.00	172.00
420577	AA278436	Hs.186649	ESTs	1.00	97.00
421262	AA286746	Hs.9343	Homo sapiens cDNA FLJ14265 fis, clone PL	1.00	64.00
421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054868, mRNA	0.88	1.51
421470	R27496	Hs.1378	annexin A3	0.05	11.26
421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	1.00	73.00
421563	NM_006433	Hs.105806	granulysin	0.82	2.42
421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	5.50	31.57
421855	F06504	Hs.27384	ESTs, Moderately similar to ALU4_HUMAN A	1.00	129.00
421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	1.00	101.00
421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	0.60	63.60
422232	D43945	Hs.113274	transcription factor EC	1.00	148.00
422386	AF105374	Hs.115830	heparan sulfate (glucosamine) 3-O-sulfot	1.40	3.98
423168	R34385	Hs.124940	GTP-binding protein	0.34	3.59
423196	AK001866	Hs.125139	hypothetical protein FLJ11004	0.55	2.00
423387	AJ012074		vasoactive intestinal peptide receptor 1	0.09	2.13
423424	AF150241	Hs.128433	prostaglandin D2 synthase, hematopoietic	1.00	141.00
423456	AL110151	Hs.128797	DKFZP586D0824 protein	1.00	66.00
423696	Z92546		Sushi domain (SCR repeat) containing	0.73	1.27
424027	AW337575	Hs.201591	ESTs	0.54	2.58
424212	NM_005814	Hs.143131	glycoprotein A33 (transmembrane)	0.77	2.47
425087	R62424	Hs.126059	ESTs	1.00	74.00
425175	AF020202	Hs.155001	UNC13 (C. elegans)-like	0.85	1.96
425771	BE561776	Hs.159494	Bruton agammaglobulinemia tyrosine kinas	1.18	2.56
426486	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	1.00	76.00
427507	AF240467	Hs.179152	toll-like receptor 7	1.00	63.00
427618	NM_000760	Hs.2175	colony stimulating factor 3 receptor (gr	0.60	2.19
427732	NM_002980	Hs.2199	secretin receptor	0.97	1.42
427952	AA765368	Hs.293941	ESTs, Moderately similar to A53959 throm	1.00	105.00
428709	BE268717	Hs.104916	hypothetical protein FLJ21940	1.00	80.00
428769	AW207175	Hs.106771	ESTs	0.09	2.55
428780	AI478578	Hs.50636	ESTs	1.00	98.00
428833	AI928355	Hs.185805	ESTs	1.00	113.00
429657	D13626	Hs.2465	KIAA0001 gene product; putative G-protei	1.00	52.00
430212	AA469153		gb:nc67f04.s1 NCI_CGAP_Pr1 Homo sapiens	1.00	132.00
430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	0.11	15.60
430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	1.00	103.00
430414	AW365665	Hs.120388	ESTs	0.50	6.96
430656	AA482900	Hs.162080	ESTs	1.00	70.00
430843	AI734149	Hs.119514	ESTs	1.00	90.00
430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	0.29	1.84
431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	1.00	79.00
431921	N46466	Hs.58879	ESTs	0.91	1.67
432176	AW090386	Hs.112278	arrestin, beta 1	0.66	2.63
432203	AA305746	Hs.49	macrophage scavenger receptor 1	1.00	76.00
432231	AA339977	Hs.274127	CLST 11240 protein	0.46	1.46
432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	0.79	2.25
432522	D11466	Hs.51	phosphatidylinositol glycan, class A (pa	1.93	4.83
432596	AJ224741	Hs.278461	matrilin 3	0.04	5.79
432850	X87723	Hs.3110	angiotensin receptor 2	1.00	167.00
433138	AB029496	Hs.59729	semaphorin sem2	0.04	9.16
433563	AI732637	Hs.277901	ESTs	1.00	91.00
433588	AI056872	Hs.133386	ESTs	120.16	315.00
434445	AI349306	Hs.11782	ESTs	0.60	1.84
435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	1.00	128.00
435974	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	1.00	108.00
436081	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	1.00	91.00
437157	BE048860	Hs.120655	ESTs	1.00	87.00
437207	T27503	Hs.15929	hypothetical protein FLJ12910	1.00	105.00
437311	AA370041	Hs.9456	SWI/SNF related, matrix associated, acti	1.00	71.00
437439	H29796	Hs.269622	ESTs	1.00	115.00
438199	AW016531	Hs.122147	ESTs	1.00	80.00
439551	W72062	Hs.11112	ESTs	0.30	3.10
440515	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene famil	1.00	77.00
440887	AI799488	Hs.135905	ESTs	1.00	85.00
441025	AA913880	Hs.176379	ESTs	1.00	82.00
441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	0.79	1.89
441735	AI738675	Hs.127346	ESTs	1.00	75.00
442200	AW590572	Hs.235768	ESTs	0.78	5.83
442832	AW206560	Hs.253569	ESTs	0.03	10.88
442957	AI949952	Hs.49397	ESTs	1.00	70.00
443282	T47764	Hs.132917	ESTs	1.00	197.00
443547	AW271273	Hs.23767	hypothetical protein FLJ12666	1.00	253.00
443951	F13272	Hs.111334	ferritin, light polypeptide	0.55	2.09
444330	AI597655	Hs.49265	ESTs	1.00	90.00

444515	AW204908	Hs.169979	ESTs	1.00	84.00
445769	AI741471	Hs.23666	ESTs	0.02	4.38
445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	1.00	97.00
446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	0.93	1.69
446917	AI347863	Hs.156672	ESTs	1.00	106.00
447261	NM_006691	Hs.17917	extracellular link domain-containing 1	0.40	47.20
447432	AW958473	Hs.301957	nudix (nucleoside diphosphate linked moi	1.00	100.00
447482	AB033059	Hs.18705	KIAA1233 protein	0.05	8.21
447997	H00656	Hs.29792	ESTs, Weakly similar to I38022 hypotheti	0.02	5.42
448299	AA497044	Hs.20887	hypothetical protein FLJ10392	1.00	79.00
448782	AL050295	Hs.22039	KIAA0758 protein	0.42	1.56
450575	NM_005859	Hs.29117	purine-rich element binding protein A	0.17	11.33
450584	AA040403	Hs.60371	ESTs	1.00	94.00
450693	AW450461	Hs.203965	ESTs	1.00	91.00
450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	1.00	152.00
451103	R52804	Hs.25956	DKFZP564D206 protein	1.00	86.00
451220	AF124251	Hs.26054	novel SH2-containing protein 3	0.60	1.30
451668	Z43948	Hs.326444	cartilage acidic protein 1	0.54	1.91
452197	AW023595	Hs.232048	ESTs	1.00	67.00
452331	AA598509	Hs.29117	purine-rich element binding protein A	4.53	11.07
452353	C18825	Hs.29191	epithelial membrane protein 2	0.72	2.24
453049	BE537217	Hs.30343	ESTs	1.00	68.00
453107	NM_016113	Hs.279746	vanilloid receptor-like protein 1	0.83	1.70
453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	1.00	132.00
453390	AA862496	Hs.28482	ESTs	1.00	72.00
453531	AA417940		ESTs, Weakly similar to JC5795 CDEP prot	1.00	68.00
454741	BE154396		gb:CM2-HT0342-091299-050-b05 HT0342 Homo	0.57	2.89
456579	AA287827	Hs.284205	up-regulated by BCG-CWS	1.00	82.00
456672	AK002016	Hs.114727	Homo sapiens, clone MGC:16327, mRNA, com	0.79	1.96
457400	AF032906	Hs.252549	cathepsin Z	1.03	3.25
457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	1.00	113.00
459696	F03027		gb:HSC1KA072 normalized infant brain cDN	1.00	544.00

TABLE 10B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
408074	103684_1	R20723 AA263003 AA333976 AA334725 AA334151 AW965490 AA310513 AI810530 D31302 AW134897 AA830127 AA046953 AI668930 C06094 AW104534
411667	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW861034
413533	1375344_1	BE146973 BE146972 BE147042 BE147018 BE146783 BE147020 BE146781 BE147019 BE146766 BE147021 BE146952 BE146767 BE147044 BE146797 BE146776 BE146985 BE146793 BE146768 BE146771 BE146954 BE146760 BE147048 BE147025 BE147030
423387	22779_1	AJ012074 U11087 L13288 X75299 L20295 AW630780 H14880 T28037 AI872991 R72136 AW449839 T81622 T79697 T29519 R94105 T83923 R73300 AI797007 R73390 AA961010 H74168 AI689932 BE045543 AI808418 AI608912 AI806573 AW884084 AW872978 AW872985 AA565655 AI022915 R50647 R73210 H45098 R46451 AW166269 T71132 AI264547 R52146 AI304920 R73391 AW884059 AW884085 H73241 T60038 T79612 R73145 R50549 AI094557 AI668793 R72302 AI564366 W01956 AA418962 W32571 R72840 H45409 R72085 R46356 R46758 AA508805 AA418798 T83751 R94072 T16182 AA928785 AA903896
423696	23112_1	Z92546 AA330586 AI570568 AW341487 AI827050 AW298668 AI792189 AI015693 AI733599 AI572251 AI672488 AW193262 AI244716 AI864375 AI206100 AA912444 AI269365 AI640254 AW772466 AI867336 AA627604 H16914 AA358477 AA338009
430212	314437_1	AA469153 AI718503 AA469225
436532	421802_1	AA721522 AW975443 T93070
453531	97026_1	AA417940 AA036735 T07025
454741	1232559_1	BE154396 AW817959 BE154393

TABLE 10C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400754	7331445	Plus	144559-144684
401045	8117619	Plus	90044-90184,91111-91345
401083	3242744	Plus	33192-33360
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
402808	6456148	Minus	114964-115136,115461-115585,115931-116047,117666-117771,118004-118102
403021	7547270	Plus	120799-120966
403421	9665041	Minus	126609-126773,139986-140205
403438	9719679	Plus	90792-90938
403687	7387384	Plus	9009-9534
403764	7717105	Minus	118692-118853
404277	1834458	Minus	91665-91946
404288	2769644	Plus	3512-3691
404394	3135305	Minus	37121-37205,37491-37762,41053-41140,41322-41593,41773-41919
404518	8151988	Plus	84494-84603
404916	7341826	Plus	91057-91188
405106	8079395	Minus	80877-81418
405257	7329310	Plus	73121-73273
405381	6006920	Minus	7636-8054

TABLE 11A: Genes Distinguishing Adenocarcinoma from Other Lung Diseases and Normal Lung

Table 11A shows about 84 genes upregulated in lung adenocarcinomas relative to other lung tumors, non-malignant lung disease, and normal lung. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 11B show the accession numbers for those Pkey's lacking UnigeneID's for table 11A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 11C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 11A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
403329			Target Exon	1.00	61.00
406399			NM_003122*:Homo sapiens serine protease	1.00	39.00
406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	226.37	350.00
407869	AI827976	Hs.24391	hypothetical protein FLJ13612	0.77	1.18
407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	1.00	10.00
408908	BE296227	Hs.250822	serine/threonine kinase 15	7.76	1.00
409103	AF251237	Hs.112208	XAGE-1 protein	80.44	40.00
409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	1.00	1.00
409269	AA576953	Hs.22972	hypothetical protein FLJ13352	1.00	1.00
410076	T05387	Hs.7991	ESTs	1.12	1.50
410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	9.89	1.00
410399	BE068889		synuclein, gamma (breast cancer-specific	0.92	1.06
411908	L27943	Hs.72924	cytidine deaminase	1.00	1.00
412612	NM_000047	Hs.74131	arylsulfatase E (chondrodysplasia puncta	1.02	1.03
414075	U11862	Hs.75741	amiloride binding protein 1 (amine oxida	0.84	1.07
416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.67	1.00
417542	J04129	Hs.82269	progestagen-associated endometrial prote	1.28	1.35
419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	1.00	1.00
419502	AU076704		fibrinogen, A alpha polypeptide	13.05	115.00
419631	AW188117	Hs.303154	popeye protein 3	1.00	13.00
420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	1.00	8.00
421155	H87879	Hs.102267	lysyl oxidase	1.00	15.00
421190	U95031	Hs.102482	mucin 5, subtype B, tracheobronchial	1.17	1.55
421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	1.46	1.76
421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, l	1.00	3.00
421582	AI910275		trefoil factor 1 (breast cancer, estroge	1.23	1.00
422026	U80736	Hs.110826	trinucleotide repeat containing 9	1.00	52.00
422095	AI868872	Hs.282804	hypothetical protein FLJ22704	4.37	2.34
422311	AF073515	Hs.114948	cytokine receptor-like factor 1	1.15	1.78
422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.69	3.17
423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	48.13	72.00
423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	1.00	50.00
424502	AF242388	Hs.149585	lengsin	1.00	1.00
424544	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci	1.00	59.00
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	21.35	1.00
424960	BE245380	Hs.153952	5' nucleotidase (CD73)	1.00	1.00
425523	AB007948	Hs.158244	KIAA0479 protein	1.00	35.00
426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	1.00	83.00
427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	7.41	34.00
428585	AB007863	Hs.185140	KIAA0403 protein	1.00	6.00
428758	AA433988	Hs.98502	hypothetical protein FLJ14303	1.06	1.13
429170	NM_001394	Hs.2359	dual specificity phosphatase 4	16.18	105.00
429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	1.07	1.00
429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.59	1.69
430508	AI015435	Hs.104637	ESTs	4.75	7.27
430985	AA490232	Hs.27323	ESTs, Weakly similar to I78885 serine/th	0.94	1.28
431548	AI834273	Hs.9711	novel protein	5.66	15.00
431566	AF176012	Hs.260720	J domain containing protein 1	49.76	37.00
431986	AA536130	Hs.149018	Novel human gene mapping to chomosome 20	1.19	1.47
432375	BE536069	Hs.2962	S100 calcium-binding protein P	1.65	1.06
432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.00	48.00
433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	1.00	19.00
433819	AW511097	Hs.112765	ESTs	3.71	8.00
434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	29.31	72.00
434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	1.00	64.00
434792	AA649253	Hs.132458	ESTs	8.52	44.00
436217	T53925	Hs.107	fibrinogen-like 1	57.97	31.00
436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	1.10	1.41
436972	AA284679	Hs.25640	claudin 3	1.59	1.46
437866	AA156781		metallothionein 1E (functional)	3.62	101.00
437935	AW939591	Hs.5940	mucin 13, epithelial transmembrane	1.60	1.39
438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.00	1.00
439451	AF086270	Hs.278554	heterochromatin-like protein 1	23.28	52.00

439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	1.00	21.00
441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	1.41	99.00
441377	BE218239	Hs.202656	ESTs	22.03	1.00
443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	1.00	16.00
443813	AA876372	Hs.93961	Homo sapiens mRNA; cDNA DKFZp667D095 (fr	1.20	1.99
443991	NM_002250	Hs.10082	potassium intermediate/small conductance	5.71	6.87
444670	H58373	Hs.332938	hypothetical protein MGC5370	1.98	38.00
444931	AV652066	Hs.75113	general transcription factor IIIA	1.00	54.00
446102	AW168067	Hs.317694	ESTs	1.00	1.00
446163	AA026880	Hs.25252	Homo sapiens cDNA FLJ13603 fis, clone PL	1.00	36.00
446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogenti	1.00	11.00
447388	AW630534	Hs.76277	Homo sapiens, clone MGC:9381, mRNA, comp	1.24	1.16
447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.23	1.63
448243	AW369771	Hs.52620	integrin, beta 8	15.84	1.00
448844	AI581519	Hs.177164	ESTs	1.00	31.00
449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	1.00	83.00
451807	W52854		hypothetical protein FLJ23293 similar to	1.55	35.00
452689	F33868	Hs.284176	transferrin	1.54	1.44
453392	U23762	Hs.32964	SRY (sex determining region Y)-box 11	1.00	16.00
453464	AI884911	Hs.32989	receptor (calcitonin) activity modifying	1.55	2.45
453735	AI066629	Hs.125073	ESTs	1.01	1.30

TABLE 11B

Pkey: *Unique Eos probeset identifier number*
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
410399	11995_1	BE068889 BE068882 AF044311 AF017256 NM_003087 AF037207 AF010126 AA633976 AA872836 BE298825 BE299889 AI016464 AI684600 AI936527 AA804675 AA394097 AI139933 AA946606 BE171313 AA722407 AA293803 AI468480 AA056035 AA055968 AW796957 AI637713 AA410737 H49348 AA486472 AA411094 AA235594 AA402624 AA443638 AW452137 AA421708 AW265211 AI493266 AA365132 AW966044
419502	18535_1	AU076704 T74854 T74860 T72098 T73265 T73873 T69180 T74658 T58786 T60385 T73410 T68781 T67845 T67593 T73952 T67864 T60630 T68367 T68401 T53959 T72360 T72099 T60377 T58961 T71712 T72821 T64738 T74645 T72037 T68688 T72063 T73258 T72826 T64242 T68220 T74673 T71800 T68355 T61227 T62738 T69317 T53850 T64692 T73768 T73962 T73382 T68914 T70975 T73400 T60631 T73277 T73203 T70498 T61409 T58925 NM_000508 M64982 T68301 T73729 T69445 T60424 T67922 T67736 T68716 T67755 T74765 T73819 T58719 T74756 T60477 T74863 T61109 T68329 T58850 T71857 T73425 T53736 T68607 T58898 T64309 T72031 T72079 T64305 T71908 T68107 T71916 T73787 T56035 T64425 T71870 T60476 T61376 T67820 T71895 T41006 T69441 T68170 T74617 T71958 T69440 T61875 R06796 H48353 T71914 T53939 T64121 AA693996 T72525 T67779 T68078 AA011465 AA345378 AV654847 AV654272 AV656001 AI064740 T82897 N33594 AA344542 AW805054 AI207457 T61743 AA026737 H94389 AA382695 AA918409 T68044 S82092 T39959 AI017721 AA312395 AA312919 T40156 H66239 AV652989 H38728 R98521 AV655200 R95790 W03250 W00913 AA344136 AV660126 R97923 AA343596 AW470774 AV651256 N54417 AA812862 AW182929 AI111192 H61463 H72060 AA344503 H38639 AI277511 AV661108 AI207625 T47810 AA235252 T27853 T47778 R95746 H70620 AA701463 AW827166 R98475 C20925 AV657287 T71959 T71313 T73920 T73333 T61618 T69293 T69283 T73931 T72178 T72456 AV645639 AV653476 T72957 T72300 T58906 T71457 T70494 T72956 T70495 T68267 T74407 T85778 AA344726 T27854 T74485 T74101 T73868 T71518 T72304 AA343853 T73909 T68070 T72065 H72149 T73493 T73495 AV645993 R02293 T70475 T64751 AA344441 AA343657 AA345732 AA344328 AI110639 AA344603 AF063513 T64696 T68516 T72223 T60507 T67633 R29500 T72517 R02292 T60599 T69206 T70452 T74677 R29366 T61277 T74914 T60352 R29675 T74843 AV645792 AA344408 T69197 T72057 T69368 T69358 T68258 AV650429 T73341 T61702 T74598 T40095 K02272 T40106 AA343045 AA341908 AA341907 AA342807 AA341964 T53747 T72042 T62764 AI064899 AA343060 T67832 T72440 T71770 T68091 T69108 T72449 T69167 T71289 T68251 AV654844 T64375 AA345234 T67598 AA011414 T68036 H48262 AI207557 T68219 W86031 T69081 T64232 R93196 T62136 AV650539 H67459 T72978 AA344583 T60362 H58121 T95711 T72803 T68055 T71715 R29036 T72793 T69122 T64595 T62888 T69139 T68291 T64652 T67971 T46862 AA693592 AI248502 R29454 T64764 T57001 T73052 T71429 T51176 T58866 AV655414 H90426 AA342489 T73666 T67848 T72512 T53835 T67837 T73317 T74273 T69420 T68245 T74380 T67862 T74474 T56068
421582	2041_1	AI910275 X00474 X52003 X05030 NM_003225 AA314326 AA308400 AA506787 AA314825 AI571948 AA507595 AA614579 AA587613 R83818 AA568312 AA614409 AA307578 AI925552 AW950155 AI910083 M12075 BE074052 AW004668 AA578674 AA582084 BE074053 BE074126 BE074140 AA514776 AA588034 BE074051 BE074068 AW009769 AW050690 AA858276 R55389 AI001051 AW050700 AW750216 AA614539 BE074045 AI307407 AW602303 BE073575 AI202532 AA524242 AI970839 AI909751 BE076078 AI909749 R55292
437866	44433_2	AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992 AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA043777 AA040926 D20160 AI536733 AA812489 AW874142 AI471883 W84421 AA156850
451807	8865_1	W52854 AL117600 BE208116 BE208432 BE206239 BE082291 AW953423 AA351619 BE180648 BE140560 W60080 AA865478 N90291 AW450652 AW449519 AA993634 AI806539 AA351618 AW449522 AI827626 AA904788 AA380381 AA886045 AA774409 BE003229 Z41756

TABLE 11C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA *sequence of human chromosome 22.*" Dunham I. et al., *Nature* (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
403329	8516120	Plus	96450-96598
406399	9256288	Minus	63448-63554

TABLE 12A: Genes Distinguishing Squamous Cell Carcinoma from Other Lung Diseases and Normal Lung

Table 12A shows about 72 genes upregulated in squamous cell carcinomas of the lung relative to other lung tumors, non-malignant lung disease, and normal lung. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 12B show the accession numbers for those Pkey's lacking UnigeneID's for table 12A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 12C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 12A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	132.45	4.00
400666			NM_002425:Homo sapiens matrix metallopro	3.26	3.22
401780			NM_005557*:Homo sapiens keratin 16 (foca	26.47	10.50
401781			Target Exon	10.33	4.61
401785			NM_002275*:Homo sapiens keratin 15 (KRT1	4.13	2.70
401994			Target Exon	61.84	47.00
402075			ENSP00000251056*:Plasma membrane calcium	1.00	1.00
404996			Target Exon	1.00	1.00
407839	AA045144	Hs.161566	ESTs	173.91	108.00
408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	151.17	8.00
408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	1.98	1.24
410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	10.04	1.00
415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.00	30.00
415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	24.30	1.00
416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	53.29	51.00
417034	NM_006183	Hs.80962	neurotensin	1.00	1.00
417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	8.97	3.27
418663	AK001100	Hs.41690	desmocollin 3	112.17	19.00
418678	NM_001327	Hs.87225	cancer/testis antigen	1.18	1.10
419121	AA374372	Hs.89626	parathyroid hormone-like hormone	1.00	1.00
420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	3.04	1.25
421773	W69233	Hs.112457	ESTs	1.12	1.14
421948	L42583	Hs.334309	keratin 6A	51.83	20.25
421978	AJ243662	Hs.110196	NICE-1 protein	1.01	0.91
422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.37	1.10
422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	47.53	32.00
423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	76.02	1.00
423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.20	1.00
423738	AB002134	Hs.132195	airway trypsin-like protease	10.14	51.00
424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	233.42	68.00
424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	1.00	1.00
424098	AF077374	Hs.139322	small proline-rich protein 3	137.82	54.00
424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	56.19	12.00
425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	33.45	1.00
427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.24	17.00
427335	AA448542	Hs.251677	G antigen 7B	51.83	4.00
428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00	1.00
428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	1.00	16.00
428748	AW593206	Hs.98785	Ksp37 protein	1.00	87.00
429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.01	1.18
429538	BE182592	Hs.11261	small proline-rich protein 2A	4.43	2.90
429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	11.80	1.00
430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	12.28	41.00
430890	X54232	Hs.2699	glypican 1	1.58	1.40
431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	60.25	28.00
431846	BE019924	Hs.271580	uroplakin 1B	4.49	2.51
433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.20	1.09
434360	AW015415	Hs.127780	ESTs	40.98	27.00
434880	U02388	Hs.101	cytochrome P450, subfamily IVF, polypept	1.00	1.00
435505	AF200492	Hs.211238	interleukin-1 homolog 1	1.00	38.00
435793	AB037734	Hs.4993	KIAA1313 protein	23.68	42.00
436511	AA721252	Hs.291502	ESTs	16.76	14.00
438403	AA806607	Hs.292206	ESTs	1.00	1.00
439285	AL133916		hypothetical protein FLJ20093	46.23	139.00
439606	W79123	Hs.58561	G protein-coupled receptor 87	33.61	1.00
439670	AF088076	Hs.59507	ESTs, Weakly similar to AC004858 3 U1 sm	1.00	1.00
439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	86.55	11.00
440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	62.88	147.00
441525	AW241867	Hs.127728	ESTs	1.53	1.42
443162	T49951	Hs.9029	DKFZP434G032 protein	31.11	38.00
444378	R41339	Hs.12569	ESTs	1.00	1.00

446292	AF081497	Hs.279682	Rh type C glycoprotein	1.55	1.26
447078	AW885727	Hs.9914	ESTs	47.24	24.00
447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	28.63	1.00
449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	1.00	1.00
449101	AA205847	Hs.23016	G protein-coupled receptor	2.58	27.00
450832	AW970602	Hs.105421	ESTs	25.17	36.00
452240	AI591147	Hs.61232	ESTs	13.42	1.00
453317	NM_002277	Hs.41696	keratin, hair, acidic, 1	1.19	1.27
453830	AA534296	Hs.20953	ESTs	24.92	25.00
454098	W27953	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.26	1.11
455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	206.11	1.00

TABLE 12B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
439285	47065_1	AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AI346341 AI867454 N54784 AI655270 AI421279 AW014882 AA775552 N62351 N59253 AA626243 AI341407 BE175639 AA456968 AI358918 AA457077

TABLE 12C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400666	8118496	Plus	17982-18115,20297-20456
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
401785	7249190	Minus	165776-165998,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450

TABLE 13A: Genes Distinguishing Non-Malignant Lung Disease from Lung Tumors and Normal lung

Table 13A shows about 23 genes upregulated in non-malignant lung disease relative to lung tumors and normal lung. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 13B show the accession numbers for those Pkey's lacking UnigeneID's for table 13A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 13C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 13A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	1.00	230.00
409031	AA376836	Hs.76728	ESTs	1.00	128.00
412372	R65998	Hs.285243	hypothetical protein FLJ22029	1.00	173.00
415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	1.00	145.00
417511	AL049176	Hs.82223	chordin-like	1.00	179.00
418819	AA228776	Hs.191721	ESTs	1.00	140.00
422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.00	156.00
424585	AA464840	Hs.131987	ESTs	1.00	167.00
426753	T89832	Hs.170278	ESTs	1.00	141.00
429496	AA453800	Hs.192793	ESTs	1.00	138.00
430719	AA488988	Hs.293796	ESTs	1.00	133.00
431089	BE041395		ESTs, Weakly similar to unknown protein	23.32	941.00
431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	1.00	157.00
431728	NM_007351	Hs.268107	multimerin	1.00	157.00
436532	AA721522		gb:nv54h12.r1 NCI_CGAP_Ew1 Homo sapiens	1.00	218.00
437960	AI669586	Hs.222194	ESTs	1.00	147.00
438202	AW169287	Hs.22588	ESTs	1.00	141.00
441499	AW298235	Hs.101689	ESTs	1.00	167.00
444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	1.00	151.00
448253	H25899	Hs.201591	ESTs	1.00	141.00
453636	R67837	Hs.169872	ESTs	1.00	116.00
458332	AI000341	Hs.220491	ESTs	1.00	192.00
459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbH	1.00	154.00

TABLE 13B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
431089	327825_1	BE041395 AA491826 AA621946 AA715980 AA666102
436532	421802_1	AA721522 AW975443 T93070

TABLE 13C

Pkey: Unique number corresponding to an Eos probeset
Ref: *Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.*
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	*Ref*	*Strand*	*Nt_position*
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076

TABLE 14A: Preferred Utility and Subcellular Localization for Potential Lung Disease Targets

Table 14A shows the subcellular localization and preferred utility for the genes appearing in Tables 9A and 10A. mAb symbolizes monoclonal antibody, diag symbolizes diagnostic, s.m. symbolizes small molecule, and CTL symbolizes cytotoxic lymphocytic ligand. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 14B show the accession numbers for those Pkey's lacking UnigeneID's for table 14A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 14C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 14A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
Pref.Utility: Preferred Utility
Pred.Loc: Predicted subcellular localization

Pkey	ExAccn	UnigeneID	Unigene Title	Pref Utility	Pred. Loc
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	mAb & diag & s.m.	extracellular
400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	mAb	plasma membrane
402075			ENSP00000251056*:Plasma membrane calcium	mAb & diag	secreted
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	diag	secreted
408243	Y00787	Hs.624	interleukin 8	diag	secreted
408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	mAb & s.m.	plasma membrane
408908	BE296227	Hs.250822	serine/threonine kinase 15	s.m.	cytoplasm
409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	CTL & diag	secreted
409103	AF251237	Hs.112208	XAGE-1 protein	CTL	nuclear
409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	diag	secreted
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	diag	secreted
409757	NM_001898	Hs.123114	cystatin SN	diag	extracellular
409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	CTL	nuclear
409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	diag	extracellular
410001	AB041036	Hs.57771	kallikrein 11	diag	extracellular
410407	X66839	Hs.63287	carbonic anhydrase IX	mAb & s.m.	plasma membrane
410418	D31382	Hs.63325	transmembrane protease, serine 4	mAb & diag & s.m.	plasma membrane
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	s.m.	
412719	AW016610	Hs.816	ESTs	s.m.	nuclear
414774	X02419	Hs.77274	plasminogen activator, urokinase	diag	extracellular
414883	AA926960		CDC28 protein kinase 1	s.m.	
415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	CTL & diag	extracellular
415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	mAb & diag & s.m.	secreted
415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	mAb & s.m.	plasma membrane
416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	diag	extracellular
417034	NM_006183	Hs.80962	neurotensin	diag	extracellular
417079	U65590	Hs.81134	interleukin 1 receptor antagonist	diag	extracellular
417308	H60720	Hs.81892	KIAA0101 gene product	s.m.	mitochondrial
417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	mAb & diag	secreted
417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	mAb	plasma membrane
417933	X02308	Hs.82962	thymidylate synthetase	s.m.	endoplasmic reticulum
418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	s.m.	cytoplasm
418506	AA084248	Hs.85339	G protein-coupled receptor 39	mAb & s.m.	plasma membrane
418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	CTL	cytoplasmic
419121	AA374372	Hs.89626	parathyroid hormone-like hormone	diag	secreted
419171	NM_002846	Hs.89655	protein tyrosine phosphatase, receptor t	mAb & s.m.	plasma membrane
419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	CTL & s.m.	mitochondrial
419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	diag	secreted
419235	AW470411	Hs.288433	neurotrimin	mAb & diag	plasma membrane
419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	mAb & s.m.	plasma membrane
419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	mAb & diag	extracellular*
420610	AI683183	Hs.99348	distal-less homeo box 5	CTL	nuclear
421110	AJ250717	Hs.1355	cathepsin E	sm & diag	extracellular
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	diag	secreted
421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	mAb & s.m.	plasma membrane
421552	AF026692	Hs.105700	secreted frizzled-related protein 4	diag	secreted
421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	mAb & s.m.	plasma membrane
421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	mAb & s.m.	plasma membrane
422109	S73265	Hs.1473	gastrin-releasing peptide	diag	secreted
422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	diag	secreted
422282	AF019225	Hs.114309	apolipoprotein L	diag	secreted
422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	s.m.	nuclear
422424	AI186431	Hs.296638	prostate differentiation factor	diag	extracellular
422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	s.m.	cytoplasm
422809	AK001379	Hs.121028	hypothetical protein FLJ10549	s.m.	nuclear
422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	diag	extracellular
422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	CTL & s.m.	
423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	diag	
423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	mAb & diag & s.m.	secreted
423961	D13666	Hs.136348	periostin (OSF-2os)	mAb & diag	extracellular
424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	diag	secreted
424381	AA285249	Hs.146329	protein kinase Chk2	s.m.	nuclear

424502	AF242388	Hs.149585	lengsin	s.m.	cytoplasmic
424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	mAb & s.m.	plasma membrane
424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	diag	extracellular
425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	mAb & diag & s.m.	secreted
425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	s.m.	cytoplasmic
425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	mAb	plasma membrane
425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	s.m.	
425776	U25128	Hs.159499	parathyroid hormone receptor 2	mAb & diag	plasma membrane
425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	mAb & s.m.	plasma membrane
426215	AW963419	Hs.155223	stanniocalcin 2	mAb & diag	secreted
426427	M86699	Hs.169840	TTK protein kinase	CTL & s.m.	nuclear
426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	mAb & diag	secreted
427335	AA448542	Hs.251677	G antigen 7B	CTL	cytoplasmic
427747	AW411425	Hs.180655	serine/threonine kinase 12	s.m.	cytoplasmic
428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	diag	
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	mAb & diag & s.m.	extracellular
428450	NM_014791	Hs.184339	KIAA0175 gene product	s.m.	nuclear
428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	s.m.	nuclear
428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	mAb & s.m.	plasma membrane
428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	CTL & s.m.	nuclear
428698	AA852773	Hs.334838	KIAA1866 protein	mAb	
428748	AW593206	Hs.98785	Ksp37 protein	diag	extracellular
428758	AA433988	Hs.98502	CA125 antigen; mucin 16	diag	mitochodria*
428969	AF120274	Hs.194689	artemin	diag	extracellular
429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	mAb & s.m.	plasma membrane
429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	mAb & s.m.	plasma membrane
429547	AW009166	Hs.99376	ESTs	diag	secreted
429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	mAb & diag	secreted
429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	s.m.	
430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	mAb & s.m.	plasma membrane
431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	diag	extracellular
431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	mAb & s.m.	plasma membrane
431846	BE019924	Hs.271580	uroplakin 1B	mAb & diag	plasma membrane
431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	mAb & diag	plasma membrane
432201	AI538613	Hs.298241	Transmembrane protease, serine 3	mAb & diag & s.m.	plasma membrane
433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	s.m.	nuclear
435505	AF200492	Hs.211238	interleukin-1 homolog 1	diag	secreted
436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	s.m.	
437016	AU076916	Hs.5398	guanine monphosphate synthetase	s.m.	cytoplasm
437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	CTL	ER
437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	CTL	nuclear
437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.sa	mAb & s.m.	plasma membrane
439223	AW238299	Hs.250618	UL16 binding protein 2	mAb	plasma membrane
439477	W69813	Hs.58042	ESTs, Moderately similar to GFR3_HUMAN G	mAb & s.m.	
439606	W79123	Hs.58561	G protein-coupled receptor 87	mAb & s.m.	plasma membrane
439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	mAb & s.m.	plasma membrane
440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-li	s.m.	nuclear
441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	s.m.	
442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	mAb & s.m.	plasma membrane
443247	BE614387	Hs.333893	c-Myc target JPO1	CTL	extracellular*
443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	CTL	
443859	NM_013409	Hs.9914	follistatin	diag	extracellular
444006	BE395085	Hs.10086	type I transmembrane protein Fn14	mAb	plasma membrane
444371	BE540274	Hs.239	forkhead box M1	s.m.	nuclear
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	diag	secreted
444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	mAb & diag	plasma membrane
445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	mAb & diag	secreted
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	diag	secreted
446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	diag	extracellular
447033	AI357412	Hs.157601	ESTs	CTL & diag	secreted
447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	CTL	
448243	AW369771	Hs.52620	integrin, beta 8	mAb & s.m.	plasma membrane
448844	AI581519	Hs.177164	ESTs	mAb & s.m.	
449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	mAb	plasma membrane
449722	BE280074	Hs.23960	cyclin B1	s.m.	cytoplasm
450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte	mAb & s.m.	plasma membrane
450375	AA009647		a disintegrin and metalloproteinase doma	mAb & diag & s.m.	plasma membrane
450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	mAb & diag	plasma membrane
450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	diag	secreted
451668	Z43948	Hs.326444	cartilage acidic protein 1	mAb & diag	plasma membrane
452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	diag	
452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	diag	extracellular
452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	mAb	plasma membrane
452838	U65011	Hs.30743	preferentially expressed antigen in mela	CTL	nuclear
453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso	CTL & s.m.	nuclear
457489	AI693815	Hs.127179	cryptic gene	diag	secreted

TABLE 14B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey CAT Number Accession

414883	15024_1	AA926960 AA926959 W76521 W24270 W21526 AA037172 BE267636 H83186 AA469909 N86396 AA001348 BE535736 AA081745 BE566245 AA082436 H72525 H77575 N49786 W80565 H78746 BE569085 W04339 R98127 T55938 BE279271 AW960304 T29812 AA476873 BE297387 AA292753 AA177048 NM_001826 X54941 BE314366 AA908783 AI719075 BE270172 BE269819 AA889955 AI204630 W25243 AI935150 AA872039 W72395 T99630 AI422691 H98460 N31428 BE255916 H03265 AI857576 AA776920 AA910644 AA459522 AA293140 AW514667 R75953 AW662396 AA662522 AI865147 AI423153 AW262230 AA584410 AA583187 AW024595 AW069734 AI828996 AA282997 AA876046 AW613002 AA527373 AW972459 AI831360 AA621337 AA100926 AA772418 AA594628 AI033892 W95096 AI034317 AA398727 AI085031 N95210 AI459432 AI041437 AA932124 AA627684 AA935829 AI004827 AI423513 AI094597 H42079 R54703 AI630359 AA617681 AA978045 AA643280 W44561 AI991988 AI537692 AI090262 AA740817 AI312104 AI911822 AA416871 AI185409 AA129784 AA701623 AI075239 AI139549 AA633648 AI339996 AI336880 AA399239 AI078708 AI085351 AI362835 AI346618 AI146955 AI989380 AI348243 N92892 AA765850 AI494230 AI278887 AA962596 AI492600 W80435 AA001979 R97424 AI129015 N24127 AA157451 AA235549 AA459292 AA037114 AA129785 AI494211 AW059601 AW886710 R92790 N59755 AI361128 AW589407 H47725 H97534 H48076 H48450 T99631 AW300758 H03431 R76789 AA954344 H77576 R96823 AI457100 N92845 N49682 H42038 BE220698 BE220715 H99552 AA701624 N74173 R54704 H79520 H72923 H03266 BE261919 AA769633 AA480310 AA507454 AA910586 AI203723 AW104725 W25611 W25071 T88980 H03513 T77589 R99156 W95095 R97470 AA702275 T77551 AA911952 H82956 N83673 AA283672
450375	83327_1	AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532 AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067

TABLE 14C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076

TABLE 15A: Information for all sequences in Table 16

Table 15A shows the Seq ID No, Pkey, ExAccn, UnigeneID, and Unigene Title for all of the sequences in Table 16.

Table 15B show the accession numbers for those Pkey's lacking UnigeneID's for table 15A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 15C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 15A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Seq ID No: Sequence ID number
Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title

Seq ID No:	Pkey	ExAccn	UnigeneID	Unigene Title
Seq ID No: 1 & 2	410407	X66839	Hs.63287	carbonic anhydrase IX
Seq ID No: 3 & 4	412719	AW016610	Hs.816	ESTs
Seq ID No: 5 & 6	417034	NM_006183	Hs.80962	neurotensin
Seq ID No: 7 & 8	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam
Seq ID No: 9 & 10	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
Seq ID No: 11 & 12	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
Seq ID No: 13 & 14	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
Seq ID No: 15 & 16	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
Seq ID No: 17 & 18	439285	AL133916		hypothetical protein FLJ20093
Seq ID No: 19 & 20	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin
Seq ID No: 21 & 22	120486	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog
Seq ID No: 23 & 24	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen
Seq ID No: 25 & 26	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines
Seq ID No: 27 & 28	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage
Seq ID No: 29 & 30	452838	U65011	Hs.30743	preferentially expressed antigen in mela
Seq ID No: 31 & 32	418663	AK001100	Hs.41690	desmocollin 3
Seq ID No: 33 & 34	418663	AK001100	Hs.41690	desmocollin 3
Seq ID No: 35 & 36	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito
Seq ID No: 37 & 38	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas
Seq ID No: 39 & 40	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad
Seq ID No: 41 & 42	431846	BE019924	Hs.271580	uroplakin 1B
Seq ID No: 43 & 44	418830	BE513731	Hs.88959	hypothetical protein MGC4816
Seq ID No: 45 & 46	424098	AF077374	Hs.139322	small proline-rich protein 3
Seq ID No: 47 & 48	443648	AI085377	Hs.143610	ESTs
Seq ID No: 49	311034	BE567130	Hs.311389	ESTs, Highly similar to NKGD_HUMAN NKG2-
Seq ID No: 50 & 51	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,
Seq ID No: 52 & 53	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
Seq ID No: 54 & 55	435505	AF200492	Hs.211238	interleukin-1 homolog 1
Seq ID No: 56 & 57	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)
Seq ID No: 58 & 59	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta
Seq ID No: 60 & 61	441020	W79283	Hs.35962	ESTs
Seq ID No: 62 & 63	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys
Seq ID No: 64 & 65	429538	BE182592	Hs.11261	small proline-rich protein 2A
Seq ID No: 66 & 67	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte
Seq ID No: 68 & 69	444371	BE540274	Hs.239	forkhead box M1
Seq ID No: 70 & 71	444371	BE540274	Hs.239	forkhead box M1
Seq ID No: 72 & 73	444371	BE540274	Hs.239	forkhead box M1
Seq ID No: 74 & 75	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias
Seq ID No: 76 & 77	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias
Seq ID No: 78 & 79	429259	AA420450	Hs.292911	Plakophilin
Seq ID No: 80 & 81	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu
Seq ID No: 82 & 83	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an
Seq ID No: 84 & 85	423662	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro
Seq ID No: 86 & 87	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino
Seq ID No: 88 & 89	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3
Seq ID No: 90 & 91	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor
Seq ID No: 92 & 93	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr
Seq ID No: 94 & 95	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated
Seq ID No: 96 & 97	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re
Seq ID No: 98 & 99	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic
Seq ID No: 100 & 101	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o
Seq ID No: 102 & 103	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3
Seq ID No: 104 & 105	409103	AF251237	Hs.112208	XAGE-1 protein
Seq ID No: 106 & 107	417542	J04129	Hs.82269	progestagen-associated endometrial prote
Seq ID No: 108 & 109	428471	X57348	Hs.184510	stratifin
Seq ID No: 110 & 111	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member
Seq ID No: 112 & 113	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2
Seq ID No: 114 & 115	418203	X54942	Hs.83758	CDC28 protein kinase 2
Seq ID No: 116	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m
Seq ID No: 117 & 118	437016	AU076916	Hs.5398	guanine monphosphate synthetase
Seq ID No: 119 & 120	449230	BE613348	Hs.211579	melanoma cell adhesion molecule
Seq ID No: 121 & 122	446989	AK001898	Hs.16740	hypothetical protein FLJ11036
Seq ID No: 123 & 124	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein
Seq ID No: 125 & 126	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B

Seq ID No: 127 & 128	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1
Seq ID No: 129 & 130	418462	BE001596	Hs.85266	integrin, beta 4
Seq ID No: 131 & 132	100668	L05424	Hs.169610	CD44 antigen (homing function and Indian
Seq ID No: 133 & 134	458933	AI638429	Hs.24763	RAN binding protein 1
Seq ID No: 135 & 136	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
Seq ID No: 137 & 138	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
Seq ID No: 139 & 140	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
Seq ID No: 141 & 142	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
Seq ID No: 143 & 144	446269	AW263155	Hs.14559	hypothetical protein FLJ10540
Seq ID No: 145 & 146	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur
Seq ID No: 147 & 148	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con
Seq ID No: 149 & 150	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma
Seq ID No: 151 & 152	439606	W79123	Hs.58561	G protein-coupled receptor 87
Seq ID No: 153 & 154	453884	AA355925	Hs.36232	KIAA0186 gene product
Seq ID No: 155 & 156	453884	AA355925	Hs.36232	KIAA0186 gene product
Seq ID No: 157 & 158	453884	AA355925	Hs.36232	KIAA0186 gene product
Seq ID No: 159 & 160	453884	AA355925	Hs.36232	KIAA0186 gene product
Seq ID No: 161 & 162	404877			NM_005365:Homo sapiens melanoma antigen,
Seq ID No: 163 & 164	413129	AF292100	Hs.104613	RP42 homolog
Seq ID No: 165 & 166	413281	AA861271	Hs.222024	transcription factor BMAL2
Seq ID No: 167 & 168	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote
Seq ID No: 169 & 170	416819	U77735	Hs.80205	pim-2 oncogene
Seq ID No: 171 & 172	451320	AW118072		diacylglycerol kinase, zeta (104kD)
Seq ID No: 173 & 174	418543	NM_005329	Hs.85962	hyaluronan synthase 3
Seq ID No: 175 & 176	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member
Seq ID No: 177 & 178	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)
Seq ID No: 179 & 180	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
Seq ID No: 181 & 182	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
Seq ID No: 183 & 184	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
Seq ID No: 185 & 186	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
Seq ID No: 187 & 188	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
Seq ID No: 189 & 190	419121	AA374372	Hs.89626	parathyroid hormone-like hormone
Seq ID No: 191 & 192	448993	AI471630	Hs.8127	KIAA0144 gene product
Seq ID No: 193 & 194	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR
Seq ID No: 195 & 196	430393	BE185030	Hs.241305	estrogen-responsive B box protein
Seq ID No: 197 & 198	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol
Seq ID No: 199 & 200	420462	AF050147	Hs.97932	chondromodulin I precursor
Seq ID No: 201 & 202	102963	X02404	Hs.274534	calcitonin-related polypeptide, beta
Seq ID No: 203 & 204	100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid
Seq ID No: 205 & 206	101175	U82671	Hs.36980	melanoma antigen, family A, 2
Seq ID No: 207 & 208	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like
Seq ID No: 209 & 210	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
Seq ID No: 211 & 212	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
Seq ID No: 213 & 214	131927	AJ003112	Hs.34780	doublecortex; lissencephaly, X-linked (d
Seq ID No: 215 & 216	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT
Seq ID No: 217 & 218	427335	AA448542	Hs.251677	G antigen 7B
Seq ID No: 219 & 220	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini
Seq ID No: 221 & 222	114346	AL137256	Hs.130489	ATPase, aminophospholipid transporter-li
Seq ID No: 223 & 224	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9
Seq ID No: 225 & 226	404440			NM_021048:Homo sapiens melanoma antigen,
Seq ID No: 227 & 228	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito
Seq ID No: 229 & 230	103312	Y12642	Hs.3185	lysosomal
Seq ID No: 231 & 232	320843	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr
Seq ID No: 233	429065	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT
Seq ID No: 234 & 235	446102	AW168067	Hs.317694	ESTs
Seq ID No: 236 & 237	330495	U47924	Hs.71642	guanine nucleotide binding protein (G pr
Seq ID No: 238	413573	AI733859	Hs.149089	ESTs
Seq ID No: 239 & 240	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to
Seq ID No: 241 & 242	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to
Seq ID No: 243 & 244	332180	AF134160	Hs.7327	claudin 1
Seq ID No: 245	437915	AI637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca
Seq ID No: 246 & 247	441553	AA281219	Hs.121296	ESTs
Seq ID No: 248 & 249	331692	AI683487	Hs.152213	wingless-type MMTV integration site fami
Seq ID No: 250 & 251	429413	NM_014058	Hs.201877	DESC1 protein
Seq ID No: 252 & 253	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis
Seq ID No: 254 & 255	448357	N20169	Hs.108923	RAB38, member RAS oncogene family
Seq ID No: 256 & 257	446292	AF081497	Hs.279682	Rh type C glycoprotein
Seq ID No: 258 & 259	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h
Seq ID No: 260 & 261	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1
Seq ID No: 262 & 263	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito
Seq ID No: 264 & 265	439223	AW238299	Hs.250618	UL16 binding protein 2
Seq ID No: 266 & 267	429228	AI553633	Hs.326447	ESTs
Seq ID No: 268 & 269	409757	NM_001898	Hs.123114	cystatin SN
Seq ID No: 270 & 271	411089	AA456454	Hs.214291	cell division cycle 2-like 1 (PITSLRE pr
Seq ID No: 272 & 273	436511	AA721252	Hs.291502	ESTs
Seq ID No: 274 & 275	428969	AF120274	Hs.194689	artemin
Seq ID No: 276 & 277	428969	AF120274	Hs.194689	artemin
Seq ID No: 278 & 279	428969	AF120274	Hs.194689	artemin
Seq ID No: 280 & 281	428969	AF120274	Hs.194689	artemin
Seq ID No: 282	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen
Seq ID No: 283 & 284	412723	AA648459	Hs.335951	hypothetical protein AF301222
Seq ID No: 285 & 286	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
Seq ID No: 287 & 288	405770			NM_002362:Homo sapiens melanoma antigen,
Seq ID No: 289 & 290	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13
Seq ID No: 291 & 292	414774	X02419	Hs.77274	plasminogen activator, urokinase

Seq ID No: 293 & 294	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub
Seq ID No: 295 & 296	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
Seq ID No: 297 & 298	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
Seq ID No: 299 & 300	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
Seq ID No: 301 & 302	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
Seq ID No: 303 & 304	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
Seq ID No: 305 & 306	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso
Seq ID No: 307 & 308	403478			NM_022342:Homo sapiens kinesin protein 9
Seq ID No: 309	441525	AW241867	Hs.127728	ESTs
Seq ID No: 310 & 311	434105	AW952124	Hs.13094	presenilins associated rhomboid-like pro
Seq ID No: 312 & 313	428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible, hep
Seq ID No: 314 & 315	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B
Seq ID No: 316 & 317	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription f
Seq ID No: 318 & 319	409228	R16811	Hs.22010	ESTs, Weakly similar to 2109260A B cell
Seq ID No: 320 & 321	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg
Seq ID No: 322 & 323	413582	AW295647	Hs.71331	hypothetical protein MGC5350
Seq ID No: 324 & 325	438403	AA806607	Hs.292206	ESTs
Seq ID No: 326 & 327	403329			unnamed protein product [Homo sapiens]
Seq ID No: 328 & 329	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.
Seq ID No: 330 & 331	119073	BE245360	Hs.279477	v-ets erythroblastosis virus E26 oncogen
Seq ID No: 332 & 333	113195	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom
Seq ID No: 334 & 335	102283	AW161552	Hs.83381	guanine nucleotide binding protein 11
Seq ID No: 336 & 337	101345	NM_005795	Hs.152175	calcitonin receptor-like
Seq ID No: 338 & 339	103280	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula
Seq ID No: 340 & 341	102012	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas
Seq ID No: 342 & 343	105729	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds
Seq ID No: 344 & 345	134299	AW580939	Hs.97199	complement component C1q receptor
Seq ID No: 346 & 347	412719	AW016610	Hs.816	ESTs
Seq ID No: 348 & 349	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
Seq ID No: 350 & 351	128924	BE279383	Hs.26557	plakophilin 3
Seq ID No: 352 & 353	100486	T19006	Hs.10842	RAN, member RAS oncogene family
Seq ID No: 354 & 355	419121	AA374372	Hs.89626	parathyroid hormone-like hormone
Seq ID No: 356 & 357	409459	D86407	Hs.54481	low density lipoprotein receptor-related
Seq ID No: 358 & 359	330493	M27826		endogenous retroviral protease
Seq ID No: 360 & 361	417866	AW067903	Hs.82772	collagen, type XI, alpha 1
Seq ID No: 362 & 363	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4
Seq ID No: 364 & 365	437016	AU076916	Hs.5398	guanine monphosphate synthetase
Seq ID No: 366 & 367	429612	AF062649	Hs.252587	pituitary tumor-transforming 1
Seq ID No: 368 & 369	440704	M69241	Hs.162	insulin-like growth factor binding prote
Seq ID No: 370 & 371	431221	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye
Seq ID No: 372 & 373	431565	AF161470	Hs.260622	butyrate-induced transcript 1
Seq ID No: 374 & 375	431565	AF161470	Hs.260622	butyrate-induced transcript 1
Seq ID No: 376 & 377	132354	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)
Seq ID No: 378 & 379	424441	X14850	Hs.147097	H2A histone family, member X
Seq ID No: 380 & 381	103768	AF086009	Hs.296398	gb:Homo sapiens full length insert cDNA
Seq ID No: 382 & 383	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb
Seq ID No: 384 & 385	425266	J00077	Hs.155421	alpha-fetoprotein
Seq ID No: 386 & 387	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,
Seq ID No: 388 & 389	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin
Seq ID No: 390 & 391	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
Seq ID No: 392 & 393	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
Seq ID No: 394 & 395	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino
Seq ID No: 396 & 397	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2
Seq ID No: 398 & 399	418506	AA084248	Hs.85339	G protein-coupled receptor 39
Seq ID No: 400 & 401	423961	D13666	Hs.136348	periostin (OSF-2os)
Seq ID No: 402 & 403	414812	X72755	Hs.77367	monokine induced by gamma interferon
Seq ID No: 404 & 405	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein
Seq ID No: 406 & 407	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein
Seq ID No: 408 & 409	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse
Seq ID No: 410 & 411	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy
Seq ID No: 412 & 413	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti
Seq ID No: 414 & 415	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated
Seq ID No: 416 & 417	411789	AF245505	Hs.72157	Adlican
Seq ID No: 418 & 419	428698	AA852773	Hs.334838	KIAA1866 protein
Seq ID No: 420 & 421	450098	W27249	Hs.8109	hypothetical protein FLJ21080
Seq ID No: 422 & 423	421552	AF026692	Hs.105700	secreted frizzled-related protein 4
Seq ID No: 424 & 425	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR
Seq ID No: 426 & 427	450375	AA009647		a disintegrin and metalloproteinase doma
Seq ID No: 428 & 429	426215	AW963419	Hs.155223	stanniocalcin 2
Seq ID No: 430 & 431	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin
Seq ID No: 432 & 433	432201	AI538613	Hs.298241	Transmembrane protease, serine 3
Seq ID No: 434 & 435	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph
Seq ID No: 436 & 437	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447
Seq ID No: 438 & 439	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn
Seq ID No: 440 & 441	447033	AI357412	Hs.157601	ESTs
Seq ID No: 442 & 443	447033	AI357412	Hs.157601	ESTs
Seq ID No: 444 & 445	447033	AI357412	Hs.157601	ESTs
Seq ID No: 446 & 447	115522	BE614387	Hs.333893	c-Myc target JPO1
Seq ID No: 448 & 449	410418	D31382	Hs.63325	transmembrane protease, serine 4
Seq ID No: 450 & 451	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119
Seq ID No: 452 & 453	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119
Seq ID No: 454 & 455	452461	N78223	Hs.108106	transcription factor
Seq ID No: 456 & 457	412420	AL035668	Hs.73853	bone morphogenetic protein 2
Seq ID No: 458 & 459	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara
Seq ID No: 460 & 461	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon

Seq ID No: 462 & 463	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.sa
Seq ID No: 464 & 465	402075			ENSP00000251056*:Plasma membrane calcium
Seq ID No: 466 & 467	421110	AJ250717	Hs.1355	cathepsin E
Seq ID No: 468 & 469	451668	Z43948	Hs.326444	cartilage acidic protein 1
Seq ID No: 470 & 471	451668	Z43948	Hs.326444	cartilage acidic protein 1
Seq ID No: 472 & 473	451668	Z43948	Hs.326444	cartilage acidic protein 1
Seq ID No: 474 & 475	422282	AF019225	Hs.114309	apolipoprotein L
Seq ID No: 476 & 477	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member
Seq ID No: 478 & 479	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),
Seq ID No: 480 & 481	427747	AW411425	Hs.180655	serine/threonine kinase 12
Seq ID No: 482 & 483	420281	AI623693	Hs.323494	Predicted cation efflux pump
Seq ID No: 484 & 485	405932			C15000305:gi|3806122|gb|AAC69198.1| (AF0
Seq ID No: 486 & 487	405932			C15000305:gi|3806122|gb|AAC69198.1| (AF0
Seq ID No: 488 & 489	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane
Seq ID No: 490 & 491	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy
Seq ID No: 492 & 493	417079	U65590	Hs.81134	interleukin 1 receptor antagonist
Seq ID No: 494 & 495	430890	X54232	Hs.2699	glypican 1
Seq ID No: 496 & 497	419721	NM_001650	Hs.288650	aquaporin 4
Seq ID No: 498 & 499	444471	AB020684	Hs.11217	KIAA0877 protein
Seq ID No: 500 & 501	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote
Seq ID No: 502 & 503	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly
Seq ID No: 504 & 505	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro
Seq ID No: 506 & 507	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro
Seq ID No: 508 & 509	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte
Seq ID No: 510 & 511	410407	X66839	Hs.63287	carbonic anhydrase IX
Seq ID No: 512 & 513	309931	AW341683		gb:hd13d01.x1 Soares_NFL_T_GBC_S1 Homo s
Seq ID No: 514 & 515	412719	AW016610	Hs.816	ESTs
Seq ID No: 516 & 517	417034	NM_006183	Hs.80962	neurotensin
Seq ID No: 518 & 519	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam
Seq ID No: 520 & 521	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin
Seq ID No: 522 & 523	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen
Seq ID No: 524 & 525	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage
Seq ID No: 526 & 527	418663	AK001100	Hs.41690	desmocollin 3
Seq ID No: 528 & 529	418663	AK001100	Hs.41690	desmocollin 3
Seq ID No: 530 & 531	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas
Seq ID No: 532 & 533	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad
Seq ID No: 534 & 535	431846	BE019924	Hs.271580	uroplakin 1B
Seq ID No: 536 & 537	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
Seq ID No: 538 & 539	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta
Seq ID No: 540 & 541	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an
Seq ID No: 542 & 543	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino
Seq ID No: 544 & 545	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3
Seq ID No: 546 & 547	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor
Seq ID No: 548 & 549	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3
Seq ID No: 550 & 551	417542	J04129	Hs.82269	progestagen-associated endometrial prote
Seq ID No: 552 & 553	449230	BE613348	Hs.211579	melanoma cell adhesion molecule
Seq ID No: 554 & 555	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma
Seq ID No: 556 & 557	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma
Seq ID No: 558 & 559	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B
Seq ID No: 560 & 561	418462	BE001596	Hs.85266	integrin, beta 4
Seq ID No: 562 & 563	410274	AA381807	Hs.61762	hypoxia-inducible protein 2
Seq ID No: 564 & 565	439606	W79123	Hs.58561	G protein-coupled receptor 87
Seq ID No: 566 & 567	404877			NM_005365:Homo sapiens melanoma antigen,
Seq ID No: 568 & 569	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote
Seq ID No: 570 & 571	418543	NM_005329	Hs.85962	hyaluronan synthase 3
Seq ID No: 572 & 573	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
Seq ID No: 574 & 575	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
Seq ID No: 576 & 577	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
Seq ID No: 578 & 579	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
Seq ID No: 580 & 581	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
Seq ID No: 582 & 583	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
Seq ID No: 584 & 585	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR
Seq ID No: 586 & 587	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
Seq ID No: 588 & 589	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
Seq ID No: 590 & 591	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini
Seq ID No: 592 & 593	332180	AF134160	Hs.7327	claudin 1
Seq ID No: 594 & 595	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,
Seq ID No: 596 & 597	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,
Seq ID No: 598 & 599	439223	AW238299	Hs.250618	UL16 binding protein 2
Seq ID No: 600 & 601	409757	NM_001898	Hs.123114	cystatin SN
Seq ID No: 602 & 603	428969	AF120274	Hs.194689	artemin
Seq ID No: 604 & 605	428969	AF120274	Hs.194689	artemin
Seq ID No: 606 & 607	428969	AF120274	Hs.194689	artemin
Seq ID No: 608 & 609	428969	AF120274	Hs.194689	artemin
Seq ID No: 610 & 611	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
Seq ID No: 612 & 613	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
Seq ID No: 614 & 615	414774	X02419	Hs.77274	plasminogen activator, urokinase
Seq ID No: 616 & 617	407944	R34008	Hs.239727	desmocollin 2
Seq ID No: 618 & 619	407944	R34008	Hs.239727	desmocollin 2
Seq ID No: 620 & 621	457489	AI693815	Hs.127179	cryptic gene
Seq ID No: 622 & 623	429547	AW009166	Hs.99376	ESTs
Seq ID No: 624 & 625	407242	M18728		gb:Human nonspecific crossreacting antig
Seq ID No: 626 & 627	407242	M18728		gb:Human nonspecific crossreacting antig
Seq ID No: 628 & 629	407242	M18728		gb:Human nonspecific crossreacting antig
Seq ID No: 630 & 631	444006	BE395085	Hs.10086	type I transmembrane protein Fn14

Seq ID No: 632 & 633	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma
Seq ID No: 634 & 635	422109	S73265	Hs.1473	gastrin-releasing peptide
Seq ID No: 636 & 637	419235	AW470411	Hs.288433	neurotrimin
Seq ID No: 638 & 639	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc
Seq ID No: 640 & 641	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy
Seq ID No: 642 & 643	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu
Seq ID No: 644 & 645	448243	AW369771	Hs.52620	integrin, beta 8
Seq ID No: 646 & 647	426427	M86699	Hs.169840	TTK protein kinase
Seq ID No: 648 & 649	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6
Seq ID No: 650 & 651	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6
Seq ID No: 652 & 653	428450	NM_014791	Hs.184339	KIAA0175 gene product
Seq ID No: 654 & 655	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,
Seq ID No: 656 & 657	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11
Seq ID No: 658 & 659	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic
Seq ID No: 660 & 661	425776	U25128	Hs.159499	parathyroid hormone receptor 2
Seq ID No: 662 & 663	425776	U25128	Hs.159499	parathyroid hormone receptor 2
Seq ID No: 664 & 665	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha
Seq ID No: 666 & 667	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7
Seq ID No: 668 & 669	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci
Seq ID No: 670 & 671	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci
Seq ID No: 672 & 673	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci
Seq ID No: 674 & 675	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci
Seq ID No: 676 & 677	410001	AB041036	Hs.57771	kallikrein 11
Seq ID No: 678 & 679	426501	AW043782	Hs.293616	ESTs
Seq ID No: 680 & 681	408369	R38438	Hs.182575	solute carrier family 15 (H??? transport
Seq ID No: 682 & 683	445413	AA151342	Hs.12677	CGI-147 protein
Seq ID No: 684 & 685	422424	AI186431	Hs.296638	prostate differentiation factor
Seq ID No: 686 & 687	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,
Seq ID No: 688 & 689	420610	AI683183	Hs.99348	distal-less homeo box 5

TABLE 15B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
309931	AW341683	
330493	33264_5	M27826 R78416 AA307645 AW957879 AW957800 AA633529 H03662
439285	47065_1	AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AI346341 AI867454 N54784 AI655270 AI421279 AW014882 AA775552 N62351 N59253 AA626243 AI341407 BE175639 AA456968 AI358918 AA457077
450375	83327_1	AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532 AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067
451320	86576_1	AW118072 AI631982 T15734 AA224195 AI701458 W20198 F26326 AA890570 N90552 AW071907 AI671352 AI375892 T03517 R88265 AI124088 AA224388 AI084316 AI354686 T33652 AI140719 AI720211 T03490 AI372637 T15415 AW205836 AA630384 T03515 T33230 AA017131 AA443303 T33623 AI222556 T33511 T33785 AI419606 D55612

TABLE 15C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
403329	8516120	Plus	96450-96598
403478	9958258	Plus	116458-116564
404440	7528051	Plus	80430-81581
404877	1519284	Plus	1095-2107
405770	2735037	Plus	61057-62075
405932	7767812	Minus	123525-123713

Table 16

Seq ID NO: 1 DNA sequence
Nucleic Acid Accession #: NM_001216
Coding sequence: 43..1422

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1          11         21         31         41         51
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GCCCGTACAC ACCGTGTGCT GGGACACCCC ACAGTCAGCC GCATGGCTCC CCTGTGCCCC     60
AGCCCCTGGC TCCCTCTGTT GATCCCGGCC CCTGCTCCAG GCCTCACTGT GCAACTGCTG    120
CTGTCACTGC TGCTTCTGAT GCCTGTCCAT CCCCAGAGGT TGCCCCGGAT GCAGGAGGAT    180
TCCCCCTTGG GAGGAGGCTC TTCTGGGGAA GATGACCCAC TGGGCGAGGA GGATCTGCCC    240
AGTGAAGAGG ATTCACCCAG AGAGGAGGAT CCACCCGGAG AGGAGGATCT ACCTGGAGAG    300
GAGGATCTAC CTGGAGAGGA GGATCTACCT GAAGTTAAGC CTAAATCAGA AGAAGAGGGC    360
TCCCTGAAGT TAGAGGATCT ACCTACTGTT GAGGCTCCTG GAGATCCTCA AGAACCCCAG    420
AATAATGCCC ACAGGGACAA AGAAGGGGAT GACCAGAGTC ATTGGCGCTA TGGAGGCGAC    480
CCGCCCTGGC CCCGGGTGTC CCCAGCCTGC GCGGGCCGCT TCCAGTCCCC GGTGGATATC    540
CGCCCCCAGC TCGCCGCCTT CTGCCCGGCC CTGCGCCCCC TGGAACTCCT GGGCTTCCAG    600
CTCCCGCCGC TCCCAGAACT GCGCCTGCGC AACAATGGCC ACAGTGTGCA ACTGACCCTG    660
CCTCCTGGGC TAGAGATGGC TCTGGGTCCC GGGCGGGAGT ACCGGGCTCT GCAGCTGCAT    720
CTGCACTGGG GGGCTGCAGG TCGTCCGGGC TCGGAGCACA CTGTGGAAGG CCACCGTTTC    780
CCTGCCGAGA TCCACGTGGT TCACCTCAGC ACCGCCTTTG CCAGAGTTGA CGAGGCCTTG    840
GGGCGCCCGG GAGGCCTGGC CGTGTTGGCC GCCTTTCTGG AGGAGGGCCC GGAAGAAAAC    900
AGTGCCTATG AGCAGTTGCT GTCTCGCTTG GAAGAAATCG CTGAGGAAGG CTCAGAGACT    960
CAGGTCCCAG GACTGGACAT ATCTGCACTC CTGCCCTCTG ACTTCAGCCG CTACTTCCAA   1020
TATGAGGGGT CTCTGACTAC ACCGCCCTGT GCCCAGGGTG TCATCTGGAC TGTGTTTAAC   1080
CAGACAGTGA TGCTGAGTGC TAAGCAGCTC CACACCCTCT CTGACACCCT GTGGGGACCT   1140
GGTGACTCTC GGCTACAGCT GAACTTCCGA GCGACGCAGC CTTTGAATGG GCGAGTGATT   1200
GAGGCCTCCT TCCCTGCTGG AGTGGACAGC AGTCCTCGGG CTGCTGAGCC AGTCCAGCTG   1260
AATTCCTGCC TGGCTGCTGG TGACATCCTA GCCCTGGTTT TTGGCCTCCT TTTTGCTGTC   1320
ACCAGCGTCG CGTTCCTTGT GCAGATGAGA AGGCAGCACA GAAGGGGAAC CAAAGGGGGT   1380
GTGAGCTACC GCCCAGCAGA GGTAGCCGAG ACTGGAGCCT AGAGGCTGGA TCTTGGAGAA   1440
TGTGAGAAGC CAGCCAGAGG CATCTGAGGG GGAGCCGGTA ACTGTCCTGT CCTGCTCATT   1500
ATGCCACTTC CTTTTAACTG CCAAGAAATT TTTTAAAATA AATATTTATA AT
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Seq ID NO: 2 Protein sequence:
Protein Accession #: NP_001207

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MAPLCPSPWL PLLIPAPAPG LTVQLLLSLL LLMPVHPQRL PRMQEDSPLG GGSSGEDDPL     60
GEEDLPSEED SPREEDPPGE EDLPGEEDLP GEEDLPEVKP KSEEEGSLKL EDLPTVEAPG    120
DPQEPQNNAH RDKEGDDQSH WRYGGDPPWP RVSPACAGRF QSPVDIRPQL AAFCPALRPL    180
ELLGFQLPPL PELRLRNNGH SVQLTLPPGL EMALGPGREY RALQLHLHWG AAGRPGSEHT    240
VEGHRFPAEI HVVHLSTAFA RVDEALGRPG GLAVLAAFLE EGPEENSAYE QLLSRLEEIA    300
EEGSETQVPG LDISALLPSD PSRYFQYEGS LTTPPCAQGV IWTVFNQTVM LSAKQLHTLS    360
DTLWGPGDSR LQLNFRATQP LNGRVIEASF PAGVDSSPRA AEPVQLNSCL AAGDILALVF    420
GLLFAVTSVA FLVQMRRQHR RGTKGGVSYR PAEVAETGA
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Seq ID NO: 3 DNA sequence
Nucleic Acid Accession #: BC013923
Coding sequence: 438-1391

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AGCGGGGTTG TCTATTAACT TGTTCAAAAA GTATCAGGAG TTGTCAAGGC AGAGAAGAGA     60
GTGTTTGCAA AAGGGGGAAA GTAGTTTGCT GCCTCTTTAA GACTAGGACT GAGAGAAAGA    120
AGAGGAGAGA GAAAGAAAGG GAGAGAAGTT TGAGCCCCAG GCTTAAGCCT TTCCAAAAAA    180
TAATAATAAC AATCATCGGC GGCGGCAGGA TCGGCCAGAG GAGGAGGGAA GCGCTTTTTT    240
TGATCCTGAT TCCAGTTTGC CTCTCTCTTT TTTTCCCCCA AATTATTCTT CGCCTGATTT    300
TCCTCGCGGA GCCCTGCGCT CCCGACACCC CCGCCCGCCT CCCCTCCTCC TCTCCCCCCG    360
CCCGCGGGCC CCCCAAAGTC CCGGCCGGGC CGAGGGTCGG CGGCCGCCGG CGGGCCGGGC    420
CCGCGCACAG CGCCCGCATG TACAACATGA TGGAGACGGA GCTGAAGCCG CCGGGCCCGC    480
AGCAAACTTC GGGGGGCGGC GGCGGCAACT CCACCGCGGC GGCGGCCGGC GGCAACCAGA    540
AAAACAGCCC GGACCGCGTC AAGCGGCCCA TGAATGCCTT CATGGTGTGG TCCCGCGGGC    600
AGCGGCGCAA GATGGCCCAG GAGAACCCCA AGATGCACAA CTCGGAGATC AGCAAGCGCC    660
TGGGCGCCGA GTGGAAACTT TTGTCGGAGA CGGAGAAGCG GCCGTTCATC GACGAGGCTA    720
AGCGGCTGCG AGCGCTGCAC ATGAAGGAGC ACCCGGATTA TAAATACCGG CCCCGGCGGA    780
AAACCAAGAC GCTCATGAAG AAGGATAAGT ACACGCTGCC CGGCGGGCTG CTGGCCCCCG    840
GCGGCAATAG CATGGCGAGC GGGGTCGGGG TGGGCGCCGG CCTGGGCGCG GGCGTGAACC    900
AGCGCATGGA CAGTTACGCG CACATGAACG GCTGGAGCAA CGGCAGCTAC AGCATGATGC    960
AGGACCAGCT GGGCTACCCG CAGCACCCGG GCCTCAATGC GCACGGCGCA GCGCAGATGC   1020
AGCCCATGCA CCGCTACGAC GTGAGCGCCC TGCAGTACAA CTCCATGACC AGCTCGCAGA   1080
CCTACATGAA CGGCTCGCCC ACCTACAGCA TGTCCTACTC GCAGCAGGGC ACCCCTGGCA   1140
TGGCTCTTGG CTCCATGGGT TCGGTGGTCA AGTCCGAGGC CAGCTCCAGC CCCCCTGTGG   1200
TTACCTCTTC CTCCCACTCC AGGGCGCCCT GCCAGGCCGG GGACCTCCGG GACATGATCA   1260
GCATGTATCT CCCCGGCGCC GAGGTGCCGG AACCCGCCGC CCCCAGCAGA CTTCACATGT   1320
CCCAGCACTA CCAGAGCGGC CCGGTGCCCG GCACGGCCAT TAACGGCACA CTGCCCCTCT   1380
CACACATGTG AGGGCCGGAC AGCGAACTGG AGGGGGGAGA AATTTTCAAA GAAAAACGAG   1440
GGAAATGGGA GGGGTGCAAA AGAGGAGAGT AAGAAACAGC ATGGAGAAAA CCCGGTACGC   1500
TCAAAAAAAA AAAAAAAAAA AAAATCCCAT CACCCACAGC AAATGACAGC TGCAAAAGAG   1560
AACACCAATC CCATCCACAC TCACGCAAAA ACCGCGATGC CGACAAGAAA ACTTTTATGA   1620
GAGAGATCCT GGACTTCTTT TKGGGGGACT ATTTTTGTAC AGAGAAAACC TGGGGAGGGT   1680
GGGGAGGGCG GGGGAATGGA CCTTGTATAG ATCTGGAGGA AAGAAAGCTA CGAAAAACTT   1740
TTTAAAAGTT CTAGTGGTAC GGTAGGAGCT TTGCAGGAAG TTTGCAAAAG TCTTTACCAA   1800
TAATATTTAG AGCTAGTCTC CAAGCGACGA AAAAAATGTT TTAATATTTG CAAGCAACTT   1860
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AATTTGCCAA TATTTTTCAA GGAGAGGCTT CTTGCTGAAT TTTGATTCTG CAGCTGAAAT  1980
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TAAAAATTGT ACAAAAGGAA AAAATTAGAA TAAGTACTGG CGAACCATCT CTGTGGTCTT  2100
GTTTAAAAAG GGCAAAAGTT TTAGACTGTA CTAAATTTTA TAACTTACTG TTAAAAGCAA  2160
AAATGGCCAT GCAGGTTGAC ACCGTTGGTA ATTTATAATA GCTTTTGTTC GATCCCAACT  2220
TTCCATTTTG TTCAGATAAA AAAAACCATG AAATTACTGT GTTTGAAATA TTTTCTTATG  2280
GTTTGTAATA TTTCTGTAAA TTTATTGTGA TATTTTAAGG TTTTCCCCCC TTTATTTTCC  2340
GTAGTTGTAT TTTAAAAGAT TCGGCTCTGT ATTATTTGAA TCAGTCTGCC GAGAATCCAT  2400
GTATATATTT GAACTAATAT CATCCTTATA ACAGGTACAT TTTCAACTTA AGTTTTTACT  2460
CCATTATGCA CAGTTTGAGA TAAATAAATT TTTGAAATAT GGACACTGAA AAAAAAAAAA  2520
AAAAAAACAA AACAAAAAAA CAAAAAACAA AAACAGAAAA AACAAAAAAA AAAACAAAAC  2580
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CCACAACACA AACAACAACA CACAGAGGG
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Seq ID NO: 4 Protein sequence:
Protein Accession #:CAA83435.1

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QENPKMHNSE ISKRLGAEWK LLSETEKRPF IDEAKRLRAL HMKEHPDYKY RPRRKTKTLM   120
KKDKYTLPGG LLAPGGNSMA SGVGVGAGLG AGVNQRMDSY AHMNGWSNGS YSMMQDQLGY   180
PQHPGLNAHG AAQMQPMHRY DVSALQYNSM TSSQTYMNGS PTYSMSYSQQ GTPGMALGSM   240
GSVVKSEASS SPPVVTSSSH SRAPCQAGDL RDMISMYLPG AEVPEPAAPS RLHMSQHYQS   300
GPVPGTAING TLPLSHM
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Seq ID NO: 5 DNA sequence
Nucleic Acid Accession #: U91618
Coding sequence: 29-541

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CATGCTACTC CTGGCTTTCA GCTCCTGGAG TCTGTGCTCA GATTCAGAAG AGGAAATGAA   120
AGCATTAGAA GCAGATTTCT TGACCAATAT GCATACATCA AAGATTAGTA AAGCACATGT   180
TCCCTCTTGG AAGATGACTC TGCTAAATGT TTGCAGTCTT GTAAATAATT TGAACAGCCC   240
AGCTGAGGAA ACAGGAGAAG TTCATGAAGA GGAGCTTGTT GCAAGAAGGA AACTTCCTAC   300
TGCTTTAGAT GGCTTTAGCT TGGAAGCAAT GTTGACAATA TACCAGCTCC ACAAAATCTG   360
TCACAGCAGG GCTTTTCAAC ACTGGGAGTT AATCCAGGAA GATATTCTTG ATACTGGAAA   420
TGACAAAAAT GGAAAGGAAG AAGTCATAAA GAGAAAAATT CCTTATATTC TGAAACGGCA   480
GCTGTATGAG AATAAACCCA GAAGACCCTA CATACTCAAA AGAGATTCTT ACTATTACTG   540
AGAGAATAAA TCATTTATTT ACATGTGATT GTGATTCATC ATCCCTTAAT TAAATATCAA   600
ATTATATTTG TGTGAAAATG TGACAAACAC ACTTATCTGT CTCTTCTACA ATTGTGGTTT   660
ATTGAATGTG TTTTTCTGCA CTAATAGAAA TTAGACTAAG TGTTTTCAAA TAAATCTAAA   720
TCTTCAAAAA AAAAAAAAAA AAATGGGGCC GCAATT
```

Seq ID NO: 6 Protein sequence:
Protein Accession #: AAB50564

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1          11         21         31         41         51
|          |          |          |          |          |
MMAGMKIQLV CMLLLAFSSW SLCSDSEEEM KALEADFLTN MHTSKISKAH VPSWKMTLLN    60
VCSLVNNLNS PAEETGEVHE EELVARRKLP TALDGFSLEA MLTIYQLHKI CHSRAFQHWE   120
LIQEDILDTG NDKNGKEEVI KRKIPYILKR QLYENKPRRP YILKRDSYYY
```

Seq ID NO: 7 DNA sequence
Nucleic Acid Accession #: NM_006536.2
Coding sequence: 109-2940

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1          11         21         31         41         51
|          |          |          |          |          |
ACCTAAAACC TTGCAAGTTC AGGAAGAAAC CATCTGCATC CATATTGAAA ACCTGACACA    60
ATGTATGCAG CAGGCTCAGT GTGAGTGAAC TGGAGGCTTC TCTACAACAT GACCCAAAGG   120
AGCATTGCAG GTCCTATTTG CAACCTGAAG TTTGTGACTC TCCTGGTTGC CTTAAGTTCA   180
GAACTCCCAT TCCTGGGAGC TGGAGTACAG CTTCAAGACA ATGGGTATAA TGGATTGCTC   240
ATTGCAATTA ATCCTCAGGT ACCTGAGAAT CAGAACCTCA TCTCAAACAT TAAGGAAATG   300
ATAACTGAAG CTTCATTTTA CCTATTTAAT GCTACCAAGA GAAGAGTATT TTTCAGAAAT   360
ATAAAGATTT TAATACCTGC CACATGGAAA GCTAATAATA ACAGCAAAAT AAAACAAGAA   420
TCATATGAAA AGGCAAATGT CATAGTGACT GACTGGTATG GGCACATGGG AGATGATCCA   480
TACACCCTAC AATACAGAGG GTGTGGAAAA GAGGGAAAAT ACATTCATTT CACACCTAAT   540
TTCCTACTGA ATGATAACTT AACAGCTGGC TACGGATCAC GAGGCCGAGT GTTTGTCCAT   600
GAATGGGCCC ACCTCCGTTG GGGTGTGTTC GATGAGTATA ACAATGACAA ACCTTTCTAC   660
ATAAATGGGC AAAATCAAAT TAAAGTGACA AGGTGTTCAT CTGACATCAC AGGCATTTTT   720
GTGTGTGAAA AAGGTCCTTG CCCCCAAGAA AACTGTATTA TTAGTAAGCT TTTTAAAGAA   780
GGATGCACCT TTATCTACAA TAGCACCCAA AATGCAACTG CATCAATAAT GTTCATGCAA   840
AGTTTATCTT CTGTGGTTGA ATTTTGTAAT GCAAGTACCC ACAACCAAGA AGCACCAAAC   900
CTACAGAACC AGATGTGCAG CCTCAGAAGT GCATGGGATG TAATCACAGA CTCTGCTGAC   960
TTTCACCACA GCTTTCCCAT GAATGGGACT GAGCTTCCAC CTCCTCCCAC ATTCTCGCTT  1020
GTACAGGCTG GTGACAAAGT GGTCTGTTTA GTGCTGGATG TGTCCAGCAA GATGGCAGAG  1080
GCTGACAGAC TCCTTCAACT ACAACAAGCC GCAGAATTTT ATTTGATGCA GATTGTTGAA  1140
ATTCATACCT TCGTGGGCAT TGCCAGTTTC GACAGCAAAG GAGAGATCAG AGCCCAGCTA  1200
CACCAAATTA ACAGCAATGA TGATCGAAAG TTGCTGGTTT CATATCTGCC CACCACTGTA  1260
TCAGCTAAAA CAGACATCAG CATTTGTTCA GGGCTTAAGA AAGGATTTGA GGTGGTTGAA  1320
AAACTGAATG GAAAAGCTTA TGGCTCTGTG ATGATATTAG TGACCAGCGG AGATGATAAG  1380
CTTCTTGGCA ATTGCTTACC CACTGTGCTC AGCAGTGGTT CAACAATTCA CTCCATTGCC  1440
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CTGGGTTCAT CTGCAGCCCC AAATCTGGAG GAATTATCAC GTCTTACAGG AGGTTTAAAG  1500
TTCTTTGTTC CAGATATATC AAACTCCAAT AGCATGATTG ATGCTTTCAG TAGAATTTCC  1560
TCTGGAACTG GAGACATTTT CCAGCAACAT ATTCAGCTTG AAAGTACAGG TGAAAATGTC  1620
AAACCTCACC ATCAATTGAA AAACACAGTG ACTGTGGATA ATACTGTGGG CAACGACACT  1680
ATGTTTCTAG TTACGTGGCA GGCCAGTGGT CCTCCTGAGA TTATATTATT TGATCCTGAT  1740
GGACGAAAAT ACTACACAAA TAATTTTATC ACCAATCTAA CTTTTCGGAC AGCTAGTCTT  1800
TGGATTCCAG GAACAGCTAA GCCTGGGCAC TGGACTTACA CCCTGAACAA TACCCATCAT  1860
TCTCTGCAAG CCCTGAAAGT GACAGTGACC TCTCGCGCCT CCAACTCAGC TGTGCCCCCA  1920
GCCACTGTGG AAGCCTTTGT GGAAAGAGAC AGCCTCCATT TTCCTCATCC TGTGATGATT  1980
TATGCCAATG TGAAACAGGG ATTTTATCCC ATTCTTAATG CCACTGTCAC TGCCACAGTT  2040
GAGCCAGAGA CTGGAGATCC TGTTACGCTG AGACTCCTTG ATGATGGAGC AGGTGCTGAT  2100
GTTATAAAAA ATGATGGAAT TTACTCGAGG TATTTTTTCT CCTTTGCTGC AAATGGTAGA  2160
TATAGCTTGA AAGTGCATGT CAATCACTCT CCCAGCATAA GCACCCCAAC CCACTCTATT  2220
CCAGGGAGTC ATGCTATGTA TGTACCAGGT TACACAGCAA ACGGTAATAT TCAGATGAAT  2280
GCTCCAAGGA AATCAGTAGG CAGAAATGAG GAGGAGCGAA AGTGGGGCTT TAGCCGAGTC  2340
AGCTCAGGAG GCTCCTTTTC AGTGCTGGGA GTTCCAGCTG GCCCCCACCC TGATGTGTTT  2400
CCACCATGCA AAATTATTGA CCTGGAAGCT GTAAAAGTAG AAGAGGAATT GACCCTATCT  2460
TGGACAGCAC CTGGAGAAGA CTTTGATCAG GGCCAGGCTA CAAGCTATGA AATAAGAATG  2520
AGTAAAAGTC TACAGAATAT CCAAGATGAC TTTAACAATG CTATTTTAGT AAATACATCA  2580
AAGCGAAATC CTCAGCAAGC TGGCATCAGG GAGATATTTA CGTTCTCACC CCAGATTTCC  2640
ACGAATGGAC CTGAACATCA GCCAAATGGA GAAACACATG AAAGCCACAG AATTTATGTT  2700
GCAATACGAG CAATGGATAG GAACTCCTTA CAGTCTGCTG TATCTAACAT TGCCCAGGCG  2760
CCTCTGTTTA TTCCCCCCAA TTCTGATCCT GTACCTGCCA GAGATTATCT TATATTGAAA  2820
GGAGTTTTAA CAGCAATGGG TTTGATAGGA ATCATTTGCC TTATTATAGT TGTGACACAT  2880
CATACTTTAA GCAGGAAAAA GAGAGCAGAC AAGAAAGAGA ATGGAACAAA ATTATTATAA  2940
ATAAATATCC AAAGTGTCTT CCTTCTTAGA TATAAGACCC ATGGCCTTCG ACTACAAAAA  3000
CATACTAACA AAGTCAAATT AACATCAAAA CTGTATTAAA ATGCATTGAG TTTTTGTACA  3060
ATACAGATAA GATTTTTACA TGGTAGATCA ACAATTCTTT TTGGGGGTAG ATTAGAAAAC  3120
CCTTACACTT TGGCTATGAA CAAATAATAA AAATTATTCT TTAAAGTAAT GTCTTTAAAG  3180
GCAAAGGGAA GGGTAAAGTC GGACCAGTGT CAAGGAAAGT TTGTTTTATT GAGGTGGAAA  3240
AATAGCCCCA AGCAGAGAAA AGGAGGGTAG GTCTGCATTA TAACTGTCTG TGTGAAGCAA  3300
TCATTTAGTT ACTTTGATTA ATTTTTCTTT TCTCCTTATC TGTGCAGTAC AGGTTGCTTG  3360
TTTACATGAA GATCATGCTA TATTTTATAT ATGTAGCCCC TAATGCAAAG CTCTTTACCT  3420
CTTGCTATTT TGTTATATAT ATTTCAGATG ACATCTCCCT GCTAATGCTC AGAGATCTTT  3480
TTTCACTGTA AGAGGTAACC TTTAACAATA TGGGTATTAC CTTTGTCTCT TCATACCGGT  3540
TTTATGACAA AGGTCTATTG AATTTATTTG TNTGTAAGTT TCTACTCCCA TCAAAGCAGC  3600
TTTCTAAGTT TATTGCCTTG GGTTATTATG GAATGATAGT TATAGCCCCN TATAATGCCT  3660
TACCTAGGAA A
```

Seq ID NO: 8 Protein sequence:
Protein Accession #: NP_006527.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MTQRSIAGPI CNLKFVTLLV ALSSELPFLG AGVQLQDNGY NGLLIAINPQ VPENQNLISN    60
IKEMITEASF YLFNATKRRV FFRNIKILIP ATWKANNNSK IKQESYEKAN VIVTDWYGAH   120
GDDPYTLQYR GCGKEGKYIH FTPNFLLNDN LTAGYGSRGR VFVHEWAHLR WGVFDEYNND   180
KPFYINGQNQ IKVTRCSSDI TGIFVCEKGP CPQENCIISK LFKEGCTFIY NSTQNATASI   240
MFMQSLSSVV EFCNASTHNQ EAPNLQNQMC SLRSAWDVIT DSADFHHSFP MNGTELPPPP   300
TFSLVQAGDK VVCLVLDVSS KMAEADRLLQ LQQAAEFYLM QIVEIHTFVG IASFDSKGEI   360
RAQLHQINSN DDRKLLVSYL PTTVSAKTDI SICSGLKKGF EVVEKLNGKA YGSVMILVTS   420
GDDKLLGNCL PTVLSSGSTI HSIALGSSAA PNLEELSRLT GGLKFFVPDI SNSNSMIDAF   480
SRISSGTGDI FQQHIQLEST GENVKPHHQL KNTVTVDNTV GNDTMFLVTW QASGPPEIIL   540
FDPDGRKYYT NNFITNLTFR TASLWIPGTA KPGHWTYTLN NTHHSLQALK VTVTSRASNS   600
AVPPATVEAF VERDSLHFPH PVMIYANVKQ GFYPILNATV TATVEPETGD PVTLRLLDDG   660
AGADVIKNDG IYSRYFFSFA ANGRYSLKVH VNHSPSISTP AHSIPGSHAM YVPGYTANGN   720
IQMNAPRKSV GRNEEERKWG FSRVSSGGSF SVLGVPAGPH PDVFPPCKII DLEAVKVEEE   780
LTLSWTAPGE DFDQGQATSY EIRMSKSLQN IQDDFNNAIL VNTSKRNPQQ AGIREIFTFS   840
PQISTNGPEH QPNGETHESH RIYVAIRAMD RNSLQSAVSN IAQAPLFIPP NSDPVPARDY   900
LILKGVLTAM GLIGIICLII VVTHHTLSRK KRADKKENGT KLL
```

Seq ID NO: 9 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 336-632

```
1          11         21         31         41         51
|          |          |          |          |          |
CTCCCCTCAC CCCGGTCCAG GATGCCCAGT CCCCACGACA CCTCCCACTT CCCACTGTGG    60
CCTGGGTGGG CTCAGGGGCT GCCCTTGACC TGGCCTAGAG CCCTCCCCCA GCTGGTGGTG   120
GAGCTGGCAC TCTCTGGGAG GGAGGGGGCT GGGAGGGAAT GAGTGGGAAT GGCAAGAGGC   180
CAGGGTTTGG TGGGATCAGG TTGAGGCAGG TTTGGTTTCC TTAAAATGCC AAGTTGGGGG   240
CCAGTGGGGC CCACATATAA ATCCTCACCC TGGGAGCCTG GCTGCCTTGC TCTCCTTCCT   300
GGGTCTGTCT CTGCCACCTG GTCTGCCACA GATCCATGAT GTGCAGTTCT CTGGAGCAGG   360
CGCTGGCTGT GCTGGTCACT ACCTTCCACA AGTACTCCTG CCAAGAGGGC GACAAGTTCA   420
AGCTGAGTAA GGGGGAAATG AAGGAACTTC TGCACAAGGA GCTGCCCAGC TTTGTGGGGG   480
AGAAAGTGGA TGAGGAGGGG CTGAAGAAGC TGATGGGCAG CCTGGATGAG AACAGTGACC   540
AGCAGGTGGA CTTCCAGGAG TATGCTGTTT TCCTGGCACT CATCACTGTC ATGTGCAATG   600
ACTTCTTCCA GGGCTGCCCA GACCGACCCT GAAGCAGAAC TCTTGACTTC CTGCCATGGA   660
TCTCTTGGGC CCAGGACTGT TGATGCCTTT GAGTTTTGTA TTCAATAAAC TTTTTTTGTC   720
TGTTGATAAT ATTTTAATTG CTCAGTGATG TTCCATAACC CGGCTGGCTC AGCTGGAGTG   780
CTGGGAGATG AGGGCCTCCT GGATCCTGCT CCCTTCTGGG CTCTGACTCT CCTGGAAATC   840
TCTCCAAGGC CAGAGCTATG CTTTAGGTCT CAATTTTGGA ATTTCAAACA CCAGCAAAAA   900
ATTGGAAATC GAGATAGGTT GCTGACTTTT ATTTTGTCAA ATAAAGATAT TAAAAAAGGC   960
AAATACCA
```

Seq ID NO: 10 Protein sequence:

Protein Accession #: NP_005969.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MMCSSLEQAL AVLVTTFHKY SCQEGDKFKL SKGEMKELLH KELPSFVGEK VDEEGLKKLM    60
GSLDENSDQQ VDFQEYAVFL ALITVMCNDF FQGCPDRP
```

Seq ID NO: 11 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 336-626

```
1          11         21         31         41         51
|          |          |          |          |          |
CTCCCCTCAC CCCGGTCCAG GATGCCCAGT CCCCACGACA CCTCCCACTT CCCACTGTGG    60
CCTGGGTGGG CTCAGGGGCT GCCCTTGACC TGGCCTAGAG CCCTCCCCCA GCTGGTGGTG   120
GAGCTGGCAC TCTCTGGGAG GGAGGGGGCT GGGAGGGAAT GAGTGGGAAT GGCAAGAGGC   180
CAGGGTTTGG TGGGATCAGG TTGAGGCAGG TTTGGTTTCC TTAAAATGCC AAGTTGGGGG   240
CCAGTGGGGC CCACATATAA ATCCTCACCC TGGGAGCCTG GCTGCCTTGC TCTCCTTCCT   300
GGGTCTGTCT CTGCCACCTG GTCTGCCACA GATCCATGAT GTGCAGTTCT CTGGAGCAGG   360
CGCTGGCTGT GCTGGTCACT ACCTTCCACA AGTACTCCTG CCAAGAGGGC GACAAGTTCA   420
AGCTGAGTAA GGGGGAAATG AAGGAACTTC TGCACAAGGA GCTGCCCAGC TTTGTGGGGC   480
ATTCCAGAGA ACCATGTGCT GTGAGGGCCT TCCGAGTCCA TCTGTTTAAT CCTGTCATTG   540
GAGACTTGAG AAACCAGAGC CCAGAAGGGA AAAGTGATTG TCCCAAGATC ACACAGCACT   600
GGAGAAAGTG GATGAGGAGG GGCTGAAGAA GCTGATGGGC AGCCTGGATG AGAACAGTGA   660
CCAGCAGGTG GACTTCCAGG AGTATGCTGT TTTCCTGGCA CTCATCACTG TCATGTGCAA   720
TGACTTCTTC CAGGGCTGCC CAGACCGACC CTGAAGCAGA ACTCTTGACT TCCTGCCATG   780
GATCTCTTGG GCCCAGGACT GTTGATGCCT TTGAGTTTTG TATTCAATAA ACTTTTTTTG   840
TCTGTTGATA ATATTTTAAT TGCTCAGTGA TGTTCCATAA CCCGGCTGGC TCAGCTGGAG   900
TGCTGGGAGA TGAGGGCCTC CTGGATCCTG CTCCCTTCTG GGCTCTGACT CTCCTGGAAA   960
TCTCTCCAAG GCCAGAGCTA TGCTTTAGGT CTCAATTTTG GAATTTCAAA CACCAGCAAA  1020
AAATTGGAAA TCGAGATAGG TTGCTGACTT TTATTTTGTC AAATAAAGAT ATTAAAAAAG  1080
GCAAATACCA
```

Seq ID NO: 12 Protein sequence:
Protein Accession #: Eos sequence

```
1          11         21         31         41         51
|          |          |          |          |          |
MMCSSLEQAL AVLVTTFHKY SCQEGDKFKL SKGEMKELLH KELPSFVGHS REPCAVRAFR    60
VHLFNPVIGD LRNQSPEGKS DCPKITQHWR KWMRRG
```

Seq ID NO: 13 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 58-354

```
1          11         21         31         41         51
|          |          |          |          |          |
GTGAGCTCAC CATGTGGGGG TGAGGCTGAG AGAAAACAAG TACACAGCCA CAGATCCATG    60
ATGTGCAGTT CTCTGGAGCA GGCGCTGGCT GTGCTGGTCA CTACCTTCCA CAAGTACTCC   120
TGCCAAGAGG GCGACAAGTT CAAGCTGAGT AAGGGGGAAA TGAAGGAACT TCTGCACAAG   180
GAGCTGCCCA GCTTTGTGGG GGAGAAAGTG GATGAGGAGG GGCTGAAGAA GCTGATGGGC   240
AGCCTGGATG AGAACAGTGA CCAGCAGGTG GACTTCCAGG AGTATGCTGT TTTCCTGGCA   300
CTCATCACTG TCATGTGCAA TGACTTCTTC CAGGGCTGCC CAGACCGACC CTGAAGCAGA   360
ACTCTTGACT TCCTGCCATG GATCTCTTGG GCCCAGGACT GTTGATGCCT TTGAGTTTTG   420
TATTCAATAA ACTTTTTTTG TCTGTTGATA ATATTTTAAT TGCTCAGTGA TGTTCCATAA   480
CCCGGCTGGC TCAGCTGGAG TGCTGGGAGA TGAGGGCCTC CTGGATCCTG CTCCCTTCTG   540
GGCTCTGACT CTCCTGGAAA TCTCTCCAAG GCCAGAGCTA TGCTTTAGGT CTCAATTTTG   600
GAATTTCAAA CACCAGCAAA AAATTGGAAA TCGAGATAGG TTGCTGACTT TTATTTTGTC   660
AAATAAAGAT ATTAAAAAAG GCAAATACCA
```

Seq ID NO: 14 Protein sequence:
Protein Accession #: NP_005969.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MMCSSLEQAL AVLVTTFHKY SCQEGDKFKL SKGEMKELLH KELPSFVGEK VDEEGLKKLM    60
GSLDENSDQQ VDFQEYAVFL ALITVMCNDF FQGCPDRP
```

Seq ID NO: 15 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 62-358

```
1          11         21         31         41         51
|          |          |          |          |          |
GGAGGGTGTG CCGCTGAGTC ACTGCCTGGG CATCTGGGCC TGGAACCTCG GCCACAGATC    60
CATGATGTGC AGTTCTCTGG AGCAGGCGCT GGCTGTGCTG GTCACTACCT TCCACAAGTA   120
CTCCTGCCAA GAGGGCGACA AGTTCAAGCT GAGTAAGGGG GAAATGAAGG AACTTCTGCA   180
CAAGGAGCTG CCCAGCTTTG TGGGGGAGAA AGTGGATGAG GAGGGGCTGA AGAAGCTGAT   240
GGGCAGCCTG GATGAGAACA GTGACCAGCA GGTGGACTTC CAGGAGTATG CTGTTTTCCT   300
GGCACTCATC ACTGTCATGT GCAATGACTT CTTCCAGGGC TGCCCAGACC GACCCTGAAG   360
CAGAACTCTT GACTTCCTGC CATGGATCTC TTGGGCCCAG GACTGTTGAT GCCTTTGAGT   420
TTTGTATTCA ATAAACTTTT TTTGTCTGTT GATAATATTT TAATTGCTCA GTGATGTTCC   480
ATAACCCGGC TGGCTCAGCT GGAGTGCTGG GAGATGAGGG CCTCCTGGAT CCTGCTCCCT   540
TCTGGGCTCT GACTCTCCTG GAAATCTCTC CAAGGCCAGA GCTATGCTTT AGGTCTCAAT   600
TTTGGAATTT CAAACACCAG CAAAAAATTG GAAATCGAGA TAGGTTGCTG ACTTTTATTT   660
```

```
TGTCAAATAA AGATATTAAA AAAGGCAAAT ACCA
```

Seq ID NO: 16 Protein sequence:
Protein Accession #: NP_005969.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MMCSSLEQAL AVLVTTFHKY SCQEGDKFKL SKGEMKELLH KELPSFVGEK VDEEGLKKLM    60
GSLDENSDQQ VDFQEYAVFL ALITVMCNDF FQGCPDRP
```

Seq ID NO: 17 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 939-2372

```
1          11         21         31         41         51
|          |          |          |          |          |
AAGACGGATT CTCAGACAAG GCTTGCAAAT GCCCCGCAGC CATCATTTAA CTGCACCCGC    60
AGAATAGTTA CGGTTTGTCA CCCGACCCTC CCGGATCGCC TAATTTGTCC CTAGTGAGAC   120
CCCGAGGCTC TGCCCGCGCC TGGCTTCTTC GTAGCTGGAT GCATATCGTG CTCCGGGCAG   180
CGCGGGCGCA GGGCACGCGT TCGCGCACAC CCTAGCACAC ATGAACACGC GCAAGAGCTG   240
AACCAAGCAC GGTTTCCATT TCAAAAAGGG AGACAGCCTC TACCGCGATT GTAGAAGAGA   300
CTGTGGTGTG AATTAGGGAC CGGGAGGCGT CGAACGGAGG AACGGTTCAT CTTAGAGACT   360
AATTTTCTGG AGTTTCTGCC CCTGCTCTGC GTCAGCCCTC ACGTCACTTC GCCAGCAGTA   420
GCAGAGGCGG CGGCGGCGGC TCCCGGAATT GGGTTGGAGC AGGAGCCTCG CTGGCTGCTT   480
CGCTCGCGCT CTACGCGCTC AGTCCCCGGC GGTAGCAGGA GCCTGGACCC AGGCGCCGCC   540
GGCGGGCGTG AGGCGCCGGA GCCCGGCCTC GAGGTGCATA CCGGACCCCC ATTCGCATCT   600
AACAAGGAAT CTGCGCCCCA GAGAGTCCCG GGAGCGCCGC CGGTCGGTGC CCGGCGCGCC   660
GGGCCATGCA GCGACGGCCG CCGCGGAGCT CCGAGCAGCG GTAGCGCCCC CCTGTAAAGC   720
GGTTCGCTAT GCCGGGGCCA CTGTGAACCC TGCCGCCTGC CGGAACACTC TTCGCTCCGG   780
ACCAGCTCAG CCTCTGATAA GCTGGACTCG GCACGCCCGC AACAAGCACC GAGGAGTTAA   840
GAGAGCCGCA AGCGCAGGGA AGGCCTCCCC GCACGGGTGG GGGAAAGCGG CCGGTGCAGC   900
GCGGGGACAG GCACTCGGGC TGGCACTGGC TGCTAGGGAT GTCGTCCTGG ATAAGGTGGC   960
ATGGACCCGC CATGGCGCGG CTCTGGGGCT TCTGCTGGCT GGTTGTGGGC TTCTGGAGGG  1020
CCGCTTTCGC CTGTCCCACG TCCTGCAAAT GCAGTGCCTC TCGGATCTGG TGCAGCGACC  1080
CTTCTCCTGG CATCGTGGCA TTTCCGAGAT TGGAGCCTAA CAGTGTAGAT CCTGAGAACA  1140
TCACCGAAAT TTTCATCGCA AACCAGAAAA GGTTAGAAAT CATCAACGAA GATGATGTTG  1200
AAGCTTATGT GGGACTGAGA AATCTGACAA TTGTGGATTC TGGATTAAAA TTTGTGGCTC  1260
ATAAAGCATT TCTGAAAAAC AGCAACCTGC AGCACATCAA TTTTACCCGA AACAAACTGA  1320
CGAGTTTGTC TAGGAAACAT TTCCGTCACC TTGACTTGTC TGAACTGATC CTGGTGGGCA  1380
ATCCATTTAC ATGCTCCTGT GACATTATGT GGATCAAGAC TCTCCAAGAG GCTAAATCCA  1440
GTCCAGACAC TCAGGATTTG TACTGCCTGA ATGAAAGCAG CAAGAATATT CCCCTGGCAA  1500
ACCTGCAGAT ACCCAATTGT GGTTTGCCAT CTGCAAATCT GGCCGCACCT AACCTCACTG  1560
TGGAGGAAGG AAAGTCTATC ACATTATCCT GTAGTGTGGC AGGTGATCCG GTTCCTAATA  1620
TGTATTGGGA TGTTGGTAAC CTGGTTTCCA AACATATGAA TGAAACAAGC CACACACAGG  1680
GCTCCTTAAG GATAACTAAC ATTTCATCCG ATGACAGTGG GAAGCAGATC TCTTGTGTGG  1740
CGGAAAATCT TGTAGGAGAA GATCAAGATT CTGTCAACCT CACTGTGCAT TTTGCACCAA  1800
CTATCACATT TCTCGAATCT CCAACCTCAG ACCACCACTG GTGCATTCCA TTCACTGTGA  1860
AAGGCAACCC CAAACCAGCG CTTCAGTGGT TCTATAACGG GGCAATATTG AATGAGTCCA  1920
AATACATCTG TACTAAAATA CATGTTACCA ATCACACGGA GTACCACGGC TGCCTCCAGC  1980
TGGATAATCC CACTCACATG AACAATGGGG ACTACACTCT AATAGCCAAG AATGAGTATG  2040
GGAAGGATGA GAAACAGATT TCTGCTCACT TCATGGGCTG GCCTGGAATT GACGATGGTG  2100
CAAACCCAAA TTATCCTGAT GTAATTTATG AAGATTATGG AACTGCAGCG AATGACATCG  2160
GGGACACCAC GAACAGAAGT AATGAAATCC CTTCCACAGA CGTCACTGAT AAAACCGGTC  2220
GGGAACATCT CTCGGTCTAT GCTGTGGTGG TGATTGCGTC TGTGGTGGGA TTTTGCCTTT  2280
TGGTAATGCT GTTTCTGCTT AAGTTGGCAA GACACTCCAA GTTTGGCATG AAAGGTTTTG  2340
TTTTGTTTCA TAAGATCCCA CTGGATGGGT AGCTGAAATA AAGGAAAAGA CAGAGAAAGG  2400
GGCTGTGGTG CTTGTTGGTT GATGCTGCCA TGTAAGCTGG ACTCCTGGGA CTGCTGTTGG  2460
CTTATCCCGG GAAGTGCTGC TTATCTGGGG TTTTCTGGTA GATGTGGGCG GTGTTTGGAG  2520
GCTGTACTAT ATGAAGCCTG CATATACTGT GAGCTGTGAT TGGGGAACAC CAATGCAGAG  2580
GTAACTCTCA GGCAGCTAAG CAGCACCTCA AGAAAACATG TTAAATTAAT GCTTCTCTTC  2640
TTACAGTAGT TCAAATACAA AACTGAAATG AAATCCCATT GGATTGTACT TCTCTTCTGA  2700
AAAGTGTGCT TTTTGACCCT ACTGGACATT TATTGACTTA ATTGCTTCTG TTTATTAAAA  2760
TTGACCTGCA AAGTTAAAAA AAAATTAAAG TTGAGAACAG GTATAAGTGC ACACTGAATA  2820
GTCTAATCTA CATGTAACAC ATATTTTAGT GTGATTTTCT ATACTCTAAT CAGCACTGAA  2880
TTCAGAGGGT TTGACTTTTT CATCTATAAC ACAGTGACTA AAAGAGTTAA GGGTATATAT  2940
ACCATCACTT TGGGACTTGG TAGTATTATT AAAAGGTTAT TTCCTTCACT GTCAATAAAA  3000
GTCCAAATGT TTAGCTTAGG TCTGAGAGTC AAACAATGTT AAGGATTGTC TTAAAGTTCC  3060
TTAGCCAGCA AAACAAAACA AAACAAAACA AACAAATGAA AAACGTTTAA AAAGAAGAAG  3120
AAGAAAAAAA ACAAGAACAA GCAGCAACAG CTGTTTTGTT GGGGCTATAG ATTTAAGTTA  3180
GGCATAGTCA ATTTCAGAAT AACTAAGAGT GGAATATATG CATATGGTGA AATTATAACC  3240
TTGCCCTTTT TTATTTGCCC TCTGCGATCC ACCTGCTTTT TAGAAGTCTG CCGAGTGAGA  3300
AGGCCACAGT ATCTCATGCT GTTTGCATTA CAGAACTGCA GCTTTTCTAC TCTGAAAAGG  3360
CCTGGGAGCA GAATGGCTGG CCTGCTGTGA GCAGGAGAGG AGATTCTAAG AAGGATAGTC  3420
CCCCCTACAA CATACTGTCA TACTGCTGGG TTTTCATGGG TAGGAAAGCT TGTCCTGACC  3480
CCAGCAGCAA AGAGGTGGCA GGTCGCTAAT GAATATATGC TTTATAATGT CCTTCTTCAT  3540
TGCTGAGAGG GCAGCCTTAG AGCTGTGGAT TTCTGCATCC CCCCTGAGTC TGACCCATGG  3600
ACACCTGTTT CATTCACTTT AGCATCACAG TGACCTTTGT ATGCTCTGTT CAGTCTGTGT  3660
CAGGCAGTAT GCTTGTCCTG AAGAGAGGTT TGGCTATCCC CACCCCACCC CACCCCACCC  3720
TGTTCCTTTT TTATCAGGAG GACTTCAGAG CCAGGCCTGC AGCATTTTGT TTGAAAACAC  3780
AATCAGCTCT GACAGTTAGA CATGCACACA GACGCCATAG CTGGATTGGA AACATTGATG  3840
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CAAGGCATTA ATCTTAATAA ACCAGGATCC ATTTAGGTAC CACTTGATAT AAAAAGGATA  4020
TCCATAATGA ATATTTTATA CTGCATCCTT TACATTAGCC ACTAAATACG TTATTGCTTG  4080
ATGAAGACCT TTCACAGAAT CCTATGGATT GCAGCATTTC ACTTGGCTAC TTCATACCCA  4140
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TCCTAACTCC ATTTGAATGT AAGGGCAGCT GGCCCCCAAT GTGGGGAGGT CCGAACATTT 4260
TCTGAATTCC CATTTTCTTG TTCGCGGCTA AATGACAGTT TCTGTCATTA CTTAGATTCC 4320
GATCTTTCCC AAAGGTGTTG ATTTACAAAG AGGCCAGCTA ATAGCAGAAA TCATGACCCT 4380
GAAAGAGAGA TGAAATTCAA GCTGTGAGCC AGGCAGGAGC TCAGTATGGC AAAGGTTCTT 4440
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AATAAAAAAA AAGGAATATT TGTACCCAAC AGCTAGAAGG ATTGCAAGGT AGATTTTTGT 4620
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Seq ID NO: 18 Protein sequence:
Protein Accession #: CAA53571

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NSVDPENITE IPIANQKRLE IINEDDVEAY VGLRNLTIVD SGLKFVAHKA FLKNSNLQHI  120
NFTRNKLTSL SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQEAKSSPD TQDLYCLNES  180
SKNIPLANLQ IPNCGLPSAN LAAPNLTVEE GKSITLSCSV AGDPVPNMYW DVGNLVSKHM  240
NETSHTQGSL RITNISSDDS GKQISCVAEN LVGEDQDSVN LTVHFAPTIT FLESPTSDHH  300
WCIPFTVKGN PKPALQWFYN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNNGDYT  360
LIAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST  420
DVTDKTGREH LSVYAVVVIA SVVGFCLLVM LFLLKLARHS KFGMKGFVLF HKIPLDG
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Seq ID NO: 19 DNA sequence
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Coding sequence: 82-3600

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CTTGTTGGGA GGACCCGGTT TCTCCGAGCT TCATCTACCT GTGGACTGAC CAAGCCTGAG  240
ACCTACTGCA CCCAGTATGG CGAGTGGCAG ATGAAATGCT GCAAGTGTGA CTCCAGGCAG  300
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CAGGTCCACG ATGTCTGTGT CTGCCAGCAC AACACTGCCG GCCCAAATTG TGAGCGCTGT  960
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GCCAGCCAGG GGGCATATGG AGGTGTGTGT GACAATTGCC GGGACCACAC CGAAGGCAAG 1140
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CTCTCAAGTC AAGGAAGCTG GGCTGGGCAG TATCCCCCGC CTTTAGTTCT CCACTGGGGA  3900
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Seq ID NO: 20 Protein sequence:
Protein Accession #: NP_000219

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MEFQGPMPAG MLIERSSDFG KTWRVYQYLA ADCTSTFPRV RQGRPQSWQD VRCQSLPQRP   180
NARLNGGKVQ LNLMDLVSGI PATQSQKIQE VGEITNLRVN FTRLAPVPQR GYHPPSAYYA   240
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HYFRNRRPGA SIQETCISCE CDPDGAVPGA PCDPVTGQCV CKEHVQGERC DLCKPGFTGL   420
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CACDPHNSPQ PTVQPVHRAV PCREGFGGLM CSAAAIRQCP DRTYGDVATG CRACDCDFRG   540
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RLQAEAEEAR SRAHAVEGQV EDVVGNLRQG TVALQEAQDT MQGTSRSLRL IQDRVAEVQQ  1020
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Seq ID NO: 21 DNA sequence
Nucleic Acid Accession #: NM_003722
Coding sequence: 145-1491

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Seq ID NO: 22 Protein sequence:
Protein Accession #: NP_003713

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FEARICACPG RDRKADEDSI RKQQVSDSTK NGDGTKRPFR QNTHGIQMTS IKKRRSPDDE 360
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Seq ID NO: 23 DNA sequence
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Coding sequence: 84-3083

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Seq ID NO: 24 Protein sequence:
Protein Accession #: NP_001935.1

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WLAVYFFTSG NEGNWFEIQT DPRTNEGILK VVKALDYEQL QSVKLSIAVK NKAEFHQSVI   360
SRYRVQSTPV TIQVINVREG IAFRPASKTF TVQKGISSKK LVDYILGTYQ AIDEDTNKAA   420
SNVKYVMGRN DGGYLMIDSK TAEIKFVKNM NRDSTFIVNK TITAEVLAID EYTGKTSTGT   480
VYVRVPDFND NCPTAVLEKD AVCSSSPSVV VSARTLNNRY TGPYTFALED QPVKLPAVWS   540
ITTLNATSAL LRAQEQIPPG VYHISLVLTD SQNNRCEMPR SLTLEVCQCD NRGICGTSYP   600
TTSPGTRYGR PHSGRLGPAA IGLLLLGLLL LLLAPLLLLT CDCGAGSTGG VTGGFIPVPD   660
GSEGTIHQWG IEGAHPEDKE ITNICVPPVT ANGADFMESS EVCTNTYARG TAVEGTSGME   720
MTTKLGAATE SGGAAGFATG TVSGAASGFG AATGVGICSS GQSGTMRTRH STGGTNKDYA   780
DGAISMNFLD SYFSQKAFAC AEEDDGQEAN DCLLIYDNEG ADATGSPVGS VGCCSFIADD   840
LDDSFLDSLG PKFKKLAEIS LGVDGEGKEV QPPSKDSGYG IESCGHPIEV QQTGFVKCQT   900
LSGSQGASAL SASGSVQPAV SIPDPLQHGN YLVTETYSAS GSLVQPSTAG FDPLLTQNVI   960
VTERVICPIS SVPGNLAGPT QLRGSHTMLC TEDPCSRLI
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Seq ID NO: 25 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 56-1642

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GCAAGGGATC CTTTCTCCGC CAGCGGGCTT GCTGTCCGAT GACGATGTCG TAGTTTCTCC   120
CATGTTTGAG TCCACAGCTG CAGATTTGGG GTCTGTGGTA CGCAAGAACC TGCTATCAGA   180
CTGCTCTGTC GTCTCTACCT CCCTAGAGGA CAAGCAGCAG GTTCCATCTG AGGACAGTAT   240
GGAGAAGGTG AAAGTATACT TGAGGGTTAG GCCCTTGTTA CCTTCAGAGT TGGAACGACA   300
GGAAGATCAG GGTTGTGTCC GTATTGAGAA TGTGGAGACC CTTGTTCTAC AAGCACCCAA   360
GGACTCTTTT GCCCTGAAGA GCAATGAACG GGGAATTGGC CAAGCCACAC ACAGGTTCAC   420
CTTTTCCCAG ATCTTTGGGC CAGAAGTGGG ACAGGCATCC TTCTTCAACC TAACTGTGAA   480
GGAGATGGTA AAGGATGTAC TCAAAGGGCA GAACTGGCTC ATCTATACAT ATGGAGTCAC   540
TAACTCAGGG AAAACCCACA CGATTCAAGG TACCATCAAG GATGGAGGGA TTCTCCCCCG   600
GTCCCTGGCG CTGATCTTCA ATAGCCTCCA AGGCCAACTT CATCCAACAC CTGATCTGAA   660
GCCCTTGCTC TCCAATGAGG TAATCTGGCT AGACAGCAAG CAGATCCGAC AGGAGGAAAT   720
GAAGAAGCTG TCCCTGCTAA ATGGAGGCCT CCAAGAGGAG GAGCTGTCCA CTTCCTTGAA   780
GAGGAGTGTC TACATCGAAA GTCGGATAGG TACCAGCACC AGCTTCGACA GTGGCATTGC   840
TGGGCTCTCT TCTATCAGTC AGTGTACCAG CAGTAGCCAG CTGGATGAAA CAAGTCATCG   900
ATGGGCACAG CCAGACACTG CCCCACTACC TGTCCCGGCA AACATTCGCT TCTCCATCTG   960
GATCTCATTC TTTGAGATCT ACAACGAACT GCTTTATGAC CTATTAGAAC CGCCTAGCCA  1020
ACAGCGCAAG AGGCAGACTT TGCGGCTATG CGAGGATCAA AATGGCAATC CCTATGTGAA  1080
AGATCTCAAC TGGATTCATG TGCAAGATGC TGAGGAGGCC TGGAAGCTCC TAAAAGTGGG  1140
TCGTAAGAAC CAGAGCTTTG CCAGCACCCA CCTCAACCAG AACTCCAGCC GCAGTCACAG  1200
CATCTTCTCA ATCAGGATCC TACACCTTCA GGGGGAAGGA GATATAGTCC CCAAGATCAG  1260
CGAGCTGTCA CTCTGTGATC TGGCTGGCTC AGAGCGCTGC AAAGATCAGA AGAGTGGTGA  1320
ACGGTTGAAG GAAGCAGGAA ACATTAACAC CTCTCTACAC ACCCTGGGCC GCTGTATTGC  1380
TGCCCTTCGT CAAAACCAGC AGAACCGGTC AAAGCAGAAC CTGGTTCCCT TCCGTGACAG  1440
CAAGTTGACT CGAGTGTTCC AAGGTTTCTT CACAGGCCGA GGCCGTTCCT GCATGATTGT  1500
CAATGTGAAT CCCTGTGCAT CTACCTATGA TGAAACTCTT CATGTGGCCA AGTTCTCAGC  1560
CATTGCTAGC CAGGTGACTT GTGCATGCCC CACCTATGCA ACTGGGATTC CCATCCCTGC  1620
ACTCGTTCAT CAAGGAACAT AGTCTTCAGG TATCCCCCAG CTTAGAGAAA GGGGCTAAGG  1680
CAGACACAGG CCTTGATGAT GATATTGAAA ATGAAGCTGA CATCTCCATG TATGGCAAAG  1740
AGGAGCTCCT ACAAGTTGTG GAAGCCATGA AGACACTGCT TTTGAAGGAA CGACAGGAAA  1800
AGCTACAGCT GGAGATGCAT CTCCGAGATG AAATTTGCAA TGAGATGGTA GAACAGATGC  1860
AACAGCGGGA ACAGTGGTGC AGTGAACATT TGGACACCCA AAAGGAACTA TTGGAGGAAA  1920
TGTATGAAGA AAAACTAAAT ATCCTCAAGG AGTCACTGAC AAGTTTTTAC CAAGAAGAGA  1980
TTCAGGAGCG GGATGAAAAG ATTGAAGAGC TAGAAGCTCT CTTGCAGGAA GCCAGACAAC  2040
AGTCAGTGGC CCATCAGCAA TCAGGGTCTG AATTGGCCCT ACGGCGGTCA CAAAGGTTGG  2100
CAGCTTCTGC CTCCACCCAG CAGCTTCAGG AGGTTAAAGC TAAATTACAG CAGTGCAAAG  2160
CAGAGCTAAA CTCTACCACT GAAGAGTTGC ATAAGTATCA GAAAATGTTA GAACCACCAC  2220
CCTCAGCCAA GCCCTTCACC ATTGATGTGG ACAAGAAGTT AGAAGAGGGC CAGAAGAATA  2280
TAAGGCTGTT GCGGACAGAG CTTCAGAAAC TTGGTGAGTC TCTCCAATCA GCAGAGAGAG  2340
CTTGTTGCCA CAGCACTGGG GCAGGAAAAC TTCGTCAAGC CTTGACCACT TGTGATGACA  2400
TCTTAATCAA ACAGGACCAG ACTCTGGCTG AACTGCAGAA CAACATGGTG CTAGTGAAAC  2460
TGGACCTTCG GAAGAAGGCA GCATGTATTG CTGAGCAGTA TCATACTGTG TTGAAACTCC  2520
AAGGCCAGGT TTCTGCCAAA AAGCGCCTTG GTACCAACCA GGAAAATCAG CAACCAAACC  2580
AACAACCACC AGGGAAGAAA CCATTCCTTC GAAATTTACT TCCCCGAACA CCAACCTGCC  2640
AAAGCTCAAC AGACTGCAGC CCTTATGCCC GGATCCTACG CTCACGGCGT TCCCCTTTAC  2700
TCAAATCTGG GCCTTTTGGC AAAAAGTACT AAGGCTGTGG GGAAAGAGAA GAGCAGTCAT  2760
GGCCCTGAGG TGGGTCAGCT ACTCTCCTGA AGAAATAGGT CTCTTTTATG CTTTACCATA  2820
TATCAGGAAT TATATCCAGG ATGCAATACT CAGACACTAG CTTTTTTCTC ACTTTTGTAT  2880
TATAACCACC TATGTAATCT CATGTTGTTG TTTTTTTTTA TTTACTTATA TGATTTCTAT  2940
GCACACAAAA ACAGTTATAT TAAAGATATT ATTGTTCACA TTTTTTATTG AATTCCAAAT  3000
GTAGCAAAAT CATTAAAACA AATTATAAAA GGGACAGAAA AA
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Seq ID NO: 26 Protein sequence:
Protein Accession #: Eos sequence

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MSQGILSPPA GLLSDDDVVV SPMFESTAAD LGSVVRKNLL SDCSVVSTSL EDKQQVPSED    60
SMEKVKVYLR VRPLLPSELE RQEDQGCVRI ENVETLVLQA PKDSFALKSN ERGIGQATHR   120
FTFSQIFGPE VGQASFFNLT VKEMVKDVLK GQNWLIYTYG VTNSGKTHTI QGTIKDGGIL   180
PRSLALIFNS LQGQLHPTPD LKPLLSNEVI WLDSKQIRQE EMKKLSLLNG GLQEEELSTS   240
LKRSVYIESR IGTSTSFDSG IAGLSSISQC TSSSQLDETS HRWAQPDTAP LPVPANIRFS   300
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IWISFFEIYN ELLYDLLEPP SQQRKRQTLR LCEDQNGNPY VKDLNWIHVQ DAEEAWKLLK   360
VGRKNQSFAS THLNQNSSRS HSIFSIRILH LQGEGDIVPK ISELSLCDLA GSERCKDQKS   420
GERLKEAGNI NTSLHTLGRC IAALRQNQQN RSKQNLVPFR DSKLTRVFQG FFTGRGRSCM   480
IVNVNPCAST YDETLHVAKF SAIASQVTCA CPTYATGIPI PALVHQGT
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Seq ID NO: 27 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 13-1424

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CTTCCCCTGA ACAGCTCTAC AAGCCTGGAA AAAAATAATG TGCTATTTGG TGAAAGATAC    120
TTAGAAAAAT TTTATGGCCT TGAGATAAAC AAACTTCCAG TGACAAAAAT GAAATATAGT    180
GGAAACTTAA TGAAGGAAAA AATCCAAGAA ATGCAGCACT TCTTGGGTCT GAAAGTGACC    240
GGGCAACTGG ACACATCTAC CCTGGAGATG ATGCACGCAC CTCGATGTGG AGTCCCCGAT    300
GTCCATCATT TCAGGGAAAT GCCAGGGGGG CCCGTATGGA GGAAACATTA TATCACCTAC    360
AGAATCAATA ATTACACACC TGACATGAAC CGTGAGGATG TTGACTACGC AATCCGGAAA    420
GCTTTCCAAG TATGGAGTAA TGTTACCCCC TTGAAATTCA GCAAGATTAA CACAGGCATG    480
GCTGACATTT TGGTGGTTTT TGCCCGTGGA GCTCATGGAG ACTTCCATGC TTTTGATGGC    540
AAAGGTGGAA TCCTAGCCCA TGCTTTTGGA CCTGGATCTG GCATTGGAGG GGATGCACAT    600
TTCGATGAGG ACGAATTCTG GACTACACAT TCAGGAGGCA CAAACTTGTT CCTCACTGCT    660
GTTCACGAGA TTGGCCATTC CTTAGGTCTT GGCCATTCTA GTGATCCAAA GGCCGTAATG    720
TTCCCCACCT ACAAATATGT TGACATCAAC ACATTTCGCC TCTCTGCTGA TGACATACGT    780
GGCATTCAGT CCCTGTATGG AGACCCAAAA GAGAACCAAC GCTTGCCAAA TCCTGACAAT    840
TCAGAACCAG CTCTCTGTGA CCCCAATTTG AGTTTTGATG CTGTCACTAC CGTGGGAAAT    900
AAGATCTTTT TCTTCAAAGA CAGGTTCTTC TGGCTGAAGG TTTCTGAGAG ACCAAAGACC    960
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GAAATTGAAG CCAGAAATCA AGTTTTTCTT TTTAAAGATG ACAAATACTG GTTAATTAGC   1080
AATTTAAGAC CAGAGCCAAA TTATCCCAAG AGCATACATT CTTTTGGTTT TCCTAACTTT   1140
GTGAAAAAAA TTGATGCAGC TGTTTTTAAC CCACGTTTTT ATAGGACCTA CTTCTTTGTA   1200
GATAACCAGT ATTGGAGGTA TGATGAAAGG AGACAGATGA TGGACCCTGG TTATCCCAAA   1260
CTGATTACCA AGAACTTCCA AGGAATCGGG CCTAAAATTG ATGCAGTCTT CTACTCTAAA   1320
AACAAATACT ACTATTTCTT CCAAGGATCT AACCAATTTG AATATGACTT CCTACTCCAA   1380
CGTATCACCA AAACACTGAA AAGCAATAGC TGGTTTGGTT GTTGAAAATG GTGTAATTAA   1440
TGGTTTTTGT TAGTTCACTT CAGCTTAATA AGTATTTATT GCATATTTGC TATGTCCTCA   1500
GTGTACCACT ACTTAGAGAT ATGTATCATA AAAATAAAAT CTGTAAACCA TAGGTAATGA   1560
TTATATAAAA TACATAATAT TTTTCAATTT TGAAAACTCT AATTGTCCAT TCTTGCTTGA   1620
CTCTACTATT AAGTTTGAAA ATAGTTACCT TCAAAGCAAG ATAATTCTAT TTGAAGCATG   1680
CTCTGTAAGT TGCTTCCTAA CATCCTTGGA CTGAGAAATT ATACTTACTT CTGGCATAAC   1740
TAAAATTAAG TATATATATT TTGGCTCAAA TAAAATTG
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Seq ID NO: 28 Protein sequence:
Protein Accession #: Eos sequence

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|          |          |          |          |          |
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KEKIQEMQHF LGLKVTGQLD TSTLEMMHAP RCGVPDVHHF REMPGGPVWR KHYITYRINN    120
YTPDMNREDV DYAIRKAFQV WSNVTPLKFS KINTGMADIL VVFARGAHGD FHAFDGKGGI    180
LAHAFGPGSG IGGDAHFDED EFWTTHSGGT NLFLTAVHEI GHSLGLGHSS DPKAVMFPTY    240
KYVDINTFRL SADDIRGIQS LYGDPKENQR LPNPDNSEPA LCDPNLSFDA VTTVGNKIFF    300
FKDRFFWLKV SERPKTSVNL ISSLWPTLPS GIEAAYEIEA RNQVFLFKDD KYWLISNLRP    360
EPNYPKSIHS FGFPNFVKKI DAAVFNPRFY RTYFFVDNQY WRYDERRQMM DPGYPKLITK    420
NFQGIGPKID AVFYSKNKYY YFFQGSNQFE YDFLLQRITK TLKSNSWFGC
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Seq ID NO: 29 DNA sequence
Nucleic Acid Accession #: NM_006115.1
Coding sequence: 236..1765

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CGGGACACCC CACCCGCTTC CCAGGCGTGA CCTGTCAACA GCAACTTCGC GGTGTGGTGA    120
ACTCTCTGAG GAAAAACCAT TTTGATTATT ACTCTCAGAC GTGCGTGGCA ACAAGTGACT    180
GAGACCTAGA AATCCAAGCG TTGGAGGTCC TGAGGCCAGC CTAAGTCGCT TCAAAATGGA    240
ACGAAGGCGT TTGTGGGGTT CCATTCAGAG CCGATACATC AGCATGAGTG TGTGGACAAG    300
CCCACGGAGA CTTGTGGAGC TGGCAGGGCA GAGCCTGCTG AAGGATGAGG CCCTGGCCAT    360
TGCCGCCCTG GAGTTGCTGC CCAGGGAGCT CTTCCCGCCA CTCTTCATGG CAGCCTTTGA    420
CGGGAGACAC AGCCAGACCC TGAAGGCAAT GGTGCAGGCC TGGCCCTTCA CCTGCCTCCC    480
TCTGGGAGTG CTGATGAAGG GACAACATCT TCACCTGGAG ACCTTCAAAG CTGTGCTTGA    540
TGGACTTGAT GTGCTCCTTG CCCAGGAGGT TCGCCCCAGG AGGTGGAAAC TTCAAGTGCT    600
GGATTTACGG AAGAACTCTC ATCAGGACTT CTGGACTGTA TGGTCTGGAA ACAGGGCCAG    660
TCTGTACTCA TTTCCAGAGC CAGAAGCAGC TCAGCCCATG ACAAAGAAGC GAAAAGTAGA    720
TGGTTTGAGC ACAGAGGCAG AGCAGCCCTT CATTCCAGTA GAGGTGCTCG TAGACCTGTT    780
CCTCAAGGAA GGTGCCTGTG ATGAATTGTT CTCCTACCTC ATTGAGAAAG TGAAGCGAAA    840
GAAAAATGTA CTACGCCTGT GCTGTAAGAA GCTGAAGATT TTTGCAATGC CCATGCAGGA    900
TATCAAGATG ATCCTGAAAA TGGTGCAGCT GGACTCTATT GAAGATTTGG AAGTGACTTG    960
TACCTGGAAG CTACCCACCT TGGCGAAATT TTCTCCTTAC CTGGGCCAGA TGATTAATCT   1020
GCGTAGACTC CTCCTCTCCC ACATCCATGC ATCTTCCTAC ATTTCCCCGG AGAAGGAAGA   1080
GCAGTATATC GCCCAGTTCA CCTCTCAGTT CCTCAGTCTG CAGTGCCTGC AGGCTCTCTA   1140
TGTGGACTCT TTATTTTTCC TTAGAGGCCG CCTGGATCAG TTGCTCAGGC ACGTGATGAA   1200
CCCCTTGGAA ACCCTCTCAA TAACTAACTG CCGGCTTTCG GAAGGGGATG TGATGCATCT   1260
GTCCCAGAGT CCCAGCGTCA GTCAGCTAAG TGTCCTGAGT CTAAGTGGGG TCATGCTGAC   1320
CGATGTAAGT CCCGAGCCCC TCCAAGCTCT GCTGGAGAGA GCCTCTGCCA CCCTCCAGGA   1380
CCTGGTCTTT GATGAGTGTG GGATCACGGA TGATCAGCTC CTTGCCCTCC TGCCTTCCCT   1440
GAGCCACTGC TCCCAGCTTA CAACCTTAAG CTTCTACGGG AATTCCATCT CCATATCTGC   1500
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CTTGCAGAGT CTCCTGCAGC ACCTCATCGG GCTGAGCAAT CTGACCCACG TGCTGTATCC  1560
TGTCCCCCTG GAGAGTTATG AGGACATCCA TGGTACCCTC CACCTGGAGA GGCTTGCCTA  1620
TCTGCATGCC AGGCTCAGGG AGTTGCTGTG TGAGTTGGGG CGGCCCAGCA TGGTCTGGCT  1680
TAGTGCCAAC CCCTGTCCTC ACTGTGGGGA CAGAACCTTC TATGACCCGG AGCCCATCCT  1740
GTGCCCCTGT TTCATGCCTA ACTAGCTGGG TGCACATATC AAATGCTTCA TTCTGCATAC  1800
TTGGACACTA AAGCCAGGAT GTGCATGCAT CTTGAAGCAA CAAAGCAGCC ACAGTTTCAG  1860
ACAAATGTTC AGTGTGAGTG AGGAAAACAT GTTCAGTGAG GAAAAAACAT TCAGACAAAT  1920
GTTCAGTGAG GAAAAAAAGG GGAAGTTGGG GATAGGCAGA TGTTGACTTG AGGAGTTAAT  1980
GTGATCTTTG GGGAGATACA TCTTATAGAG TTAGAAATAG AATCTGAATT TCTAAAGGGA  2040
GATTCTGGCT TGGGAAGTAC ATGTAGGAGT TAATCCCTGT GTAGACTGTT GTAAAGAAAC  2100
TGTTGAAAAT AAAGAGAAGC AATGTGAAGC AAAAAAAAAA AAAAAAAA
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Seq ID NO: 30 Protein sequence:
Protein Accession #: NP_006106.1

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CGGGACACCC CACCCGCTTC CCAGGCGTGA CCTGTCAACA GCAACTTCGC GGTGTGGTGA   120
ACTCTCTGAG GAAAAACCAT TTTGATTATT ACTCTCAGAC GTGCGTGGCA ACAAGTGACT   180
GAGACCTAGA AATCCAAGCG TTGGAGGTCC TGAGGCCAGC CTAAGTCGCT TCAAAATGGA   240
ACGAAGGCGT TTGTGGGGTT CCATTCAGAG CCGATACATC AGCATGAGTG TGTGGACAAG   300
CCCACGGAGA CTTGTGGAGC TGGCAGGGCA GAGCCTGCTG AAGGATGAGG CCCTGGCCAT   360
TGCCGCCCTG GAGTTGCTGC CCAGGGAGCT CTTCCCGCCA CTCTTCATGG CAGCCTTTGA   420
CGGGAGACAC AGCCAGACCC TGAAGGCAAT GGTGCAGGCC TGGCCCTTCA CCTGCCTCCC   480
TCTGGGAGTG CTGATGAAGG GACAACATCT TCACCTGGAG ACCTTCAAAG CTGTGCTTGA   540
TGGACTTGAT GTGCTCCTTG CCCAGGAGGT TCGCCCCAGG AGGTGGAAAC TTCAAGTGCT   600
GGATTTACGG AAGAACTCTC ATCAGGACTT CTGGACTGTA TGGTCTGGAA ACAGGGCCAG   660
TCTGTACTCA TTTCCAGAGC CAGAAGCAGC TCAGCCCATG ACAAAGAAGC GAAAAGTAGA   720
TGGTTTGAGC ACAGAGGCAG AGCAGCCCTT CATTCCAGTA GAGGTGCTCG TAGACCTGTT   780
CCTCAAGGAA GGTGCCTGTG ATGAATTGTT CTCCTACCTC ATTGAGAAAG TGAAGCGAAA   840
GAAAAATGTA CTACGCCTGT GCTGTAAGAA GCTGAAGATT TTTGCAATGC CCATGCAGGA   900
TATCAAGATG ATCCTGAAAA TGGTGCAGCT GGACTCTATT GAAGATTTGG AAGTGACTTG   960
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GCGTAGACTC CTCCTCTCCC ACATCCATGC ATCTTCCTAC ATTTCCCCGG AGAAGGAAGA  1080
GCAGTATATC GCCCAGTTCA CCTCTCAGTT CCTCAGTCTG CAGTGCCTGC AGGCTCTCTA  1140
TGTGGACTCT TTATTTTTCC TTAGAGGCCG CCTGGATCAG TTGCTCAGGC ACGTGATGAA  1200
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GTCCCAGAGT CCCAGCGTCA GTCAGCTAAG TGTCCTGAGT CTAAGTGGGG TCATGCTGAC  1320
CGATGTAAGT CCCGAGCCCC TCCAAGCTCT GCTGGAGAGA GCCTCTGCCA CCCTCCAGGA  1380
CCTGGTCTTT GATGAGTGTG GGATCACGGA TGATCAGCTC CTTGCCCTCC TGCCTTCCCT  1440
GAGCCACTGC TCCCAGCTTA CAACCTTAAG CTTCTACGGG AATTCCATCT CCATATCTGC  1500
CTTGCAGAGT CTCCTGCAGC ACCTCATCGG GCTGAGCAAT CTGACCCACG TGCTGTATCC  1560
TGTCCCCCTG GAGAGTTATG AGGACATCCA TGGTACCCTC CACCTGGAGA GGCTTGCCTA  1620
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TAGTGCCAAC CCCTGTCCTC ACTGTGGGGA CAGAACCTTC TATGACCCGG AGCCCATCCT  1740
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TTGGACACTA AAGCCAGGAT GTGCATGCAT CTTGAAGCAA CAAAGCAGCC ACAGTTTCAG  1860
ACAAATGTTC AGTGTGAGTG AGGAAAACAT GTTCAGTGAG GAAAAAACAT TCAGACAAAT  1920
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GTGATCTTTG GGGAGATACA TCTTATAGAG TTAGAAATAG AATCTGAATT TCTAAAGGGA  2040
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Seq ID NO: 31 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 64-2754

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CCGATGGCCG CCGCTGGGCC CCGGCGCTCC GTGCGCGGAG CCGTCTGCCT GCATCTGCTG   120
CTGACCCTCG TGATCTTCAG TCGTGATGGT GAAGCCTGCA AAAAGGTGAT ACTTAATGTA   180
CCTTCTAAAC TAGAGGCAGA CAAAATAATT GGCAGAGTTA ATTTGGAAGA GTGCTTCAGG   240
TCTGCAGACC TCATCCGGTC AAGTGATCCT GATTTCAGAG TTCTAAATGA TGGGTCAGTG   300
TACACAGCCA GGGCTGTTGC GCTGTCTGAT AAGAAAAGAT CATTTACCAT ATGGCTTTCT   360
GACAAAAGGA AACAGACACA GAAAGAGGTT ACTGTGCTGC TAGAACATCA GAAGAAGGTA   420
TCGAAGACAA GACACACTAG AGAAACTGTT CTCAGGCGTG CCAAGAGGAG ATGGGCACCT   480
ATTCCTTGCT CTATGCAAGA GAATTCCTTG GGCCCTTTCC CATTGTTTCT TCAACAAGTT   540
GAATCTGATG CAGCACAGAA CTATACTGTC TTCTACTCAA TAAGTGGACG TGGAGTTGAT   600
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CCTGTGGATC GTGAAGAATA TGATGTTTTT GATTTGATTG CTTATGCGTC AACTGCAGAT   720
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ACTACAGTGG GGGTGGTTTG TGCCACAGAC AGAGATGAAC CGGACACAAT GCATACGCGC   900
CTGAAATACA GCATTTTGCA GCAGACACCA AGGTCACCTG GGCTCTTTTC TGTGCATCCC   960
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TCATTGATAA TGAAAGTACA AGACATGGAT GGCCAGTTTT TTGGATTGAT AGGCACATCA  1080
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TATGAAGCAT TTGTAGAGGA AAATGCATTC AATGTGGAAA TCTTACGAAT ACCTATAGAA  1200
GATAAGGATT TAATTAACAC TGCCAATTGG AGAGTCAATT TTACCATTTT AAAGGGAAAT  1260
GAAAATGGAC ATTTCAAAAT CAGCACAGAC AAAGAAACTA ATGAAGGTGT TCTTTCTGTT  1320
GTAAAGCCAC TGAATTATGA AGAAAACCGT CAAGTGAACC TGGAAATTGG AGTAAACAAT  1380
GAAGCGCCAT TTGCTAGAGA TATTCCCAGA GTGACAGCCT TGAACAGAGC CTTGGTTACA  1440
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ATTAAAGAAA ACTTAGCAGT GGGGTCAAAG ATCAACGGCT ATAAGGCATA TGACCCCGAA  1560
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CCCAAAAATG AGTTGTATAA TATTACAGTC CTGGCAATAG ACAAAGATGA TAGATCATGT 1740
ACTGGAACAC TTGCTGTGAA CATTGAAGAT GTAAATGATA ATCCACCAGA AATACTTCAA 1800
GAATATGTAG TCATTTGCAA ACCAAAAATG GGGTATACCG ACATTTTAGC TGTTGATCCT 1860
GATGAACCTG TCCATGGAGC TCCATTTTAT TTCAGTTTGC CCAATACTTC TCCAGAAATC 1920
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GCAACAAAAT TATTGAGAGT TAATCTGTGT GAATGTACTC ATCCAACTCA GTGTCGTGCG 2100
ACTTCAAGGA GTACAGGAGT AATACTTGGA AAATGGGCAA TCCTTGCAAT ATTACTGGGT 2160
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GAAGACCGCA TGCCATCCCA AGATTATGTC CTCACTTATA ACTATGAGGG AAGAGGATCT 2640
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Protein Accession #: NP_001932.1

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Seq ID NO: 33 DNA sequence
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GAAGAAATTT CCTGAATCAG AAACAAAAGA ATGTCCTTTC AGACTCAACA AGACAGACAC  720
CAAACCAGTG CAGATGATGA ACATGGAGGC CACGTTCTGT ATGGGAAACA TTGACAGTAT  780
CAATTGTAAG ATCATAGAGC TTCCTTTTCA AAATAAGCAT CTCAGCATGT TCATCCTACT  840
ACCCAAGGAT GTGGAGGATG AGTCCACAGG CTTGGAGAAG ATTGAAAAAC AACTCAACTC  900
AGAGTCACTG TCACAGTGGA CTAATCCCAG CACCATGGCC AATGCCAAGG TCAAACTCTC  960
CATTCCAAAA TTTAAGGTGG AAAAGATGAT TGATCCCAAG GCTTGTCTGG AAAATCTAGG 1020
GCTGAAACAT ATCTTCAGTG AAGACACATC TGATTTCTCT GGAATGTCAG AGACCAAGGG 1080
AGTGGCCCTA TCAAATGTTA TCCACAAAGT GTGCTTAGAA ATAACTGAAG ATGGTGGGGA 1140
TTCCATAGAG GTGCCAGGAG CACGGATCCT GCAGCACAAG GATGAATTGA ATGCTGACCA 1200
TCCCTTTATT TACATCATCA GGCACAACAA AACTCGAAAC ATCATTTTCT TTGGCAAATT 1260
CTGTTCTCCT TAAGTGGCAT AGCCCATGTT AAGTCCTCCC TGACTTTTCT GTGGATGCCG 1320
ATTTCTGTAA ACTCTGCATC CAGAGATTCA TTTTCTAGAT ACAATAAATT GCTAATGTTG 1380
CTGGATCAGG AAGCCGCCAG TACTTGTCAT ATGTAGCCTT CACACAGATA GACCTTTTTT 1440
TTTTTCCAAT TCTATCTTTT GTTTCCTTTT TTCCCATAAG ACAATGACAT ACGCTTTTAA 1500
TGAAAAGGAA TCACGTTAGA GGAAAAATAT TTATTCATTA TTTGTCAAAT TGTCCGGGGT 1560
AGTTGGCAGA AATACAGTCT TCCACAAAGA AAATTCCTAT AAGGAAGATT TGGAAGCTCT 1620
TCTTCCCAGC ACTATGCTTT CCTTCTTTGG GATAGAGAAT GTTCCAGACA TTCTCGCTTC 1680
CCTGAAAGAC TGAAGAAAGT GTAGTGCATG GGACCCACGA AACTGCCCTG GCTCCAGTGA 1740
AACTTGGGCA CATGCTCAGG CTACTATAGG TCCAGAAGTC CTTATGTTAA GCCCTGGCAG 1800
GCAGGTGTTT ATTAAAATTC TGAATTTTGG GGATTTTCAA AAGATAATAT TTTACATACA 1860
CTGTATGTTA TAGAACTTCA TGGATCAGAT CTGGGGCAGC AACCTATAAA TCAACACCTT 1920
AATATGCTGC AACAAAATGT AGAATATTCA GACAAAATGG ATACATAAAG ACTAAGTAGC 1980
CCATAAGGGG TCAAAATTTG CTGCCAAATG CGTATGCCAC CAACTTACAA AAACACTTCG 2040
TTCGCAGAGC TTTTCAGATT GTGGAATGTT GGATAAGGAA TTATAGACCT CTAGTAGCTG 2100
AAATGCAAGA CCCCAAGAGG AAGTTCAGAT CTTAATATAA ATTCACTTTC ATTTTTGATA 2160
GCTGTCCCAT CTGGTCATGT GGTTGGCACT AGACTGGTGG CAGGGGCTTC TAGCTGACTC 2220
GCACAGGGAT TCTCACAATA GCCGATATCA GAATTTGTGT TGAAGGAACT TGTCTCTTCA 2280
TCTAATATGA TAGCGGGAAA AGGAGAGGAA ACTACTGCCT TTAGAAAATA TAAGTAAAGT 2340
GATTAAAGTG CTCACGTTAC CTTGACACAT AGTTTTTCAG TCTATGGGTT TAGTTACTTT 2400
AGATGGCAAG CATGTAACTT ATATTAATAG TAATTTGTAA AGTTGGGTGG ATAAGCTATC 2460
CCTGTTGCCG GTTCATGGAT TACTTCTCTA TAAAAAATAT ATATTTACCA AAAAATTTTG 2520
TGACATTCCT TCTCCCATCT CTTCCTTGAC ATGCATTGTA AATAGGTTCT TCTTGTTCTG 2580
AGATTCAATA TTGAATTTCT CCTATGCTAT TGACAATAAA ATATTATTGA ACTACC
```

Seq ID NO: 36 Protein sequence:
Protein Accession #: NP_002630.1

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1          11         21         31         41         51
|          |          |          |          |          |
MDALQLANSA FAVDLFKQLC EKEPLGNVLF SPICLSTSLS LAQVGAKGDT ANEIGQVLHF   60
ENVKDIPFGF QTVTSDVNKL SSFYSLKLIK RLYVDKSLNL STEFISSTKR PYAKELETVD  120
FKDKLEETKG QINNSIKDLT DGHFENILAD NSVNDQTKIL VVNAAYFVGK WMKKFPESET  180
KECPFRLNKT DTKPVQMMNM EATFCMGNID SINCKIIELP FQNKHLSMFI LLPKDVEDES  240
TGLEKIEKQL NSESLSQWTN PSTMANAKVK LSIPKFKVEK MIDPKACLEN LGLKHIFSED  300
TSDFSGMSET KGVALSNVIH KVCLEITEDG GDSIEVPGAR ILQHKDELNA DHPFIYIIRH  360
NKTRNIIFFG KFCSP
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Seq ID NO: 37 DNA sequence
Nucleic Acid Accession #: NM_0168583
Coding sequence: 72-842

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1          11         21         31         41         51
|          |          |          |          |          |
GGAGTGGGGG AGAGAGAGGA GACCAGGACA GCTGCTGAGA CCTCTAAGAA GTCCAGATAC   60
TAAGAGCAAA GATGTTTCAA ACTGGGGGCC TCATTGTCTT CTACGGGCTG TTAGCCCAGA  120
CCATGGCCCA GTTTGGAGGC CTGCCCGTGC CCCTGGACCA GACCCTGCCC TTGAATGTGA  180
ATCCAGCCCT GCCCTTGAGT CCCACAGGTC TTGCAGGAAG CTTGACAAAT GCCCTCAGCA  240
ATGGCCTGCT GTCTGGGGGC CTGTTGGGCA TTCTGGAAAA CCTTCCGCTC CTGGACATCC  300
TGAAGCCTGG AGGAGGTACT TCTGGTGGCC TCCTTGGGGG ACTGCTTGGA AAAGTGACGT  360
CAGTGATTCC TGGCCTGAAC AACATCATTG ACATAAAGGT CACTGACCCC CAGCTGCTGG  420
AACTTGGCCT TGTGCAGAGC CCTGATGGCC ACCGTCTCTA TGTCACCATC CCTCTCGGCA  480
TAAAGCTCCA AGTGAATACG CCCCTGGTCG GTGCAAGTCT GTTGAGGCTG GCTGTGAAGC  540
TGGACATCAC TGCAGAAATC TTAGCTGTGA GAGATAAGCA GGAGAGGATC CACCTGGTCC  600
TTGGTGACTG CACCCATTCC CCTGGAAGCC TGCAAATTTC TCTGCTTGAT GGACTTGGCC  660
CCCTCCCCAT TCAAGGTCTT CTGGACAGCC TCACAGGGAT CTTGAATAAA GTCCTGCCTG  720
AGTTGGTTCA GGGCAACGTG TGCCCTCTGG TCAATGAGGT TCTCAGAGGC TTGGACATCA  780
CCCTGGTGCA TGACATTGTT AACATGCTGA TCCACGGACT ACAGTTTGTC ATCAAGGTCT  840
AAGCCTTCCA GGAAGGGGCT GGCCTCTGCT GAGCTGCTTC CCAGTGCTCA CAGATGGCTG  900
GCCCATGTGC TGGAAGATGA CACAGTTGCC TTCTCTCCGA GGAACCTGCC CCCTCTCCTT  960
TCCCACCAGG CGTGTGTAAC ATCCCATGTG CCTCACCTAA TAAAATGGCT CTTCTTCTGC 1020
AAAAAAAAAA AAAAAAAAAA AAAAAAAAA
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Seq ID NO: 38 Protein sequence:
Protein Accession #: NP_057667

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1          11         21         31         41         51
|          |          |          |          |          |
MFQTGGLIVF YGLLAQTMAQ FGGLPVPLDQ TLPLNVNPAL PLSPTGLAGS LTNALSNGLL    60
SGGLLGILEN LPLLDILKPG GGTSGGLLGG LLGKVTSVIP GLNNIIDIKV TDPQLLELGL   120
VQSPDGHRLY VTIPLGIKLQ VNTPLVGASL LRLAVKLDIT AEILAVRDKQ ERIHLVLGDC   180
THSPGSLQIS LLDGLGPLPI QGLLDSLTGI LNKVLPELVQ GNVCPLVNEV LRGLDITLVH   240
DIVNMLIHGL QFVIKV
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Seq ID NO: 39 DNA sequence
Nucleic Acid Accession #: NM_004363.1
Coding sequence: 115-2223

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1          11         21         31         41         51
|          |          |          |          |          |
CTCAGGGCAG AGGGAGGAAG GACAGCAGAC CAGACAGTCA CAGCAGCCTT GACAAAACGT    60
TCCTGGAACT CAAGCTCTTC TCCACAGAGG AGGACAGAGC AGACAGCAGA GACCATGGAG   120
TCTCCCTCGG CCCCTCCCCA CAGATGGTGC ATCCCCTGGC AGAGGCTCCT GCTCACAGCC   180
TCACTTCTAA CCTTCTGGAA CCCGCCCACC ACTGCCAAGC TCACTATTGA ATCCACGCCG   240
TTCAATGTCG CAGAGGGGAA GGAGGTGCTT CTACTTGTCC ACAATCTGCC CCAGCATCTT   300
TTTGGCTACA GCTGGTACAA AGGTGAAAGA GTGGATGGCA ACCGTCAAAT TATAGGATAT   360
GTAATAGGAA CTCAACAAGC TACCCCAGGG CCCGCATACA GTGGTCGAGA GATAATATAC   420
CCCAATGCAT CCCTGCTGAT CCAGAACATC ATCCAGAATG ACACAGGATT CTACACCCTA   480
CACGTCATAA AGTCAGATCT TGTGAATGAA GAAGCAACTG GCCAGTTCCG GGTATACCCG   540
GAGCTGCCCA AGCCCTCCAT CTCCAGCAAC AACTCCAAAC CCGTGGAGGA CAAGGATGCT   600
GTGGCCTTCA CCTGTGAACC TGAGACTCAG GACGCAACCT ACCTGTGGTG GGTAAACAAT   660
CAGAGCCTCC CGGTCAGTCC CAGGCTGCAG CTGTCCAATG GCAACAGGAC CCTCACTCTA   720
TTCAATGTCA CAAGAAATGA CACAGCAAGC TACAAATGTG AAACCCAGAA CCCAGTGAGT   780
GCCAGGCGCA GTGATTCAGT CATCCTGAAT GTCCTCTATG GCCCGGATGC CCCCACCATT   840
TCCCCTCTAA ACACATCTTA CAGATCAGGG GAAAATCTGA ACCTCTCCTG CCACGCAGCC   900
TCTAACCCAC CTGCACAGTA CTCTTGGTTT GTCAATGGGA CTTTCCAGCA ATCCACCCAA   960
GAGCTCTTTA TCCCCAACAT CACTGTGAAT AATAGTGGAT CCTATACGTG CCAAGCCCAT  1020
AACTCAGACA CTGGCCTCAA TAGGACCACA GTCACGACGA TCACAGTCTA TGCAGAGCCA  1080
CCCAAACCCT TCATCACCAG CAACAACTCC AACCCCGTGG AGGATGAGGA TGCTGTAGCC  1140
TTAACCTGTG AACCTGAGAT TCAGAACACA ACCTACCTGT GGTGGGTAAA TAATCAGAGC  1200
CTCCCGGTCA GTCCCAGGCT GCAGCTGTCC AATGACAACA GGACCCTCAC TCTACTCAGT  1260
GTCACAAGGA ATGATGTAGG ACCCTATGAG TGTGGAATCC AGAACGAATT AAGTGTTGAC  1320
CACAGCGACC CAGTCATCCT GAATGTCCTC TATGGCCCAG ACGACCCCAC CATTTCCCCC  1380
TCATACACCT ATTACCGTCC AGGGGTGAAC CTCAGCCTCT CCTGCCATGC AGCCTCTAAC  1440
CCACCTGCAC AGTATTCTTG GCTGATTGAT GGGAACATCC AGCAACACAC ACAAGAGCTC  1500
TTTATCTCCA ACATCACTGA GAAGAACAGC GGACTCTATA CCTGCCAGGC CAATAACTCA  1560
GCCAGTGGCC ACAGCAGGAC TACAGTCAAG ACAATCACAG TCTCTGCGGA GCTGCCCAAG  1620
CCCTCCATCT CCAGCAACAA CTCCAAACCC GTGGAGGACA AGGATGCTGT GGCCTTCACC  1680
TGTGAACCTG AGGCTCAGAA CACAACCTAC CTGTGGTGGG TAAATGGTCA GAGCCTCCCA  1740
GTCAGTCCCA GGCTGCAGCT GTCCAATGGC AACAGGACCC TCACTCTATT CAATGTCACA  1800
AGAAATGACG CAAGAGCCTA TGTATGTGGA ATCCAGAACT CAGTGAGTGC AAACCGCAGT  1860
GACCCAGTCA CCCTGGATGT CCTCTATGGG CCGGACACCC CCATCATTTC CCCCCCAGAC  1920
TCGTCTTACC TTTCGGGAGC GAACCTCAAC CTCTCCTGCC ACTCGGCCTC TAACCCATCC  1980
CCGCAGTATT CTTGGCGTAT CAATGGGATA CCGCAGCAAC ACACACAAGT TCTCTTTATC  2040
GCCAAAATCA CGCCAAATAA TAACGGGACC TATGCCTGTT TTGTCTCTAA CTTGGCTACT  2100
GGCCGCAATA ATTCCATAGT CAAGAGCATC ACAGTCTCTG CATCTGGAAC TTCTCCTGGT  2160
CTCTCAGCTG GGGCCACTGT CGGCATCATG ATTGGAGTGC TGGTTGGGGT TGCTCTGATA  2220
TAGCAGCCCT GGTGTAGTTT CTTCATTTCA GGAAGACTGA CAGTTGTTTT GCTTCTTCCT  2280
TAAAGCATTT GCAACAGCTA CAGTCTAAAA TTGCTTCTTT ACCAAGGATA TTTACAGAAA  2340
AGACTCTGAC CAGAGATCGA GACCATCCTA GCCAACATCG TGAAACCCCA TCTCTACTAA  2400
AAATACAAAA ATGAGCTGGG CTTGGTGGCG CGCACCTGTA GTCCCAGTTA CTCGGGAGGC  2460
TGAGGCAGGA GAATCGCTTG AACCCGGGAG GTGGAGATTG CAGTGAGCCC AGATCGCACC  2520
ACTGCACTCC AGTCTGGCAA CAGAGCAAGA CTCCATCTCA AAAAGAAAAG AAAAGAAGAC  2580
TCTGACCTGT ACTCTTGAAT ACAAGTTTCT GATACCACTG CACTGTCTGA GAATTTCCAA  2640
AACTTTAATG AACTAACTGA CAGCTTCATG AAACTGTCCA CCAAGATCAA GCAGAGAAAA  2700
TAATTAATTT CATGGGACTA AATGAACTAA TGAGGATTGC TGATTCTTTA AATGTCTTGT  2760
TTCCCAGATT TCAGGAAACT TTTTTTCTTT TAAGCTATCC ACTCTTACAG CAATTTGATA  2820
AAATATACTT TTGTGAACAA AAATTGAGAC ATTTACATTT TCTCCCTATG TGGTCGCTCC  2880
AGACTTGGGA AACTATTCAT GAATATTTAT ATTGTATGGT AATATAGTTA TTGCACAAGT  2940
TCAATAAAAA TCTGCTCTTT GTATAACAGA AAAA
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Seq ID NO: 40 Protein sequence:
Protein Accession #: NP_004354.1

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1          11         21         31         41         51
|          |          |          |          |          |
MESPSAPPHR WCIPWQRLLL TASLLTFWNP PTTAKLTIES TPFNVAEGKE VLLLVHNLPQ    60
HLFGYSWYKG ERVDGNRQII GYVIGTQQAT PGPAYSGREI IYPNASLLIQ NIIQNDTGFY   120
TLHVIKSDLV NEEATGQFRV YPELPKPSIS SNNSKPVEDK DAVAFTCEPE TQDATYLWWV   180
NNQSLPVSPR LQLSNGNRTL TLFNVTRNDT ASYKCETQNP VSARRSDSVI LNVLYGPDAP   240
TISPLNTSYR SGENLNLSCH AASNPPAQYS WFVNGTFQQS TQELFIPNIT VNNSGSYTCQ   300
AHNSDTGLNR TTVTTITVYA EPPKPFITSN NSNPVEDEDA VALTCEPEIQ NTTYLWWVNN   360
QSLPVSPRLQ LSNDNRTLTL LSVTRNDVGP YECGIQNELS VDHSDPVILN VLYGPDDPTI   420
SPSYTYYRPG VNLSLSCHAA SNPPAQYSWL IDGNIQQHTQ ELFISNITEK NSGLYTCQAN   480
NSASGHSRTT VKTITVSAEL PKPSISSNNS KPVEDKDAVA FTCEPEAQNT TYLWWVNGQS   540
LPVSPRLQLS NGNRTLTLFN VTRNDARAYV CGIQNSVSAN RSDPVTLDVL YGPDTPIISP   600
PDSSYLSGAN LNLSCHSASN PSPQYSWRIN GIPQQHTQVL FIAKITPNNN GTYACFVSNL   660
ATGRNNSIVK SITVSASGTS PGLSAGATVG IMIGVLVGVA LI
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Seq ID NO: 41 DNA sequence
Nucleic Acid Accession #: NM_006952.1
Coding sequence: 11-793

1          11         21         31         41         51
|          |          |          |          |          |
AATCCCGACA ATGGCGAAAG ACAACTCAAC TGTTCGTTGC TTCCAGGGCC TGCTGATTTT    60
TGGAAATGTG ATTATTGGTT GTTGCGGCAT TGCCCTGACT GCGGAGTGCA TCTTCTTTGT   120
ATCTGACCAA CACAGCCTCT ACCCACTGCT TGAAGCCACC GACAACGATG ACATCTATGG   180
GGCTGCCTGG ATCGGCATAT TTGTGGGCAT CTGCCTCTTC TGCCTGTCTG TTCTAGGCAT   240
TGTAGGCATC ATGAAGTCCA GCAGGAAAAT TCTTCTGGCG TATTTCATTC TGATGTTTAT   300
AGTATATGCC TTTGAAGTGG CATCTTGTAT CACAGCAGCA ACACAACGAG ACTTTTTCAC   360
ACCCAACCTC TTCCTGAAGC AGATGCTAGA GAGGTACCAA AACAACAGCC CTCCAAACAA   420
TGATGACCAG TGGAAAAACA ATGGAGTCAC CAAAACCTGG GACAGGCTCA TGCTCCAGGA   480
CAATTGCTGT GGCGTAAATG GTCCATCAGA CTGGCAAAAA TACACATCTG CCTTCCGGAC   540
TGAGAATAAT GATGCTGACT ATCCCTGGCC TCGTCAATGC TGTGTTATGA ACAATCTTAA   600
AGAACCTCTC AACCTGGAGG CTTGTAAACT AGGCGTGCCT GGTTTTTATC ACAATCAGGG   660
CTGCTATGAA CTGATCTCTG GTCCAATGAA CCGACACGCC TGGGGGGTTG CCTGGTTTGG   720
ATTTGCCATT CTCTGCTGGA CTTTTTGGGT TCTCCTGGGT ACCATGTTCT ACTGGAGCAG   780
AATTGAATAT TAAGAA

Seq ID NO: 42 Protein sequence:
Protein Accession #: NP_008883.1

1          11         21         31         41         51
|          |          |          |          |          |
MAKDNSTVRC FQGLLIFGNV IIGCCGIALT AECIFFVSDQ HSLYPLLEAT DNDDIYGAAW    60
IGIFVGICLF CLSVLGIVGI MKSSRKILLA YFILMFIVYA FEVASCITAA TQRDFFTPNL   120
FLKQMLERYQ NNSPPNNDDQ WKNNGVTKTW DRLMLQDNCC GVNGPSDWQK YTSAFRTENN   180
DADYPWPRQC CVMNNLKEPL NLEACKLGVP GFYHNQGCYE LISGPMNRHA WGVAWFGFAI   240
LCWTFWVLLG TMFYWSRIEY

Seq ID NO: 43 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 83-2605

1          11         21         31         41         51
|          |          |          |          |          |
GCCGGACAGA TCTGCGCGTA TCCTGGAGCC GGCCCAGTTG TGAACTAGGA GAGCTTTGGG    60
ACCTCTGTCC CAAGCAAGAG AGATGAATGG AGAGTATAGA GGCAGAGGAT TTGGACGAGG   120
AAGATTTCAA AGCTGGAAAA GGGGAAGAGG TGGTGGGAAC TTCTCAGGAA AATGGAGAGA   180
AAGAGAACAC AGACCTGATC TGAGTAAAAC CACAGGAAAA CGTACTTCTG AACAAACCCC   240
ACAGTTTTTG CTTTCAACAA AGACCCCACA GTCAATGCAG TCAACATTGG ATCGATTCAT   300
ACCATATAAA GGCTGGAAGC TTTATTTCTC TGAAGTTTAC AGCGATAGCT CTCCTTTGAT   360
TGAGAAGATT CAAGCATTTG AAAAATTTTT CACAAGGCAT ATTGATTTGT ATGACAAGGA   420
TGAAATAGAA AGAAAGGGAA GTATTTTGGT AGATTTTAAA GAACTGACAG AAGGTGGTGA   480
AGTAACTAAC TTGATACCAG ATATAGCAAC TGAACTAAGA GATGCACCTG AGAAAACCTT   540
GGCTTGCATG GGTTTGGCAA TACATCAGGT GTTAACTAAG GACCTTGAAA GGCATGCAGC   600
TGAGTTACAA GCCCAGGAAG GATTGTCTAA TGATGGAGAA ACAATGGTAA ATGTGCCACA   660
TATTCATGCA AGGGTGTACA ACTATGAGCC TTTGACACAG CTCAAGAATG TCAGAGCAAA   720
TTACTATGGA AAATACATTG CTCTAAGAGG GACAGTGGTT CGTGTCAGTA ATATAAAGCC   780
TCTTTGCACC AAGATGGCTT TTCTTTGTGC TGCATGTGGA GAAATTCAGA GCTTTCCTCT   840
TCCAGATGGA AAATACAGTC TTCCCACAAA GTGTCCTGTG CCTGTGTGTC GAGGCAGGTC   900
ATTTACTGCT CTCCGCAGCT CTCCTCTCAC AGTTACGATG GACTGGCAGT CAATCAAAAT   960
CCAGGAATTG ATGTCTGATG ATCAGAGAGA AGCAGGTCGG ATTCCACGAA CAATAGAATG  1020
TGAGCTTGTT CATGATCTTG TGGATAGCTG TGTCCCGGGA GACACAGTGA CTATTACTGG  1080
AATTGTCAAA GTCTCAAATG CGGAAGAAGG TTCTCGAAAT AAGAATGACA AGTGTATGTT  1140
CCTTTTGTAT ATTGAAGCAA ATTCTATTAG TAATAGCAAA GGACAGAAAA CAAAGAGTTC  1200
TGAGGATGGG TGTAAGCATG GAATGTTGAT GGAGTTCTCA CTTAAAGACC TTTATGCCAT  1260
CCAAGAGATT CAAGCTGAAG AAAACCTGTT TAAACTCATT GTCAACTCGC TTTGCCCTGT  1320
CATTTTTGGT CATGAACTTG TTAAAGCAGG TTTGGCATTA GCACTCTTTG GAGGAAGCCA  1380
GAAATACGCA GATGACAAAA ACAGAATTCC AATTCGGGGA GACCCCCACA TCCTTGTTGT  1440
TGGAGATCCA GGCCTAGGAA AAAGTCAAAT GCTACAGGCA GCGTGCAATG TTGCCCCACG  1500
TGGCGTGTAT GTTTGTGGTA ACACCACGAC CACCTCTGGT CTGACGGTAA CTCTTTCAAA  1560
AGATAGTTCC TCTGGAGATT TTGCTTTGGA AGCTGGTGCC CTGGTACTTG GTGATCAAGG  1620
TATTTGTGGA ATCGATGAAT TTGATAAGAT GGGGAATCAA CATCAAGCCT TGTTGGAAGC  1680
CATGGAGCAG CAAAGTATTA GTCTTGCTAA GGCTGGTGTG GTTTGTAGCC TTCCTGCAAG  1740
AACTTCCATT ATTGCTGCTG CAAATCCAGT TGGAGGACAT TACAATAAAG CCAAAACAGT  1800
TTCTGAGAAT TTAAAAATGG GGAGTGCACT ACTATCCAGA TTTGATTTGG TCTTTATCCT  1860
GTTAGATACT CCAAATGAGC ATCATGATCA CTTACTCTCT GAACATGTGA TTGCAATAAG  1920
AGCTGGAAAG CAGAGAACCA TTAGCAGTGC CACAGTAGCT CGTATGAATA GTCAAGATTC  1980
AAATACTTCC GTACTTGAAG TAGTTTCTGA GAAGCCATTA TCAGAAAGAC TAAAGGTGGT  2040
TCCTGGAGAA ACAATAGATC CCATTCCCCA CCAGCTATTG AGAAAGTACA TTGGCTATGC  2100
TCGGCAGTAT GTGTACCCAA GGCTATCCAC AGAAGCTGCT CGAGTTCTTC AAGATTTTTA  2160
CCTTGAGCTC CGGAAACAGA GCCAGAGGTT AAATAGCTCA CCAATCACTA CCAGGCAGCT  2220
GGAATCTTTG ATTCGTCTGA CAGAGGCACG AGCAAGGTTG GAATTGAGAG AGGAAGCAAC  2280
CAAAGAAGAC GCTGAGGATA TAGTGGAAAT TATGAAATAT AGCATGCTAG GAACTTACTC  2340
TGATGAATTT GGGAACCTAG ATTTTGAGCG ATCCCAGCAT GGTTCTGGAA TGAGCAACAG  2400
GTCAACAGCG AAAAGATTTA TTTCTGCTCT CAACAACGTT GCTGAAAGAA CTTATAATAA  2460
TATATTTCAA TTTCATCAAC TTCGGCAGAT TGCCAAAGAA CTAAACATTC AGGTTGCTGA  2520
TTTTGAAAAT TTTATTGGAT CACTAAATGA CCAGGGTTAC CTCTTGAAAA AAGGCCCAAA  2580
AGTTTACCAG CTTCAAACTA TGTAAAAGGA CTTCACCAAG TTAGGGCCTC CTGGGTTTAT  2640
TGCAGATTAA AGCCATCTCA GTGAAGATAT GCGTGCACGC ACAGACAGAC AGACACACAC  2700
ACACACACAC ACACACACAC ACACACACAC ACACACAGTC AAATACTGTT CTCTGAAAAA  2760
TGATGTCCCA AAAGTATTAT AATAGGAAAA AAGCATTAAA TATAATAAAC TAATTTAAGA  2820
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AGTGATAAAG TCTCCAGATG CAGTAGCTCA CACTGTAATC ACAGTGACTC AGGAGGCTGA  2880
GGTGAGAGGA TTCCTTGAGG CCAGGGTTCG AGACCAACCT TGGGCAACAT AGCAAGACCC  2940
CATTTCTTAA AAAAAAAAAA AAAAAATTTA AACTTAGCTG GGTATGGTGG CACATGCCTA  3000
TAGTCTCAGC TACTTGTGAG GCTGAGGCAG GAGGATTCTT TGAGCCCAGG AGTTTGAGGT  3060
TACAGTGAGC CACAATCACA CCAATCACTG CACTCCAGCC TGGGCAATAA AGTAACTCTT  3120
GACTCAAAAA AATAAAAAAA ATTGTAGTGG TAGCCATGTG TTAATTGTTA AATAAATTCT  3180
CCAAAGGGCT AAAAGTAAAT TACTTATAAA TTTTTTATAG TTGTATTTTT GACCTGCCTT  3240
TTATATGTAT GAATATTTCA TAGTTTTGCA TATCAGATGT AGGCATACAG ACAAATACAT  3300
AAACCAATGA ATATATTACA TATTCTGTGT TCCAATAAAA CTTTATTTAT GGACACTAAA  3360
ATTTGAATTT CATAAAATTT TCCCATGTCA AGAATACAAA ATACTTGAGT TTTGTTTTTA  3420
GCTATTTAAT AATAGGTCTC ATTTATTCCA CAGGCTGTAG TTTGTAGTCT TGCTTGAAAC  3480
AATAGAAACA GACTGATTAA GCAGGAGAAG TTTTTTGAAA GAATTTTGTT TGGCTCACGG  3540
AATTATTAGA AGGCAGGTGA ACCAGGAGGG TAAGCTTCCA GCAGCAATTT GTAAAACCAT  3600
GCCTTAGAAT TGGACTAAGG AAGAAGCTGC TGACACTCCA CTGCCACACA GGGCACTGGA  3660
AGAAAGTGCT GCTGCCTCCC TGCCCCACCT TTGCCACTTC TGCAGCAGGA ATAGGTAGAA  3720
GAATGCCCCC ACCCGCACCG GAACAGCAAC AAAAGGATTC TGCATGAGAT GCCTCCCTAA  3780
ATTGCTGAAT TCAAAAAAGA AGTTGCATAC AAAGACATCT GATTGAAAAA GGGTATGTTA  3840
TATGCCCCTT TCATAGGCTG CTAGGGAGTT TTCCTGGTTC TACTTTCAGG TGGTGGGATC  3900
AATAAGACCA GAATTTCTCA TATGTTGTGA GAGGATTCAA ATGTTACAGG GTTGCCAGCC  3960
AAACTATCAA TCATGTATAA ATCCAACAAA CACTTTGTAA CATACAAGAA CTCAGGAAAT  4020
GTGAACCATT GTTGGAGAAT CTACTAAAAT ACGGCTTCCC GCAAACGAAG ATGAATGGAA  4080
AATGTAAATA AAAAGAACTG GCAGTGTATA TCAGATGTTT AACTATAGGA CCAGAACTAA  4140
GATGTGGAGA CTATTGCCAT AGACCACAAT GTAAATTTTT AAGTGAGGAA GGAAAAATCA  4200
GGAATCAAAA GGGGCCAGGT GCAGTGGCTC ACATCTATAA TCCCAGAGCT TTGGGAGTTC  4260
GAGGCAGGAG GATCACTTGA AGCCAGTTTT GAGACCAGCC TATGCAACAC ATTGAGACCC  4320
TATCTCTACA AAAAATAGAT TAGCTGGGCA CGGTGGTGCA TGCCTATTGT CCTACCTACT  4380
GTGGAGGCTG AAGTAGGAAA TCACTTGAGC CCGAGAGTTT GAGGTTACAG TGAGCTATGA  4440
TTATACCACT GCACTCCAGC CTGGGCAAGA GAGCAAGACC TTGTCTCTT
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Seq ID NO: 44 Protein sequence:
Protein Accession #: CAB55276.2

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1          11         21         31         41         51
|          |          |          |          |          |
MNGEYRGRGF GRGRFQSWKR GRGGGNFSGK WREREHRPDL SKTTGKRTSE QTPQFLLSTK    60
TPQSMQSTLD RFIPYKGWKL YPSEVYSDSS PLIEKIQAFE KFFTRHIDLY DKDEIERKGS   120
ILVDFKELTE GGEVTNLIPD IATELRDAPE KTLACMGLAI HQVLTKDLER HAAELQAQEG   180
LSNDGETMVN VPHIHARVYN YEPLTQLKNV RANYYGKYIA LRGTVVRVSN IKPLCTKMAF   240
LCAACGEIQS FPLPDGKYSL PTKCPVPVCR GRSFTALRSS PLTVTMDWQS IKIQELMSDD   300
QREAGRIPRT IECELVHDLV DSCVPGDTVT ITGIVKVSNA EEGSRNKNDK CMFLLYIEAN   360
SISNSKGQKT KSSEDGCKHG MLMEFSLKDL YAIQEIQAEE NLFKLIVNSL CPVIFGHELV   420
KAGLALALFG GSQKYADDKN RIPIRGDPHI LVVGDPGLGK SQMLQAACNV APRGVYVCGN   480
TTTTSGLTVT LSKDSSSGDF ALEAGALVLG DQGICGIDEF DKMGNQHQAL LEAMEQQSIS   540
LAKAGVVCSL PARTSIIAAA NPVGGHYNKA KTVSENLKMG SALLSRFDLV FILLDTPNEH   600
HDHLLSEHVI AIRAGKQRTI SSATVARMNS QDSNTSVLEV VSEKPLSERL KVVPGETIDP   660
IPHQLLRKYI GYARQYVYPR LSTEAARVLQ DFYLELRKQS QRLNSSPITT RQLESLIRLT   720
EARARLELRE EATKEDAEDI VEIMKYSMLG TYSDEFGNLD FERSQHGSGM SNRSTAKRFI   780
SALNNVAERT YNNIFQFHQL RQIAKELNIQ VADFENFIGS LNDQGYLLKK GPKVYQLQTM
```

Seq ID NO: 45 DNA sequence
Nucleic Acid Accession #: NM_005416.1
Coding sequence: 149..658

```
1          11         21         31         41         51
|          |          |          |          |          |
ACCAGATCCC AGAGGCTGAA CACCTCGACC TTCTCTGCAC AGCAGATGAT CCCTGAGCAG    60
CTGAAGACCA GAAAAGCCAC TAAGACTTTC TGCTTAATTC AGGAGCTTAG AGGATTCTTC   120
AAAGAGTGTG TCCACGATCC TTTGAAGCAT GAGTTCTTAC CAGCAGAAGC AGACCTTTAC   180
CCCACCACCT CAGCTTCAAC AGCAGCAGGT GAAACAACCC AGCCAGCCTC CACCTCAGGA   240
AATATTTGTT CCCACAACCA AGGAGCCATG CCACTCAAAG GTTCCACAAC CTGGAAACAC   300
AAAGATTCCA GAGCCAGGCT GTACCAAGGT CCCTGAGCCA GGCTGTACCA AGGTCCCTGA   360
GCCAGGCTGT ACCAAGGTCC CTGAGCCAGG TTGTACCAAG GTCCCTGAGC CAGGCTGTAC   420
CAAGGTCCCT GAGCCAGGTT GTACCAAGGT CCCTGAGCCA GGCTACACCA AGGTCCCTGA   480
ACCAGGCAGC ATCAAGGTCC CTGACCAAGG CTTCATCAAG TTTCCTGAGC CAGGTGCCAT   540
CAAAGTTCCT GAGCAAGGAT ACACCAAAGT TCCTGTGCCA GGCTACACAA AGCTACCAGA   600
GCCATGTCCT TCAACGGTCA CTCCAGGCCC AGCTCAGCAG AAGACCAAGC AGAAGTAATT   660
TGGTGCACAG ACAAGCCCTT GAGAAGCCAA CCACCAGATG CTGGACACCC TCTTCCCATC   720
TGTTTCTGTG TCTTAATTGT CTGTAGACCT TGTAATCAGC ACATTGTCAC CCCAAGCCAT   780
AGTCTCTCTC TTATTTGTAT CCTAAAAATA CGTACTATAA AGCTTTTGTT CACACACACT   840
CTGAAGAATC CTGTAAGCCC CTGAATTAAG CAGAAAGTCT TCATGGCTTT TCTGGTCTTC   900
GGCTGCTCAG GGTTCATCTG AAGATTCGAA TGAAAAGAAA TGCATGTTTC CTGCTCTTCC   960
CTCATTAAAT TGCTTTTAAT TCCA
```

Seq ID NO: 46 Protein sequence:
Protein Accession #: NP_005407.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MSSYQQKQTF TPPPQLQQQQ VKQPSQPPPQ EIFVPTTKEP CHSKVPQPGN TKIPEPGCTK    60
VPEPGCTKVP EPGCTKVPEP GCTKVPEPGC TKVPEPGCTK VPEPGYTKVP EPGSIKVPDQ   120
GFIKFPEPGA IKVPEQGYTK VPVPGYTKLP EPCPSTVTPG PAQQKTKQK
```

Seq ID NO: 47 DNA sequence
Nucleic Acid Accession #: Eos sequence

```
1          11         21         31         41         51
|          |          |          |          |          |
GCGTCGTGTG CAGGCGTCCC CGGGCTGTGG ATAATTAGAC ACGTTCTTCC CTCATTGCCC    60
AAGGCTCGTT AGAATTCGCC CTAGAGCTGT ATCATGTATT TTCTTTCAAA TTAACTTTGC   120
TTGCAATTAA GCTTAGGGAA CCAGCAACAA AAGCAAACTT GGCCCGAGGT CGTTCACCGC   180
GAAAATGGAT TAGAGAAACT TCTTCCCCGA TTTAAGGGGA AAGATTCCTG CGGCCAGCGC   240
TTTGGGGAAA GTGCCCCGAC CGCAGAGGCG ACGACAGGGG AGCAGGAAGC TGCTCACGGT   300
AGTCGGCGTT GGCGGCAGCG GTGGCCTTCC TCATCTGGGC GATGTGGGCT CCTAGAAGAG   360
TAAGGATAAC ATCCTGGAAA TGACTTCTGT ACGGTTTGAG CCCAACTGCA CACTCATGAC   420
TTGGAGCTGC CCTGTGGAGT TACAGTTTAC CAAACACATT CATGAACATA ATCTCATTTA   480
CTAAAAACTT TGTGAGAATT TTCTTTTACT AAAATTTTTT CTTATTACAA A
```

Seq ID NO: 48 DNA sequence:
Nucleic Acid Accession #: CAT cluster

```
1          11         21         31         41         51
|          |          |          |          |          |
TTCCAAATTT TTTTTTTTGT AATAAGAAAA AATTTTAGTA AAAGAAAATT CTCACAAAGT    60
TTTTAGTAAA TGAGATTATG TTCATGAATG TGTTTGGTAA ACTGTAACTC CACAGGGCAG   120
CTCCAAGTCA TGAGTGTGCA GTTGGGCTCA AACCGTACAG AAGTCATTTC CAGGATGTTA   180
TCCTTACTCT TCTCGGAGCC CACATCGCCC AGATGAGGAA GGCCACCGCT GCCGCCAACG   240
CCGACTACCG TGAGCAGCTT CCTGCTCCCC TGTCGTCGCC TCTGCGGTCG GGGCACTTTC   300
CCCAAAGCGC TGGCCGCAGG AATCTTTCCC CTTAAATCGG GGAAGAAGTT TCTCTAATCC   360
ATTTTCGCGG TGAACGACCT CGGGCCAAGT TTGCTTTTGT TGCTGGTTCC CTAAGCTTAA   420
TTGCAAGCAA AGTTAATTTG AAAGAAAATA CATGATACAG CTCTAGGGCG AATTCTAACG   480
AGCCTTGGGC AATGAGGGAA GAACGTGTCT AGTTATCCAC AGCCCGGGGA CGCCTGCACA   540
CGACGCT
```

Seq ID NO: 49 DNA sequence
Nucleic Acid Accession #: CAT cluster

```
1          11         21         31         41         51
|          |          |          |          |          |
TCTTTCTTCT GCTGCTCGTT TGTCTCTCCT GTGCTCTTCT TCTTTCTTTC CCTCGCCGCT    60
CCTGCCGACC TCTGTTGTCT CTTCTCTGAT GGCGGGGGGC GGGAGAAGCT GACCGGTGAG   120
ACCGTAGACC CGAAACCATT GGGTGTCACA AGCCGGTCGC CGGCTTTTTT GGGAGAACCC   180
GACACATGCA GACCAGTTTT CCTGGAACNG CATGACCATG TTATTACTAT GGGCCGCCTC   240
CCCAACCAAA GTGTTTAAAA CTTTTTAGGG CACCCCCAAA ATTTTTTTTT TTTTTTTTTT   300
TTCATTTAAA AAACTCTAAT ATTTATATTA AATACAAAGA TACCCAAACC CTTTATGCTT   360
CTTTCTCTGA TCTGTGTCTT TTTTCTTTGA CAGCATCTCC ATTTTTTTTC TGCTGCTTCA   420
TCGCTGTAGC CATGGGAATC CGTTTCATTA TTATGGTAGC AATATGGAGT GCTGTATTCC   480
TAAAGAAACT GACACAGGAG AATCACTTGA ACTTGGGAGG CAGAGTTTGC AGTGAGCCGA   540
GATTGAACCA GTGCACTCCA GCCTTGGCAG CGGAGCAAGA TTCTGTCACA GTTCCTGAAG   600
TGCTGGTATC GTCCTGCAGC CCCATCCTCG GTTCCATTGC GCTGCCAGGC AGGGTGCTGG   660
GACGTGGGGA GAGCTGGTCT ATATATCCGG GTGAAGCTCA GCTGTGGCAC ACCTTGGATG   720
CCGGGTCTCT CCTGGCCCCG GGGACCTAGT ATTTTTGCCA CGAGTGTACA CCAAACAAAG   780
GAGACAGCAT CATTTATGAG CCTGCAGCAT CCACCCTACT GCTGTATCCA GTTTCCATTG   840
ACTG
```

Seq ID NO: 50 DNA sequence
Nucleic Acid Accession #: L05187
Coding sequence: 1991..2260

```
1          11         21         31         41         51
|          |          |          |          |          |
CTGCAGGGAG GCAGGTAGAA AAGGCTTTTG GGTTTTCAGG TGGGGGGCAG TCTAGCCTGA    60
TCAGAAAGGA GGAAAAGGCC AGGGCAGATG TCTGGGTGGA GTGAAGGGAA AAAGTGATCC   120
CAGAAGAAGG ATTAGCCCCT GAAAGTCCCT GAAGTAGGAG AAGGGTAAAG GTGTGGTTGG   180
TGAAGGAAAG CAGGTTTTCC CAGATTAGCA ACCAGTCAGG GGGAGGAAGG TGAGAGTGGG   240
AGAGTCATAA GTAAATTATT CTGAATGTGT GTAGTTTAAT GGAATTGGGA AAAAGATGGG   300
GGAAATGGAT GGAAGGTCTT GGACTCTGAG ACAAGGGGTC TATAATCAGT CCATTTCATT   360
ATTTCTAGCT TCCACCTTCA CCAAGGCAGA CAAGGAGGGC CCACCTCAGC TCCTCTGCTC   420
CCCCTCCCTT TCCCACCTAT TCATGTGTGC AAGAGTGCCC TGTCCCACAG AACACGGGGA   480
ACAACCATCT CAATGACAAG GACAGCAGGT GGCAAGGCTC AACAGGACTC AGATGTCCCC   540
CCAGGGTTAA CTCATGAAAC CCTCCATGAA GCCTGCTGCT CACCCCTCCC TCAAGGCAAG   600
CCCTGCACCT GGGTCTGAGG ATGAGGGTGG CAGTGAAAAT TAGGCCAGTG ACATCATTTT   660
CAGCCAGCTA GTGCCAAAAA ATATCAGGTG GTGTTCATCA AATAAGCCGA GCCAACCGGT   720
GATGAGGATG GTAGTGTGAG TCATGTGTGA CAGGTGAGGA ATGAAAACAG AGTGCCCGAG   780
AGCTTCTATT TCCTTGAGGC AGGGCTCATT CATCTTATAA AAGCCAGCTG GCCATTGCCT   840
TCACACCAAA CCCAAGGGAC CACACAGCCC ATTCTGCTCC GTATACCAGG TAAGTCTCTG   900
ATTGCAACAA ACTGGCAATT CTAGTGTACT TTTTCATTAT TAGAAATTAG CTAAAGGCAA   960
ATATGTGTAA GCAGGTTAAT CCAGGGTTTC AATGGGAGAT AGAGAATAGT GGAATATCTT  1020
TATTTTAAGT TAAATTACAG TCTGGATTTG AAAGGACCTT AGAGATGGTT AGGGCTCCCA  1080
CCTCAGTAGA TAGTCATTGA ACTGGGAGTC CTGGAGAAGA TTGTTCAAAT GCCCATGGGA  1140
AGTTCATAGC AGAACTAGAA CTCAGGCCAG AGCACTCTCA GTAACACTGC AATTTCCCCC  1200
TGACAAGATA TTTATAGAAA TTTTAATTTA TTAGATGGAT CTCTACTGAG CATTTATTCC  1260
ATTTAAGGCA GTATGCTAGG CACTTTGGAC AAATCAATGC CCTAACGTAC TTACTTAACA  1320
AACATAAAAC CTAGCAGGAA GGTAATACAT ATATATAAAT AAATGAAATG CAAAGTAGAT  1380
AGTAATTGGC ATGACGGAGA TGGGCAGAGA AGGGCTGTGC ACTTTTGGGA GACTTGCTCA  1440
AGGAGACCTC TAGGGTGTCA AGTGATGTGA GCTATGATGG AGGGGTATTT GGACAAGCAG  1500
AGATGGGAAG AAAAGCATTT GGAAGGGACT GTGTAAGCAC AGACCAGAAG CAAAACCATA  1560
GAGGCTTAGA TGAATATAAA GCCATCCTAT AAGTCACAGG CTTTCTACAT GGTACTAGGA  1620
GAGGAAAGTG GTCTGATGCC ATTTTCCAAA AGACCTAATA TGCGGACCTC ATGTCCCTCA  1680
GAAGCCAGCT TTAGTAGGGC ATTTTTCCAG AACAGATATA AGGTGCCTTG GGTAGGAAGG  1740
GAGCCAAGAA GAGAACTCCA ATAAAATGGA GCAGAAGAAA TTGCCTTTTA GCTCCTCCTC  1800
TTCAAAGGGC CTGAAAATTA TCCAAGCTTA TTTCATTTTT AAATGTAATG GGGGAGCTAA  1860
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GGGAGATGAA AGGCTTTCTC TTCTAAAGGG TCCTGAAATA AAATCTGTTT GGCATTGAAT  1920
TTGTATCCAT CTTTCTTTAA TTGAATCACT GTGTCAGCTT TCTGTCTCTA GAAAAAAACA  1980
CATTTGAAGC ATGAATTCTC AGCAGCAGAA GCAGCCTTGC ACCCCACCCC CTCAGCCTCA  2040
GCAGCAGCAG GTGAAACAAC CTTGCCAGCC TCCACCCCAG GAACCATGCA TCCCCAAAAC  2100
CAAGGAGCCC TGCCAACCCA AGGTGCCTGA GCCCTGCCAC CCCAAAGTGC CTGAGCCCTG  2160
CCAGCCCAAG ATTCCAGAGC CCTGCCAGCC CAAGGTGCCT GAGCCCTGCC CTTCAACGGT  2220
CACTCCAGCA CCAGCCCAGC AGAAGACCAA GCAGAAGTAA TGTGGTCCAC AGCCATGCCC  2280
TTGAGGAGCT GGCCACTGGA TACTGAACAC CCTACTCCAT TCTGCTTATG AATCCCATTT  2340
GCCTATTGAC CCTGCAGTTA GCATGCTGTC ACCCTGAATC ATAATCGCTC CTTTGCACCT  2400
CTAAAAAGAT GTCCCTTACC CTCATTCTGG AGGCTCCTGA GCCTCTGCGT AAGGCTGAAC  2460
GTCTCACTGA CTGAGCTAGT CTTCTTGTTG CTCGGGTGCA TTTGAGGATG GATTTGGGGA  2520
AGGTCAAGTG ACCATCCCTA G
```

Seq ID NO: 51 Protein sequence:
Protein Accession #:AAC26838

```
1          11         21         31         41         51
|          |          |          |          |          |
MNSQQQKQPC TPPPQPQQQQ VKQPCQPPPQ EPCIPKTKEP CQPKVPEPCH PKVPEPCQPK    60
IPEPCQPKVP EPCPSTVTPA PAQQKTKQK
```

Seq ID NO: 52 DNA sequence
Nucleic Acid Accession #: NM_002638.1
Coding sequence: 120-473

```
1          11         21         31         41         51
|          |          |          |          |          |
CAATACAGCT AAGGAATTAT CCCTTGTAAA TACCACAGAC CCGCCCTGGA GCCAGGCCAA    60
GCTGGACTGC ATAAAGATTG GTATGGCCTT AGCTCTTAGC CAAACACCTT CCTGACACCA   120
TGAGGGCCAG CAGCTTCTTG ATCGTGGTGG TGTTCCTCAT CGCTGGGACG CTGGTTCTAG   180
AGGCAGCTGT CACGGGAGTT CCTGTTAAAG GTCAAGACAC TGTCAAAGGC CGTGTTCCAT   240
TCAATGGACA AGATCCCGTT AAAGGACAAG TTTCAGTTAA AGGTCAAGAT AAAGTCAAAG   300
CGCAAGAGCC AGTCAAAGGT CCAGTCTCCA CTAAGCCTGG CTCCTGCCCC ATTATCTTGA   360
TCCGGTGCGC CATGTTGAAT CCCCCTAACC GCTGCTTGAA AGATACTGAC TGCCCAGGAA   420
TCAAGAAGTG CTGTGAAGGC TCTTGCGGGA TGGCCTGTTT CGTTCCCCAG TGAAGGGAGC   480
CGGTCCTTGC TGCACCTGTG CCGTCCCCAG AGCTACAGGC CCCATCTGGT CCTAAGTCCC   540
TGCTGCCCTT CCCCTTCCCA CACTGTCCAT TCTTCCTCCC ATTCAGGATG CCCACGGCTG   600
GAGCTGCCTC TCTCATCCAC TTTCCAATAA A
```

Seq ID NO: 53 Protein sequence:
Protein Accession #: NP_002629.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MRASSFLIVV VFLIAGTLVL EAAVTGVPVK GQDTVKGRVP FNGQDPVKGQ VSVKGQDKVK    60
AQEPVKGPVS TKPGSCPIIL IRCAMLNPPN RCLKDTDCPG IKKCCEGSCG MACFVPQ
```

Seq ID NO: 54 DNA sequence
Nucleic Acid Accession #: NM_019618
Coding sequence: 75-584

```
1          11         21         31         41         51
|          |          |          |          |          |
GGCACGAGCC ACGATTCAGT CCCCTGGACT GTAGATAAAG ACCCTTTCTT GCCAGGTGCT    60
GAGACAACCA CACTATGAGA GGCACTCCAG GAGACGCTGA TGGTGGAGGA AGGGCCGTCT   120
ATCAATCAAT GTGTAAACCT ATTACTGGGA CTATTAATGA TTTGAATCAG CAAGTGTGGA   180
CCCTTCAGGG TCAGAACCTT GTGGCAGTTC CACGAAGTGA CAGTGTGACC CCAGTCACTG   240
TTGCTGTTAT CACATGCAAG TATCCAGAGG CTCTTGAGCA AGGCAGAGGG GATCCCATTT   300
ATTTGGGAAT CCAGAATCCA GAAATGTGTT TGTATTGTGA GAAGGTTGGA GAACAGCCCA   360
CATTGCAGCT AAAAGAGCAG AAGATCATGG ATCTGTATGG CCAACCCGAG CCCGTGAAAC   420
CCTTCCTTTT CTACCGTGCC AAGACTGGTA GGACCTCCAC CCTTGAGTCT GTGGCCTTCC   480
CGGACTGGTT CATTGCCTCC TCCAAGAGAG ACCAGCCCAT CATTCTGACT TCAGAACTTG   540
GGAAGTCATA CAACACTGCC TTTGAATTAA ATATAAATGA CTGAACTCAG CCTAGAGGTG   600
GCAGCTTGGT CTTTGTCTTA AAGTTTCTGG TTCCCAATGT GTTTTCGTCT ACATTTTCTT   660
AGTGTCATTT TCACGCTGGT GCTGAGACAG GGGCAAGGCT GCTGTTATCA TCTCATTTTA   720
TAATGAAGAA GAAGCAATTA CTTCATAGCA ACTGAAGAAC AGGATGTGGC CTCAGAAGCA   780
GGAGAGCTGG GTGGTATAAG GCTGTCCTCT CAAGCTGGTG CTGTGTAGGC CACAAGGCAT   840
CTGCATGAGT GACTTTAAGA CTCAAAGACC AAACACTGAG CTTTCTTCTA GGGGTGGGTA   900
TGAAGATGCT TCAGAGCTCA TGCGCGTTAC CCACGATGGC ATGACTAGCA CAGAGCTGAT   960
CTCTGTTTCT GTTTTGCTTT ATTCCCTCTT GGGATGATAT CATCCAGTCT TTATATGTTG  1020
CCAATATACC TCATTGTGTG TAATAGAACC TTCTTAGCAT TAAGACCTTG TAAACAAAAA  1080
TAATTCTTGT GTTAAGTTAA ATCATTTTTG TCCTAATTGT AATGTGTAAT CTTAAAGTTA  1140
AATAAACTTT GTGTATTTAT ATAATAAAAA AAAAAAAAAA AAA
```

Seq ID NO: 55 Protein sequence:
Protein Accession #: NP_062564

```
1          11         21         31         41         51
|          |          |          |          |          |
MRGTPGDADG GGRAVYQSMC KPITGTINDL NQQVWTLQGQ NLVAVPRSDS VTPVTVAVIT    60
CKYPEALEQG RGDPIYLGIQ NPEMCLYCEK VGEQPTLQLK EQKIMDLYGQ PEPVKPFLFY   120
RAKTGRTSTL ESVAFPDWFI ASSKRDQPII LTSELGKSYN TAFELNIND
```

Seq ID NO: 56 DNA sequence
Nucleic Acid Accession #: NM_003125
Coding sequence: 65-334

```
1          11         21         31         41         51
|          |          |          |          |          |
AGCAGTTCTA AGGGACCATA CAGAGTATTC CTCTCTTCAC ACCAGGACCA GCCACTGTTG   60
CAGCATGAGT TCCCAGCAGC AGAAGCAGCC CTGCATCCCA CCCCCTCAGC TTCAGCAGCA  120
GCAGGTGAAA CAGCCTTGCC AGCCTCCACC TCAGGAACCA TGCATCCCCA AAACCAAGGA  180
GCCCTGCCAC CCCAAGGTGC CTGAGCCCTG CCACCCCAAA GTGCCTGAGC CCTGCCAGCC  240
CAAGCTTCCA GAGCCATGCC ACCCCAAGGT GCCTGAGCCC TGCCCTTCAA TAGTCACTCC  300
AGCACCAGCC CAGCAGAAGA CCAAGCAGAA GTAATGTGGT CCACAGCCAT GCCCTTGAGG  360
AGCCGGCCAC CAGATGCTGA ATCCCCTATC CCATTCTGTG TATGAGTCCC ATTTGCCTTG  420
CAATTAGCAT TCTGTCTCCC CCAAAAAAGA ATGTGCTATG AAGCTTTCTT TCCTACACAC  480
TCTGAGTCTC TGAATGAAGC TGAAGGTCTT AGTACCAGAG CTAGTTTTCA GCTGCTCAGA  540
ATTCATCTGA AGAGAGACTT AAGATGAAAG CAAATGATTC AGCTCCCTTA TACCCCCATT  600
AAATTCACTT TCAATTCCA
```

Seq ID NO: 57 Protein sequence:
Protein Accession #: NP_003116

```
1          11         21         31         41         51
|          |          |          |          |          |
MSSQQQKQPC IPPPQLQQQQ VKQPCQPPPQ EPCIPKTKEP CHPKVPEPCH PKVPEPCQPK   60
LPEPCHPKVP EPCPSIVTPA PAQQKTKQK
```

Seq ID NO: 58 DNA sequence
Nucleic Acid Accession #: NM_001793.2
Coding sequence: 71-2560

```
1          11         21         31         41         51
|          |          |          |          |          |
AAAGGGGCAA GAGCTGAGCG GAACACCGGC CCGCCGTCGC GGCAGCTGCT TCACCCCTCT   60
CTCTGCAGCC ATGGGGCTCC CTCGTGGACC TCTCGCGTCT CTCCTCCTTC TCCAGGTTTG  120
CTGGCTGCAG TGCGCGGCCT CCGAGCCGTG CCGGGCGGTC TTCAGGGAGG CTGAAGTGAC  180
CTTGGAGGCG GGAGGCGCGG AGCAGGAGCC CGGCCAGGCG CTGGGGAAAG TATTCATGGG  240
CTGCCCTGGG CAAGAGCCAG CTCTGTTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA  300
TGGCGAGACA GTCCAGGAAA GAAGGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC  360
ATCCAAACGT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCCAA TATCTGTCCC  420
TGAAAATGGC AAGGGTCCCT TCCCCCAGAG ACTGAATCAG CTCAAGTCTA ATAAAGATAG  480
AGACACCAAG ATTTTCTACA GCATCACGGG GCCGGGGGCA GACAGCCCCC CTGAGGGTGT  540
CTTCGCTGTA GAGAAGGAGA CAGGCTGGTT GTTGTTGAAT AAGCCACTGG ACCGGGAGGA  600
GATTGCCAAG TATGAGCTCT TTGGCCACGC TGTGTCAGAG AATGGTGCCT CAGTGGAGGA  660
CCCCATGAAC ATCTCCATCA TCGTGACCGA CCAGAATGAC CACAAGCCCA AGTTTACCCA  720
GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCCTACCA GGTACTTCTG TGATGCAGGT  780
GACAGCCACG GATGAGGATG ATGCCATCTA CACCTACAAT GGGGTGGTTG CTTACTCCAT  840
CCATAGCCAA GAACCAAAGG ACCCACACGA CCTCATGTTC ACCATTCACC GGAGCACAGG  900
CACCATCAGC GTCATCTCCA GTGGCCTGGA CCGGGAAAAA GTCCCTGAGT ACACACTGAC  960
CATCCAGGCC ACAGACATGG ATGGGGACGG CTCCACCACC ACGGCAGTGG CAGTAGTGGA 1020
GATCCTTGAT GCCAATGACA ATGCTCCCAT GTTTGACCCC CAGAAGTACG AGGCCCATGT 1080
GCCTGAGAAT GCAGTGGGCC ATGAGGTGCA GAGGCTGACG GTCACTGATC TGGACGCCCC 1140
CAACTCACCA GCGTGGCGTG CCACCTACCT TATCATGGGC GGTGACGACG GGGACCATTT 1200
TACCATCACC ACCCACCCTG AGAGCAACCA GGGCATCCTG ACAACCAGGA AGGGTTTGGA 1260
TTTTGAGGCC AAAAACCAGC ACACCCTGTA CGTTGAAGTG ACCAACGAGG CCCCTTTTGT 1320
GCTGAAGCTC CCAACCTCCA CAGCCACCAT AGTGGTCCAC GTGGAGGATG TGAATGAGGC 1380
ACCTGTGTTT GTCCCACCCT CCAAAGTCGT TGAGGTCCAG GAGGGCATCC CCACTGGGGA 1440
GCCTGTGTGT GTCTACACTG CAGAAGACCC TGACAAGGAG AATCAAAAGA TCAGCTACCG 1500
CATCCTGAGA GACCCAGCAG GGTGGCTAGC CATGGACCCA GACAGTGGGC AGGTCACAGC 1560
TGTGGGCACC CTCGACCGTG AGGATGAGCA GTTTGTGAGG AACAACATCT ATGAAGTCAT 1620
GGTCTTGGCC ATGGACAATG GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGCTAAC 1680
ACTGATTGAT GTCAATGACC ATGGCCCAGT CCCTGAGCCC CGTCAGATCA CCATCTGCAA 1740
CCAAAGCCCT GTGCGCCAGG TGCTGAACAT CACGGACAAG GACCTGTCTC CCCACACCTC 1800
CCCTTTCCAG GCCCAGCTCA CAGATGACTC AGACATCTAC TGGACGGCAG AGGTCAACGA 1860
GGAAGGTGAC ACAGTGGTCT TGTCCCTGAA GAAGTTCCTG AAGCAGGATA CATATGACGT 1920
GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT 1980
GTGCGACTGC CATGGCCATG TCGAAACCTG CCCTGGACCC TGGAAGGGAG GTTTCATCCT 2040
CCCTGTGCTG GGGGCTGTCC TGGCTCTGCT GTTCCTCCTG CTGGTGCTGC TTTTGTTGGT 2100
GAGAAAGAAG CGGAAGATCA AGGAGCCCCT CCTACTCCCA GAAGATGACA CCCGTGACAA 2160
CGTCTTCTAC TATGGCGAAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCACCCA 2220
GCTCCACCGA GGTCTGGAGG CCAGGCCGGA GGTGGTTCTC CGCAATGACG TGGCACCAAC 2280
CATCATCCCG ACACCCATGT ACCGTCCTCG GCCAGCCAAC CCAGATGAAA TCGGCAACTT 2340
TATAATTGAG AACCTGAAGG CGGCTAACAC AGACCCCACA GCCCCGCCCT ACGACACCCT 2400
CTTGGTGTTC GACTATGAGG GCAGCGGCTC CGACGCCGCG TCCCTGAGCT CCCTCACCTC 2460
CTCCGCCTCC GACCAAGACC AAGATTACGA TTATCTGAAC GAGTGGGGCA GCCGCTTCAA 2520
GAAGCTGGCA GACATGTACG GTGGCGGGGA GGACGACTAG GCGGCCTGCC TGCAGGGCTG 2580
GGGACCAAAC GTCAGGCCAC AGAGCATCTC CAAGGGGTCT CAGTTCCCCC TTCAGCTGAG 2640
GACTTCGGAG CTTGTCAGGA AGTGGCCGTA GCAACTTGGC GGAGACAGGC TATGAGTCTG 2700
ACGTTAGAGT GGTTGCTTCC TTAGCCTTTC AGGATGGAGG AATGTGGGCA GTTTGACTTC 2760
AGCACTGAAA ACCTCTCCAC CTGGGCCAGG GTTGCCTCAG AGGCCAAGTT TCCAGAAGCC 2820
TCTTACCTGC CGTAAAATGC TCAACCCTGT GTCCTGGGCC TGGGCCTGCT GTGACTGACC 2880
TACAGTGGAC TTTCTCTCTG GAATGGAACC TTCTTAGGCC TCCTGGTGCA ACTTAATTTT 2940
TTTTTTTAAT GCTATCTTCA AAACGTTAGA GAAAGTTCTT CAAAAGTGCA GCCCAGAGCT 3000
GCTGGGCCCA CTGGCCGTCC TGCATTTCTG GTTTCCAGAC CCCAATGCCT CCCATTCGGA 3060
TGGATCTCTG CGTTTTTATA CTGAGTGTGC CTAGGTTGCC CCTTATTTTT TATTTTCCCT 3120
GTTGCGTTGC TATAGATGAA GGGTGAGGAC AATCGTGTAT ATGTACTAGA ACTTTTTTAT 3180
TAAAGAAACT TTTCCCAGAA AAAAA
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Seq ID NO: 59 Protein sequence:

Protein Accession #: NP_001784.2

```
1          11         21         31         41         51
|          |          |          |          |          |
MGLPRGPLAS LLLLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVFMGCPG   60
QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG  120
KGPFPQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLLLN KPLDREEIAK  180
YELFGHAVSE NGASVEDPMN ISIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT  240
DEDDAIYTYN GVVAYSIHSQ EPKDPHDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA  300
TDMDGDGSTT TAVAVVEILD ANDNAPMFDP QKYEAHVPEN AVGHEVQRLT VTDLDAPNSP  360
AWRATYLIMG GDDGDHFTIT THPESNQGIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL  420
PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR  480
DPAGWLAMDP DSGQVTAVGT LDREDEQFVR NNIYEVMVLA MDNGSPPTTG TGTLLLTLID  540
VNDHGPVPEP RQITICNQSP VRQVLNITDK DLSPHTSPFQ AQLTDDSDIY WTAEVNEEGD  600
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Seq ID NO: 60 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 162-428

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Seq ID NO: 61 Protein sequence:
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CCAAAGTGCC CAGAGCCATG TCCACCCCCG AAGTGCCCTG AGCCCTGCCC ACCACCAAAG   120
TGTCCACAGC CCTGCCCACC TCAGCAGTGC CAGCAGAAAT ATCCTCCTGT GACACCTTCC   180
CCACCCTGCC AGCCAAAGTA TCCACCGAAG AGCAAGTAA
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Seq ID NO: 65 Protein sequence:
Protein Accession #: NP_008876

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1          11         21         31         41         51
|          |          |          |          |          |
MSYQQQCKQ PCQPPPVCPT PKCPEPCPPP KCPEPCPPPK CPQPCPPQQC QQKYPPVTPS    60
PPCQPKYPPK SK
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Seq ID NO: 66 DNA sequence
Nucleic Acid Accession #: NM_005629.1
Coding sequence: 639-2546

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1          11         21         31         41         51
|          |          |          |          |          |
TAGTCGGAGC GAGGTGGCGA GTCGCTGAGC CCGCCGCGGC CCCGAGAGCG GCTGCAGCCG    60
CCGCCGCCGG GAAGGAGAGG GCGAGGCGCG CCCGAGCCGC CGCCGCCGCC GCCACCGCCG   120
CCGCCGCCAC CACCGCCACC GGAGTCGCGG GCCAGCCGGG CAGCCTCCGC GGGCCCCGGC   180
CGGGGCGGGG GGCGCGGGCC ACAGGCCCCT GCTCCGGCCG TCGTTTGCAG ACCGCGGGCG   240
CCGATGTCGC CCGCGCCCCG TTAGGATGAG TCTCGGGTCG GGCGAGGAGC CGCCGCAGCC   300
GCCGCCGCCC GAGCCGCGGG CAGGAGCCTC GGGAGCCGCC GCCGCCGCCG CCGCCGCCCG   360
GCCGGGCCCC GACGCCGCCC GCGCGCCCCC GGGCCCCCGA CACACATGAG ATTCTTCAGG   420
CTCACTTTCA AGTGCTTCGT GGACTGCTTC TGACTGCGCC GCCCGCGCCC CGCACCCCGC   480
CGTCCGCCCG CCGCCCCGTC CCCCGGCCCG GCCGCCCCCC GGCCCCCGGC CGGCCCGCGC   540
CCTCGGGGCC CTCCCCGGTG CCGCCGGTGC CCCCCGCCTG ACCGCCGCCC CCCGTGAGGC   600
GCCGCGACCC CGGCCCGGCC GTGCGGCCCG CCGGGGCCAT GGCGAAGAAG AGCGCCGAGA   660
ACGGCATCTA TAGCGTGTCC GGCGACGAGA AGAAGGGCCC CCTCATCGCG CCCGGGCCCG   720
ACGGGGCCCC GGCCAAGGGC GACGGCCCCG TGGGCCTGGG GACACCCGGC GGCCGCCTGG   780
CCGTGCCGCC GCGCGAGACC TGGACGCGCC AGATGGACTT CATCATGTCG TGCGTGGGCT   840
TCGCCGTGGG CTTGGGCAAC GTGTGGCGCT TCCCCTACCT GTGCTACAAG AACGGCGGAG   900
GTGTGTTCCT TATTCCCTAC GTCCTGATCG CCCTGGTTGG AGGAATCCCC ATTTTCTTCT   960
TAGAGATCTC GCTGGGCCAG TTCATGAAGG CCGGCAGCAT CAATGTCTGG AACATCTGTC  1020
CCCTGTTCAA AGGCCTGGGC TACGCCTCCA TGGTGATCGT CTTCTACTGC AACACCTACT  1080
ACATCATGGT GCTGGCCTGG GGCTTCTATT ACCTGGTCAA GTCCTTTACC ACCACGCTGC  1140
CCTGGGCCAC ATGTGGCCAC ACCTGGAACA CTCCCGACTG CGTGGAGATC TTCCGCCATG  1200
AAGACTGTGC CAATGCCAGC CTGGCCAACC TCACCTGTGA CCAGCTTGCT GACCGCCGGT  1260
CCCCTGTCAT CGAGTTCTGG GAGAACAAAG TCTTGAGGCT GTCTGGGGGA CTGGAGGTGC  1320
CAGGGGCCCT CAACTGGGAG GTGACCCTTT GTCTGCTGGC CTGCTGGGTG CTGGTCTACT  1380
TCTGTGTCTG GAAGGGGGTC AAATCCACGG GAAAGATCGT GTACTTCACT GCTACATTCC  1440
CCTACGTGGT CCTGGTCGTG CTGCTGGTGC GTGGAGTGCT GCTGCCTGGC GCCCTGGATG  1500
GCATCATTTA CTATCTCAAG CCTGACTGGT CAAAGCTGGG GTCCCCTCAG GTGTGGATAG  1560
ATGCGGGGAC CCAGATTTTC TTTTCTTACG CCATTGGCCT GGGGGCCCTC ACAGCCCTGG  1620
GCAGCTACAA CCGCTTCAAC AACAACTGCT ACAAGGACGC CATCATCCTG GCTCTCATCA  1680
ACAGTGGGAC CAGCTTCTTT GCTGGCTTCG TGGTCTTCTC CATCCTGGGC TTCATGGCTG  1740
CAGAGCAGGG CGTGCACATC TCCAAGGTGG CAGAGTCAGG GCCGGGCCTG GCCTTCATCG  1800
CCTACCCGCG GGCTGTCACG CTGATGCCAG TGGCCCCACT CTGGGCTGCC CTGTTCTTCT  1860
TCATGCTGTT GCTGCTTGGT CTCGACAGCC AGTTTGTAGG TGTGGAGGGC TTCATCACCG  1920
GCCTCCTCGA CCTCCTCCCG GCCTCCTACT ACTTCCGTTT CCAAAGGGAG ATCTCTGTGG  1980
CCCTCTGTTG TGCCCTCTGC TTTGTCATCG ATCTCTCCAT GGTGACTGAT GGCGGGATGT  2040
ACGTCTTCCA GCTGTTTGAC TACTACTCGG CCAGCGGCAC CACCCTGCTC TGGCAGGCCT  2100
TTTGGGAGTG CGTGGTGGTG GCCTGGGTGT ACGGAGCTGA CCGCTTCATG GACGACATTG  2160
CCTGTATGAT CGGGTACCGA CCTTGCCCCT GGATGAAATG GTGCTGGTCC TTCTTCACCC  2220
CGCTGGTCTG CATGGGCATC TTCATCTTCA ACGTTGTGTA CTACGAGCCG CTGGTCTACA  2280
ACAACACCTA CGTGTACCCG TGGTGGGGTG AGGCCATGGG CTGGGCCTTC GCCCTGTCCT  2340
CCATGCTGTG CGTGCCGCTG CACCTCCTGG GCTGCCTCCT CAGGGCCAAG GGCACCATGG  2400
CTGAGCGCTG GCAGCACCTG ACCCAGCCCA TCTGGGGCCT CCACCACTTG GAGTACCGAG  2460
CTCAGGACGC AGATGTCAGG GGCCTGACCA CCCTGACCCC AGTGTCCGAG AGCAGCAAGG  2520
TCGTCGTGGT GGAGAGTGTC ATGTGACAAC TCAGCTCACA TCACCAGCTC ACCTCTGGTA  2580
GCCATAGCAG CCCCTGCTTC AGCCCCACCG CACCCCTCCA GGGGGCCTGC CTTTCCCTGA  2640
CACTTTTGGG GTCTGCCTGG GGGAGGAGGG GAGAAAGCAC CATGAGTGCT CACTAAAACA  2700
ACTTTTTCCA TTTTTAATAA AACGCCAAAA ATATCACAAC CCACCAAAAA TAGATGCCTC  2760
TCCCCCTCCA GCCCTAGCCG AGCTGGTCCT AGGCCCCGCC TAGTGCCCCA CCCCCACCCA  2820
CAGTGCTGCA CTCCTCCTGC CCCTGCCACG CCCACCCCCT GCCCACCTCT CCAGGCTCTG  2880
CTCTGCAGCA CACCCGTGGG TGACCCCTCA CCCCAGAAGC AGCAGTGGCA GCTTGGGAAA  2940
TGTGAGGAAG GGAAGGAGGG AGAGACGGGA GGGAGGAGAG AGAGGAGAAG GGAGGCAGGG  3000
GAGGGGCAGC AGAACCAAGG CAAATATTTC AGCTGGGCTA TACCCCTCTC CCCATCCCTG  3060
TTATAGAAGC TTAGAGAGCC AGCCAGCAAT GGAACCTTCT GGTTCCTGCG CCAATCGCCA  3120
CCAGTATCAA TTGTGTGAGC TTGGGTGCGA GTGCACGCGT GCGTGAGTAC GGAGAGTATA  3180
TATAGATCTC TATCTCTTAG CAAAGGTGAA TGCCAGATGT AAATGGCGCC TCTGGGCAAA  3240
GGAGGCTTGT ATTTTGCACA TTTTATAAAA ACTTGAGAGA ATGAGATTTC TGCTTGTATA  3300
TTTCTAAAAA GAGGAAGGAG CCCAAACCAT CCTCTCCTTA CCACTCCCAT CCCTGTGAGC  3360
CCTACCTTAC CCCTCTGCCC CTAGCCAAGG AGTGTGAATT TATAGATCTA ACTTTCATAG  3420
GCAAAACAAA AGCTTCGAGC TGTTGCGTGT GTGAGTCTGT TGTGTGGATG TGCGTGTGTG  3480
GTCCCCAGCC CCAGACTGGA TTGGAAAAGT GCATGGTGGG GGCCTCGGGG CTGTCCCCAC  3540
GCTGTCCCTT TGCCACAAGT CTGTGGGGCA AGAGGCTGCA ATATTCCGTC CTGGGTGTCT  3600
GGGCTGCTAA CCTGGCCTGC TCAGGCTTCC CACCCTGTGC GGGGCACACC CCCAGGAAGG  3660
GACCCTGGAC ACGGCTCCCA CGTCCAGGCT TAAGGTGGAT GCACTTCCCG CACCTCCAGT  3720
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CTTCTGTGTA GCAGCTTTAA CCCACGTTTG TCTGTCACGT CCAGTCCCGA GACGGCTGAG  3780
TGACCCCAAG AAAGGCTTCC CCGACACCCA GACAGAGGCT GCAGGGCTGG GGCTGGGTGA  3840
GGGTGGCGGG CCTGCGGGGA CATTCTACTG TGCTAAAAAG CCACTGCAGA CATAGCAATA  3900
AAAACATGTC ATTTTCC
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Seq ID NO: 67 Protein sequence:
Protein Accession #: NP_005620.1

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1          11         21         31         41         51
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MAKKSAENGI YSVSGDEKKG PLIAPGPDGA PAKGDGPVGL GTPGGRLAVP PRETWTRQMD   60
FIMSCVGFAV GLGNVWRFPY LCYKNGGGVF LIPYVLIALV GGIPIFFLEI SLGQFMKAGS  120
INVWNICPLF KGLGYASMVI VFYCNTYYIM VLAWGFYYLV KSFTTTLPWA TCGHTWNTPD  180
CVEIFRHEDC ANASLANLTC DQLADRRSPV IEFWENKVLR LSGGLEVPGA LNWEVTLCLL  240
ACWVLVYFCV WKGVKSTGKI VYFTATFPYV VLVVLLVRGV LLPGALDGII YYLKPDWSKL  300
GSPQVWIDAG TQIFFSYAIG LGALTALGSY NRFNNNCYKD AIILALINSG TSFFAGFVVF  360
SILGFMAAEQ GVHISKVAES GPGLAFIAYP RAVTLMPVAP LWAALFFFML LLLGLDSQFV  420
GVEGFITGLL DLLPASYYFR FQREISVALC CALCFVIDLS MVTDGGMYVF QLFDYYSASG  480
TTLLWQAFWE CVVVAWVYGA DRFMDDIACM IGYRPCPWMK WCWSFFTPLV CMGIFIFNVV  540
YYEPLVYNNT YVYPWWGEAM GWAFALSSML CVPLHLLGCL LRAKGTMAER WQHLTQPIWG  600
LHHLEYRAQD ADVRGLTTLT PVSESSKVVV VESVM
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Seq ID NO: 68 DNA sequence
Nucleic Acid Accession #: NM_021953.1
Coding sequence: 178-2469

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1          11         21         31         41         51
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CCAGGTTGGA GGAGCCCGGA GCCCGCCTTC GGAGCTACGG CCTAACGGCG GCGGCGACTG   120
CAGTCTGGAG GGTCCACACT TGTGATTCTC AATGGAGAGT GAAAACGCAG ATTCATAATG   180
AAAGCTAGCC CCCGTCGGCC ACTGATTCTC AAAAGACGGA GGCTGCCCCT TCCTGTTCAA   240
AATGCCCCAA GTGAAACATC AGAGGAGGAA CCTAAGAGAT CCCCTGCCCA ACAGGAGTCT   300
AATCAAGCAG AGGCCTCCAA GGAAGTGGCG GAGTCCAACT CTTGCAAGTT TCCAGCTGGG   360
ATCAAGATTA TTAACCACCC CACCATGCCC AACACGCAAG TAGTGGCCAT CCCCAACAAT   420
GCTAATATTC ACAGCATCAT CACAGCACTG ACTGCCAAGG GAAAAGAGAG TGGCAGTAGT   480
GGGCCCAACA AATTCATCCT CATCAGCTGT GGGGGAGCCC CAACTCAGCC TCCAGGACTC   540
CGGCCTCAAA CCCAAACCAG CTATGATGCC AAAAGGACAG AAGTGACCCT GGAGACCTTG   600
GGACCAAAAC CTGCAGCTAG GGATGTGAAT CTTCCTAGAC CACCTGGAGC CCTTTGCGAG   660
CAGAAACGGG AGACCTGTGC AGATGGTGAG GCAGCAGGCT GCACTATCAA CAATAGCCTA   720
TCCAACATCC AGTGGCTTCG AAAGATGAGT TCTGATGGAC TGGGCTCCCG CAGCATCAAG   780
CAAGAGATGG AGGAAAAGGA GAATTGTCAC CTGGAGCAGC GACAGGTTAA GGTTGAGGAG   840
CCTTCGAGAC CATCAGCGTC CTGGCAGAAC TCTGTGTCTG AGCGGCCACC CTACTCTTAC   900
ATGGCCATGA TACAATTCGC CATCAACAGC ACTGAGAGGA AGCGCATGAC TTTGAAAGAC   960
ATCTATACGT GGATTGAGGA CCACTTTCCC TACTTTAAGC ACATTGCCAA GCCAGGCTGG  1020
AAGAACTCCA TCCGCCACAA CCTTTCCCTG CACGACATGT TTGTCCGGGA GACGTCTGCC  1080
AATGGCAAGG TCTCCTTCTG GACCATTCAC CCCAGTGCCA ACCGCTACTT GACATTGGAC  1140
CAGGTGTTTA AGCCACTGGA CCCAGGGTCT CCACAATTGC CCGAGCACTT GGAATCACAG  1200
CAGAAACGAC CGAATCCAGA GCTCCGCCGG AACATGACCA TCAAAACCGA ACTCCCCCTG  1260
GGCGCACGGC GGAAGATGAA GCCACTGCTA CCACGGGTCA GCTCATACCT GGTACCTATC  1320
CAGTTCCCGG TGAACCAGTC ACTGGTGTTG CAGCCCTCGG TGAAGGTGCC ATTGCCCCTG  1380
GCGGCTTCCC TCATGAGCTC AGAGCTTGCC CGCCATAGCA AGCGAGTCCG CATTGCCCCC  1440
AAGGTGCTGC TAGCTGAGGA GGGGATAGCT CCTCTTTCTT CTGCAGGACC AGGGAAAGAG  1500
GAGAAACTCC TGTTTGGAGA AGGGTTTTCT CCTTTGCTTC CAGTTCAGAC TATCAAGGAG  1560
GAAGAAATCC AGCCTGGGGA GGAAATGCCA CACTTAGCGA GACCCATCAA AGTGGAGAGC  1620
CCTCCCTTGG AAGAGTGGCC CTCCCCGGCC CCATCTTTCA AAGAGGAATC ATCTCACTCC  1680
TGGGAGGATT CGTCCCAATC TCCCACCCCA AGACCCAAGA AGTCCTACAG TGGGCTTAGG  1740
TCCCCAACCC GGTGTGTCTC GGAAATGCTT GTGATTCAAC ACAGGGAGAG GAGGGAGAGG  1800
AGCCGGTCTC GGAGGAAACA GCATCTACTG CCTCCCTGTG TGGATGAGCC GGAGCTGCTC  1860
TTCTCAGAGG GGCCCAGTAC TTCCCGCTGG GCCGCAGAGC TCCCGTTCCC AGCAGACTCC  1920
TCTGACCCTG CCTCCCAGCT CAGCTACTCC CAGGAAGTGG GAGGACCTTT TAAGACACCC  1980
ATTAAGGAAA CGCTGCCCAT CTCCTCCACC CCGAGCAAAT CTGTCCTCCC CAGAACCCCT  2040
GAATCCTGGA GGCTCACGCC CCCAGCCAAA GTAGGGGGAC TGGATTTCAG CCCAGTACAA  2100
ACCTCCCAGG GTGCCTCTGA CCCCTTGCCT GACCCCCTGG GGCTGATGGA TCTCAGCACC  2160
ACTCCCTTGC AAAGTGCTCC CCCCCTTGAA TCACCGCAAA GGCTCCTCAG TTCAGAACCC  2220
TTAGACCTCA TCTCCGTCCC CTTTGGCAAC TCTTCTCCCT CAGATATAGA CGTCCCCAAG  2280
CCAGGCTCCC CGGAGCCACA GGTTTCTGGC CTTGCAGCCA ATCGTTCTCT GACAGAAGGC  2340
CTGGTCCTGG ACACAATGAA TGACAGCCTC AGCAAGATCC TGCTGGACAT CAGCTTTCCT  2400
GGCCTGGACG AGGACCCACT GGGCCCTGAC AACATCAACT GGTCCCAGTT TATTCCTGAG  2460
CTACAGTAGA GCCCTGCCCT TGCCCCTGTG CTCAAGCTGT CCACCATCCC GGGCACTCCA  2520
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ATAGCTCCCT GCTGCCTGAT TATGCAAAAG TAGCAGTCAC ACCCTAGCCA CTGCTGGGAC  2640
CTTGTGTTCC CCAAGAGTAT CTGATTCCTC TGCTGTCCCT GCCAGGAGCT GAAGGGTGGG  2700
AACAACAAAG GCAATGGTGA AAAGAGATTA GGAACCCCCC AGCCTGTTTC CATTCTCTGC  2760
CCAGCAGTCT CTTACCTTCC CTGATCTTTG CAGGGTGGTC CGTGTAAATA GTATAAATTC  2820
TCCAAATTAT CCTCTAATTA TAAATGTAAG CTTATTTCCT TAGATCATTA TCCAGAGACT  2880
GCCAGAAGGT GGGTAGGATG ACCTGGGGTT TCAATTGACT TCTGTTCCTT GCTTTTAGTT  2940
TTGATAGAAG GGAAGACCTG CAGTGCACGG TTTCTTCCAG GCTGAGGTAC CTGGATCTTG  3000
GGTTCTTCAC TGCAGGGACC CAGACAAGTG GATCTGCTTG CCAGAGTCCT TTTTGCCCCT  3060
CCCTGCCACC TCCCCGTGTT TCCAAGTCAG CTTTCCTGCA AGAAGAAATC CTGGTTAAAA  3120
AAGTCTTTTG TATTGGGTCA GGAGTTGAAT TTGGGGTGGG AGGATGGATG CAACTGAAGC  3180
AGAGTGTGGG TGCCCAGATG TGCGCTATTA GATGTTTCTC TGATAATGTC CCCAATCATA  3240
CCAGGGAGAC TGGCATTGAC GAGAACTCAG GTGGAGGCTT GAGAAGGCCG AAAGGGCCCC  3300
TGACCTGCCT GGCTTCCTTA GCTTGCCCCT CAGCTTTGCA AAGAGCCACC CTAGGCCCCA  3360
GCTGACCGCA TGGGTGTGAG CCAGCTTGAG AACACTAACT ACTCAATAAA AGCGAAGGTG  3420
GACCNAAAAA AAAAAAAAAA AAAA
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Seq ID NO: 69 Protein sequence:
Protein Accession #: NP_068772.1

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1          11         21         31         41         51
|          |          |          |          |          |
MKASPRRPLI LKRRRLPLPV QNAPSETSEE EPKRSPAQQE SNQAEASKEV AESNSCKFPA    60
GIKIINHPTM PNTQVVAIPN NANIHSIITA LTAKGKESGS SGPNKFILIS CGGAPTQPPG   120
LRPQTQTSYD AKRTEVTLET LGPKPAARDV NLPRPPGALC EQKRETCADG EAAGCTINNS   180
LSNIQWLRKM SSDGLGSRSI KQEMEEKENC HLEQRQVKVE EPSRPSASWQ NSVSERPPYS   240
YMAMIQFAIN STERKRMTLK DIYTWIEDHP PYFKHIAKPG WKNSIRHNLS LHDMFVRETS   300
ANGKVSFWTI HPSANRYLTL DQVFKPLDPG SPQLPEHLES QQKRPNPELR RNMTIKTELP   360
LGARRKMKPL LPRVSSYLVP IQFPVNQSLV LQPSVKVPLP LAASLMSSEL ARHSKRVRIA   420
PKVLLAEEGI APLSSAGPGK EEKLLFGEGF SPLLPVQTIK EEEIQPGEEM PHLARPIKVE   480
SPPLEEWPSP APSFKEESSH SWEDSSQSPT PRPKKSYSGL RSPTRCVSEM LVIQHRERRE   540
RSRSRRKQHL LPPCVDEPEL LFSEGPSTSR WAAELPFPAD SSDPASQLSY SQEVGGPFKT   600
PIKETLPISS TPSKSVLPRT PESWRLTPPA KVGGLDFSPV QTSQGASDPL PDPLGLMDLS   660
TTPLQSAPPL ESPQRLLSSE PLDLISVPFG NSSPSDIDVP KPGSPEPQVS GLAANRSLTE   720
GLVLDTMNDS LSKILLDISF PGLDEDPLGP DNINWSQFIP ELQ
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Seq ID NO: 70 DNA sequence
Nucleic Acid Accession #: BC006529.1
Coding sequence: 178-2424

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1          11         21         31         41         51
|          |          |          |          |          |
GGCACGAGGG GGACCCGGCC GGTCCGGCGC GAGCCCCCGT CCGGGGCCCT GGCTCGGCCC    60
CCAGGTTGGA GGAGCCCGGA GCCCGCCTTC GGAGCTACGG CCTAACGGCG GCGGCGACTG   120
CAGTCTGGAG GGTCCACACT TGTGATTCTC AATGGAGAGT GAAAACGCAG ATTCATAATG   180
AAAACTAGCC CCCGTCGGCC ACTGATTCTC AAAAGACGGA GGCTGCCCCT TCCTGTTCAA   240
AATGCCCCAA GTGAAACATC AGAGGAGGAA CCTAAGAGAT CCCCTGCCCA ACAGGAGTCT   300
AATCAAGCAG AGGCCTCCAA GGAAGTGGCA GAGTCCAACT CTTGCAAGTT TCCAGCTGGG   360
ATCAAGATTA TTAACCACCC CACCATGCCC AACACGCAAG TAGTGGCCAT CCCCAACAAT   420
GCTAATATTC ACAGCATCAT CACAGCACTG ACTGCCAAGG GAAAAGAGAG TGGCAGTAGT   480
GGGCCCAACA AATTCATCCT CATCAGCTGT GGGGGAGCCC CAACTCAGCC TCCAGGACTC   540
CGGCCTCAAA CCCAAACCAG CTATGATGCC AAAAGGACAG AAGTGACCCT GGAGACCTTG   600
GGACCAAAAC CTGCAGCTAG GGATGTGAAT CTTCCTAGAC CACCTGGAGC CCTTTGCGAG   660
CAGAAACGGG AGACCTGTGC AGATGGTGAG GCAGCAGGCT GCACTATCAA CAATAGCCTA   720
TCCAACATCC AGTGGCTTCG AAAGATGAGT TCTGATGGAC TGGGCTCCCG CAGCATCAAG   780
CAAGAGATGG AGGAAAAGGA GAATTGTCAC CTGGAGCAGC GACAGGTTAA GGTTGAGGAG   840
CCTTCGAGAC CATCAGCGTC CTGGCAGAAC TCTGTGTCTG AGCGGCCACC CTACTCTTAC   900
ATGGCCATGA TACAATTCGC CATCAACAGC ACTGAGAGGA AGCGCATGAC TTTGAAAGAC   960
ATCTATACGT GGATTGAGGA CCACTTTCCC TACTTTAAGC ACATTGCCAA GCCAGGCTGG  1020
AAGAACTCCA TCCGCCACAA CCTTTCCCTG CACGACATGT TTGTCCGGGA GACGTCTGCC  1080
AATGGCAAGG TCTCCTTCTG GACCATTCAC CCCAGTGCCA ACCGCTACTT GACATTGGAC  1140
CAGGTGTTTA AGCAGCAGAA ACGACCGAAT CCAGAGCTCC GCCGGAACAT GACCATCAAA  1200
ACCGAACTCC CCCTGGGCGC ACGGCGGAAG ATGAAGCCAC TGCTACCACG GGTCAGCTCA  1260
TACCTGGTAC CTATCCAGTT CCCGGTGAAC CAGTCACTGG TGTTGCAGCC CTCGGTGAAG  1320
GTGCCATTGC CCCTGGCGGC TTCCCTCATG AGCTCAGAGC TTGCCCGCCA TAGCAAGCGA  1380
GTCCGCATTG CCCCCAAGGT GCTGCTAGCT GAGGAGGGGA TAGCTCCTCT TTCTTCTGCA  1440
GGACCAGGGA AAGAGGAGAA ACTCCTGTTT GGAGAAGGGT TTTCTCCTTT GCTTCCAGTT  1500
CAGACTATCA AGGAGGAAGA AATCCAGCCT GGGGAGGAAA TGCCACACTT AGCGAGACCC  1560
ATCAAAGTGG AGAGCCCTCC CTTGGAAGAG TGGCCCTCCC CGGCCCCATC TTTCAAAGAG  1620
GAATCATCTC ACTCCTGGGA GGATTCGTCC CAATCTCCCA CCCCAAGACC CAAGAAGTCC  1680
TACAGTGGGC TTAGGTCCCC AACCCGGTGT GTCTCGGAAA TGCTTGTGAT TCAACACAGG  1740
GAGAGGAGGG AGAGGAGCCG GTCTCGGAGG AAACAGCATC TACTGCCTCC CTGTGTGGAT  1800
GAGCCGGAGC TGCTCTTCTC AGAGGGGCCC AGTACTTCCC GCTGGGCCGC AGAGCTCCCG  1860
TTCCCAGCAG ACTCCTCTGA CCCTGCCTCC CAGCTCAGCT ACTCCCAGGA AGTGGGAGGA  1920
CCTTTTAAGA CACCCATTAA GGAAACGCTG CCCATCTCCT CCACCCCGAG CAAATCTGTC  1980
CTCCCCAGAA CCCCTGAATC CTGGAGGCTC ACGCCCCCAG CCAAAGTAGG GGGACTGGAT  2040
TTCAGCCCAG TACAAACCCC CCAGGGTGCC TCTGACCCCT TGCCTGACCC CCTGGGGCTG  2100
ATGGATCTCA GCACCACTCC CTTGCAAAGT GCTCCCCCCC TTGAATCACC GCAAAGGCTC  2160
CTCAGTTCAG AACCCTTAGA CCTCATCTCC GTCCCCTTTG GCAACTCTTC TCCCTCAGAT  2220
ATAGACGTCC CCAAGCCAGG CTCCCCGGAG CCACAGGTTT CTGGCCTTGC AGCCAATCGT  2280
TCTCTGACAG AAGGCCTGGT CCTGGACACA ATGAATGACA GCCTCAGCAA GATCCTGCTG  2340
GACATCAGCT TTCCTGGCCT GGACGAGGAC CCACTGGGCC CTGACAACAT CAACTGGTCC  2400
CAGTTTATTC CTGAGCTACA GTAGAGCCCT GCCCTTGCCC CTGTGCTCAA GCTGTCCACC  2460
ATCCCGGGCA CTCCAAGGCT CAGTGCACCC CAAGCCTCTG AGTGAGGACA GCAGGCAGGG  2520
ACTGTTCTGC TCCTCATAGC TCCCTGCTGC CTGATTATGC AAAAGTAGCA GTCACACCCT  2580
AGCCACTGCT GGGACCTTGT GTTCCCCAAG AGTATCTGAT TCCTCTGCTG TCCCTGCCAG  2640
GAGCTGAAGG GTGGGAACAA CAAAGGCAAT GGTGAAAAGA GATTAGGAAC CCCCCAGCCT  2700
GTTTCCATTC TCTGCCCAGC AGTCTCTTAC CTTCCCTGAT CTTTGCAGGG TGGTCCGTGT  2760
AAATAGTATA AATTCTCCAA ATTATCCTCT AATTATAAAT GTAAGCTTAT TTCCTTAGAT  2820
CATTATCCAG AGACTGCCAG AAGGTGGGTA GGATGACCTG GGGTTTCAAT TGACTTCTGT  2880
TCCTTGCTTT TAGTTTTGAT AGAAGGGAAG ACCTGCAGTG CACGGTTTCT TCCAGGCTGA  2940
GGTACCTGGA TCTTGGGTTC TTCACTGCAG GGACCCAGAC AAGTGGATCT GCTTGCCAGA  3000
GTCCTTTTTG CCCCTCCCTG CCACCTCCCC GTGTTTCCAA GTCAGCTTTC CTGCAAGAAG  3060
AAATCCTGGT TAAAAAAGTC TTTTGTATTG GGTCAGGAGT TGAATTTGGG GTGGGAGGAT  3120
GGATGCAACT GAAGCAGAGT GTGGGTGCCC AGATGTGCGC TATTAGATGT TTCTCTGATA  3180
ATGTCCCCAA TCATACCAGG GAGACTGGCA TTGACGAGAA CTCAGGTGGA GGCTTGAGAA  3240
GGCCGAAAGG GCCCCTGACC TGCCTGGCTT CCTTAGCTTG CCCCTCAGCT TTGCAAAGAG  3300
CCACCCTAGG CCCCAGCTGA CCGCATGGGT GTGAGCCAGC TTGAGAACAC TAACTACTCA  3360
ATAAAAGCGA AGGTGGAAAA AAAAAAAAAA AAAAAAA
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Seq ID NO: 71 Protein sequence:
Protein Accession #: AAH06529.1

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1          11         21         31         41         51
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GIKIINHPTM PNTQVVAIPN NANIHSIITA LTAKGKESGS SGPNKFILIS CGGAPTQPPG   120
LRPQTQTSYD AKRTEVTLET LGPKPAARDV NLPRPPGALC EQKRETCADG EAAGCTINNS   180
LSNIQWLRKM SSDGLGSRSI KQEMEEKENC HLEQRQVKVE EPSRPSASWQ NSVSERPPYS   240
YMAMIQFAIN STERKRMTLK DIYTWIEDHF PYFKHIAKPG WKNSIRHNLS LHDMFVRETS   300
ANGKVSFWTI HPSANRYLTL DQVFKQQKRP NPELRRNMTI KTELPLGARR KMKPLLPRVS   360
SYLVPIQFPV NQSLVLQPSV KVPLPLAASL MSSELARHSK RVRIAPKVLL AEEGIAPLSS   420
AGPGKEEKLL FGEGFSPLLP VQTIKEEEIQ PGEEMPHLAR PIKVESPPLE EWPSPAPSFK   480
EESSHSWEDS SQSPTPRPKK SYSGLRSPTR CVSEMLVIQH RERRERSRSR RKQHLLPPCV   540
DEPELLFSEG PSTSRWAAEL PFPADSSDPA SQLSYSQEVG GPFKTPIKET LPISSTPSKS   600
VLPRTPESWR LTPPAKVGGL DFSPVQTPQG ASDPLPDPLG LMDLSTTPLQ SAPPLESPQR   660
LLSSEPLDLI SVPFGNSSPS DIDVPKPGSP EPQVSGLAAN RSLTEGLVLD TMNDSLSKIL   720
LDISFPGLDE DPLGPDNINW SQFIPELQ
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Seq ID NO: 72 DNA sequence
Nucleic Acid Accession #: U74612.1
Coding sequence: 178-2583

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CCAGGTTGGA GGAGCCCGGA GCCCGCCTTC GGAGCTACGG CCTAACGGCG GCGGCGACTG   120
CAGTCTGGAG GGTCCACACT TGTGATTCTC AATGGAGAGT GAAAACGCAG ATTCATAATG   180
AAAACTAGCC CCCGTCGGCC ACTGATTCTC AAAAGACGGA GGCTGCCCCT TCCTGTTCAA   240
AATGCCCCAA GTGAAACATC AGAGGAGGAA CCTAAGAGAT CCCCTGCCCA ACAGGAGTCT   300
AATCAAGCAG AGGCCTCCAA GGAAGTGGCA GAGTCCAACT CTTGCAAGTT TCCAGCTGGG   360
ATCAAGATTA TTAACCACCC CACCATGCCC AACACGCAAG TAGTGGCCAT CCCCAACAAT   420
GCTAATATTC ACAGCATCAT CACAGCACTG ACTGCCAAGG GAAAAGAGAG TGGCAGTAGT   480
GGGCCCAACA AATTCATCCT CATCAGCTGT GGGGGAGCCC CAACTCAGCC TCCAGGACTC   540
CGGCCTCAAA CCCAAACCAG CTATGATGCC AAAAGGACAG AAGTGACCCT GGAGACCTTG   600
GGACCAAAAC CTGCAGCTAG GGATGTGAAT CTTCCTAGAC CACCTGGAGC CCTTTGCGAG   660
CAGAAACGGG AGACCTGTGC AGATGGTGAG GCAGCAGGCT GCACTATCAA CAATAGCCTA   720
TCCAACATCC AGTGGCTTCG AAAGATGAGT TCTGATGGAC TGGGCTCCCG CAGCATCAAG   780
CAAGAGATGG AGGAAAAGGA GAATTGTCAC CTGGAGCAGC GACAGGTTAA GGTTGAGGAG   840
CCTTCGAGAC CATCAGCGTC CTGGCAGAAC TCTGTGTCTG AGCGGCCACC CTACTCTTAC   900
ATGGCCATGA TACAATTCGC CATCAACAGC ACTGAGAGGA AGCGCATGAC TTTGAAAGAC   960
ATCTATACGT GGATTGAGGA CCACTTTCCC TACTTTAAGC ACATTGCCAA GCCAGGCTGG  1020
AAGAACTCCA TCCGCCACAA CCTTTCCCTG CACGACATGT TTGTCCGGGA GACGTCTGCC  1080
AATGGCAAGG TCTCCTTCTG GACCATTCAC CCCAGTGCCA ACCGCTACTT GACATTGGAC  1140
CAGGTGTTTA AGCCACTGGA CCCAGGGTCT CCACAATTGC CCGAGCACTT GGAATCACAG  1200
CAGAAACGAC CGAATCCAGA GCTCCGCCGG AACATGACCA TCAAAACCGA ACTCCCCCTG  1260
GGCGCACGGC GGAAGATGAA GCCACTGCTA CCACGGGTCA GCTCATACCT GGTACCTATC  1320
CAGTTCCCGG TGAACCAGTC ACTGGTGTTG CAGCCCTCGG TGAAGGTGCC ATTGCCCCTG  1380
GCGGCTTCCC TCATGAGCTC AGAGCTTGCC CGCCATAGCA AGCGAGTCCG CATTGCCCCC  1440
AAGGTTTTTG GGGAACAGGT GGTGTTTGGT TACATGAGTA AGTTCTTTAG TGGCGATCTG  1500
CGAGATTTTG GTACACCCAT CACCAGCTTG TTTAATTTTA TCTTTCTTTG TTTATCAGTG  1560
CTGCTAGCTG AGGAGGGGAT AGCTCCTCTT TCTTCTGCAG GACCAGGGAA AGAGGAGAAA  1620
CTCCTGTTTG GAGAAGGGTT TTCTCCTTTG CTTCCAGTTC AGACTATCAA GGAGGAAGAA  1680
ATCCAGCCTG GGGAGGAAAT GCCACACTTA GCGAGACCCA TCAAAGTGGA GAGCCCTCCC  1740
TTGGAAGAGT GGCCCTCCCC GGCCCCATCT TTCAAAGAGG AATCATCTCA CTCCTGGGAG  1800
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TCTCGGAGGA AACAGCATCT ACTGCCTCCC TGTGTGGATG AGCCGGAGCT GCTCTTCTCA  1980
GAGGGGCCCA GTACTTCCCG CTGGGCCGCA GAGCTCCCGT TCCCAGCAGA CTCCTCTGAC  2040
CCTGCCTCCC AGCTCAGCTA CTCCCAGGAA GTGGGAGGAC CTTTTAAGAC ACCCATTAAG  2100
GAAACGCTGC CCATCTCCTC CACCCCGAGC AAATCTGTCC TCCCCAGAAC CCCTGAATCC  2160
TGGAGGCTCA CGCCCCCAGC CAAAGTAGGG GGACTGGATT TCAGCCCAGT ACAAACCTCC  2220
CAGGGTGCCT CTGACCCCTT GCCTGACCCC CTGGGGCTGA TGGATCTCAG CACCACTCCC  2280
TTGCAAAGTG CTCCCCCCCT TGAATCACCG CAAAGGCTCC TCAGTTCAGA ACCCTTAGAC  2340
CTCATCTCCG TCCCCTTTGG CAACTCTTCT CCCTCAGATA TAGACGTCCC CAAGCCAGGC  2400
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TAGAGCCCTG CCCTTGCCCC TGTGCTCAAG CTGTCCACCA TCCCGGGCAC TCCAAGGCTC  2640
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AGGTGGGTAG GATGACCTGG GGTTTCAATT GACTTCTGTT CCTTGCTTTT AGTTTTGATA  3060
GAAGGGAAGA CCTGCAGTGC ACGGTTTCTT CCAGGCTGAG GTACCTGGAT CTTGGGTTCT  3120
TCACTGCAGG GACCCAGACA AGTGGATCTG CTTGCCAGAG TCCTTTTTGC CCCTCCCTGC  3180
CACCTCCCCG TGTTTCCAAG TCAGCTTTCC TGCAAGAAGA AATCCTGGTT AAAAAAGTCT  3240
TTTGTATTGG GTCAGGAGTT GAATTTGGGG TGGGAGGATG GATGCAACTG AAGCAGAGTG  3300
TGGGTGCCCA GATGTGCGCT ATTAGATGTT TCTCTGATAA TGTCCCCAAT CATACCAGGG  3360
AGACTGGCAT TGACGAGAAC TCAGGTGGAG GCTTGAGAAG GCCGAAAGGG CCCCTGACCT  3420
GCCTGGCTTC CTTAGCTTGC CCCTCAGCTT TGCAAAGAGC CACCCTAGGC CCCAGCTGAC  3480
CGCATGGGTG TGAGCCAGCT TGAGAACACT AACTACTCAA TAAAAGCGAA GGTGGACAAA  3540
AAAAAAAAAA AAAAA
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Seq ID NO: 73 Protein sequence:
Protein Accession #: AAC51128.1

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GIKIINHPTM PNTQVVAIPN NANIHSIITA LTAKGKESGS SGPNKFILIS CGGAPTQPPG   120
LRPQTQTSYD AKRTEVTLET LGPKPAARDV NLPRPPGALC EQKRETCADG EAAGCTINNS   180
LSNIQWLRKM SSDGLGSRSI KQEMEEKENC HLEQRQVKVE EPSRPSASWQ NSVSERPPYS   240
YMAMIQFAIN STERKRMTLK DIYTWIEDHF PYFKHIAKPG WKNSIRHNLS LHDMFVRETS   300
ANGKVSFWTI HPSANRYLTL DQVFKPLDPG SPQLPEHLES QQKRPNPELR RNMTIKTELP   360
LGARRKMKPL LPRVSSYLVP IQFPVNQSLV LQPSVKVPLP LAASLMSSEL ARHSKRVRIA   420
PKVFGEQVVF GYMSKFFSGD LRDFGTPITS LFNFIFLCLS VLLAEEGIAP LSSAGPGKEE   480
KLLFGEGFSP LLPVQTIKEE EIQPGEEMPH LARPIKVESP PLEEWPSPAP SFKEESSHSW   540
EDSSQSPTPR PKKSYSGLRS PTRCVSEMLV IQHRERRERS RSRRKQHLLP PCVDEPELLF   600
SEGPSTSRWA AELPFPADSS DPASQLSYSQ EVGGPFKTPI KETLPISSTP SKSVLPRTPE   660
SWRLTPPAKV GGLDFSPVQT SQGASDPLPD PLGLMDLSTT PLQSAPPLES PQRLLSSEPL   720
DLISVPFGNS SPSDIDVPKP GSPEPQVSGL AANRSLTEGL VLDTMNDSLS KILLDISPPG   780
LDEDPLGPDN INWSQFIPEL Q
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Seq ID NO: 74 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 111-416

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CTCAAGCTGA GAGGTCCATA ATAGGCATGA TCGACATGTT TCACAAATAC ACCAGACGTG   180
ATGACAAGAT TGAGAAGCCA AGCCTGCTGA CGATGATGAA GGAGAACTTC CCCAACTTCC   240
TTAGTGCCTG TGACAAAAAG GGCACAAATT ACCTCGCCGA TGTCTTTGAG AAAAAGGACA   300
AGAATGAGGA TAAGAAGATT GATTTTTCTG AGTTTCTGTC CTTGCTGGGA GACATAGCCA   360
CAGACTACCA CAAGCAGAGC CATGGAGCAG CGCCCTGTTC CGGGGGCAGC CAGTGACCCA   420
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Seq ID NO: 75 Protein sequence:
Protein Accession #: Eos sequence

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|          |          |          |          |          |
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KKDKNEDKKI DFSEFLSLLG DIATDYHKQS HGAAPCSGGS Q
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Seq ID NO: 76 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 111-416

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1          11         21         31         41         51
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TCATCCTTCT ACTCGTGACA CTTCCCAGTT CTGGCTTTTT GAAAGCAAAG ATGAGCAACA   120
CTCAAGCTGA GAGGTCCATA ATAGGCATGA TCGACATGTT TCACAAATAC ACCGGACGTG   180
ATGGCAAGAT TGAGAAGCCA AGCCTGCTGA CGATGATGAA GGAGAACTTC CCCAATTTCC   240
TCAGTGCCTG TGACAAAAAG GGCATACATT ACCTCGCCAC TGTCTTTGAG AAAAAGGACA   300
AGAATGAGGA TAAGAAGATT GATTTTTCTG AGTTTCTGTC CTTGCTGGGA GACATAGCCG   360
CAGACTACCA CAAGCAGAGC CATGGAGCGG CGCCCTGTTC TGGGGGAAGC CAGTGATCCA   420
GCCCCACCAA GGGGCCTCCA GAGACCCCAG GAACAATAAG TGTCTCCTCC CACCAGA
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Seq ID NO: 77 Protein sequence:
Protein Accession #: XP_048124.1

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KKDKNEDKKI DFSEFLSLLG DIAADYHKQS HGAAPCSGGS Q
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Seq ID NO: 78 DNA sequence
Nucleic Acid Accession #: Z73678.1
Coding sequence: 253-2433

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CCTCGCACTC TATGGCCGTA GGGAGCCGCT GAGAGCGAGA AGAGCACGCT CCTGCCCGCC   180
CGCTGCACCG CACCTCGCCT CGCCTCTCTG CTCTCCTAGG CCCCGGCCGC GCGCCACCCG   240
CCTCCCGCCA CCATGAACCA CTCGCCGCTC AAGACCGCCT TGGCGTACGA ATGCTTCCAG   300
GACCAGGACA ACTCCACGTT GGCTTTGCCG TCGGACCAAA AGATGAAAAC AGGCACGTCT   360
GGCAGGCAGC GCGTGCAGGA GCAGGTGATG ATGACCGTCA AGCGGCAGAA GTCCAAGTCT   420
TCCCAGTCGT CCACCCTGAG CCACTCCAAT CGAGGTTCCA TGTATGATGG CTTGGCTGAC   480
AATTACAACT ATGGGACCAC CAGCAGGAGC AGCTACTACT CCAAGTTCCA GGCAGGGAAT   540
GGCTCATGGG GATATCCGAT CTACAATGGA ACCCTCAAGC GGGAGCCTGA CAACAGGCGC   600
TTCAGCTCCT ACAGCCAGAT GGAGAACTGG AGCCGGCACT ACCCCCGGGG CAGCTGTAAC   660
ACCACCGGCG CAGGCAGCGA CATCTGCTTC ATGCAGAAAA TCAAGGCGAG CCGCAGTGAG   720
CCCGACCTCT ACTGTGACCC ACGGGGCACC CTGCGCAAGG GCACGCTGGG CAGCAAGGGC   780
CAGAAGACCA CCCAGAACCG CTACAGCTTT TACAGCACCT GCAGTGGTCA GAAGGCCATA   840
AAGAAGTGCC CTGTGCGCCC GCCCTCTTGT GCCTCCAAGC AGGACCCTGT GTATATCCCG   900
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CCCATCTCCT GCAACAAGGA CCTGTCCTTT GGCCACTCTA GGGCCAGCTC CAAGATCTGC 960
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CAGGATGAGA AGTACCAGGC CATTGGGGCC TATTACATCC AGCATACCTG CTTCCAGGAT 1080
GAATCTGCCA AGCAACAGGT CTATCAGCTG GGAGGCATCT GCAAGCTGGT GGACCTCCTC 1140
CGCAGCCCCA ACCAGAACGT CCAGCAGGCC GCGGCAGGGG CCCTGCGCAA CCTGGTGTTC 1200
AGGAGCACCA CCAACAAGCT GGAGACCCGG AGGCAGAATG GGATCCGCGA GGCAGTCAGC 1260
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GTGGTGGACC CTGAGGTCTT CTTCAATGCC ACAGGCTGCT TGAGGAACCT GAGCTCGGCC 1500
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GTTCTGCACA ACCTCTCCTA CCGCCTGGAC GCCGAGGTGC CCACCCGCTA CCGCCAGCTG 1680
GAGTATAACG CCCGCAACGC CTACACCGAG AAGTCCTCCA CTGGCTGCTT CAGCAACAAG 1740
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CCACAAATTG CCCGCCTCCT GCAATCTGGC AACTCTGATG TGGTGCGGTC CGGAGCCTCC 2040
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TGTGAGGGAT CTTGGAGCTT CCCTGTAGCC CACCTTCCCC TTGCTTCATG TTTGTAGAGG 5280
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Seq ID NO: 79 Protein sequence:
Protein Accession #: CAA98022.1

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QNRYSFYSTC SGQKAIKKCP VRPPSCASKQ DPVYIPPISC NKDLSFGHSR ASSKICSEDI 240
ECSGLTIPKA VQYLSSQDEK YQAIGAYYIQ HTCFQDESAK QQVYQLGGIC KLVDLLRSPN 300
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DELKEELIAD ALPVLADRVI IPPSGWCDGN SNMSREVVDP EVFFNATGCL RNLSSADAGR   420
QTMRNYSGLI DSLMAYVQNC VAASRCDDKS VENCMCVLHN LSYRLDAEVP TRYRQLEYNA   480
RNAYTEKSST GCFSNKSDKM MNNNYDCPLP EEETNPKGSG WLYHSDAIRT YLNLMGKSKK   540
DATLEACAGA LQNLTASKGL MSSGMSQLIG LKEKGLPQIA RLLQSGNSDV VRSGASLLSN   600
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SSMLNNIINL CRSSASPKAA EAARLLLSDM WSSKELQGVL RQQGFDRNML GTLAGANSLR   720
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Seq ID NO: 80 DNA sequence
Nucleic Acid Accession #: NM_006516.1
Coding sequence: 180-1658

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TGGAGCCCAG CAGCAAGAAG CTGACGGGTC GCCTCATGCT GGCTGTGGGA GGAGCAGTGC   240
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GAGGGTGGAG ACTAAGCCCT GTCGAGACAC TTGCCTTCTT CACCCAGCTA ATCTGTAGGG  2040
CTGGACCTAT GTCCTAAGGA CACACTAATC GAACTATGAA CTACAAAGCT TCTATCCCAG  2100
GAGGTGGCTA TGGCCACCCG TTCTGCTGGC CTGGATCTCC CCACTCTAGG GGTCAGGCTC  2160
CATTAGGATT TGCCCCTTCC CATCTCTTCC TACCCAACCA CTCAAATTAA TCTTTCTTTA  2220
CCTGAGACCA GTTGGGAGCA CTGGAGTGCA GGGAGGAGAG GGGAAGGGCC AGTCTGGGCT  2280
GCCGGGTTCT AGTCTCCTTT GCACTGAGGG CCACACTATT ACCATGAGAA GAGGGCCTGT  2340
GGGAGCCTGC AAACTCACTG CTCAAGAAGA CATGGAGACT CCTGCCCTGT TGTGTATAGA  2400
TGCAAGATAT TTATATATAT TTTTGGTTGT CAATATTAAA TACAGACACT AAGTTATAGT  2460
ATATCTGGAC AAGCCAACTT GTAAATACAC CACCTCACTC CTGTTACTTA CCTAAACAGA  2520
TATAAATGGC TGGTTTTTAG AAACATGGTT TTGAAATGCT TGTGGATTGA GGGTAGGAGG  2580
TTTGGATGGG AGTGAGACAG AAGTAAGTGG GGTTGCAACC ACTGCAACGG CTTAGACTTC  2640
GACTCAGGAT CCAGTCCCTT ACACGTACCT CTCATCAGTG TCCTCTTGCT CAAAAATCTG  2700
TTTGATCCCT GTTACCCAGA GAATATATAC ATTCTTTATC TTGACATTCA AGGCATTTCT  2760
ATCACATATT TGATAGTTGG TGTTCAAAAA AACACTAGTT TTGTGCCAGC CGTGATGCTC  2820
AGGCTTGAAA TCGCATTATT TTGAATGTGA AGGGAA
```

Seq ID NO: 81 Protein sequence:
Protein Accession #: NP_006507.1

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1          11         21         31         41         51
|          |          |          |          |          |
MEPSSKKLTG RLMLAVGGAV LGSLQFGYNT GVINAPQKVI EEFYNQTWVH RYGESILPTT    60
LTTLWSLSVA IFSVGGMIGS FSVGLFVNRF GRRNSMLMMN LLAFVSAVLM GFSKLGKSFE   120
MLILGRFIIG VYCGLTTGFV PMYVGEVSPT AFRGALGTLH QLGIVVGILI AQVFGLDSIM   180
GNKDLWPLLL SIIFIPALLQ CIVLPFCPES PRFLLINRNE ENRAKSVLKK LRGTADVTHD   240
LQEMKEESRQ MMREKKVTIL ELFRSPAYRQ PILIAVVLQL SQQLSGINAV FYYSTSIFEK   300
AGVQQPVYAT IGSGIVNTAF TVVSLFVVER AGRRTLHLIG LAGMAGCAIL MTIALALLEQ   360
LPWMSYLSIV AIFGFVAFFE VGPGPIPWFI VAELFSQGPR PAAIAVAGFS NWTSNFIVGM   420
CFQYVEQLCG PYVFIIFTVL LVLFFIFTYF KVPETKGRTF DEIASGFRQG GASQSDKTPE   480
ELFHPLGADS QV
```

Seq ID NO: 82 DNA sequence
Nucleic Acid Accession #: BC001291
Coding sequence: 44-541

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1          11         21         31         41         51
|          |          |          |          |          |
GGGGGCGCCG CGCGCTGACC CTCCCTGGGC ACCGCTGGGG ACGATGGCGC TGCTCGCCTT    60
GCTGCTGGTC GTGGCCCTAC CGCGGGTGTG GACAGACGCC AACCTGACTG CGAGACAACG   120
```

```
AGATCCAGAG GACTCCCAGC GAACGGACGA GGGTGACAAT AGAGTGTGGT GTCATGTTTG   180
TGAGAGAGAA AACACTTTCG AGTGCCAGAA CCCAAGGAGG TGCAAATGGA CAGAGCCATA   240
CTGCGTTATA GCGGCCGTGA AAATATTTCC ACGTTTTTTC ATGGTTGCGA AGCAGTGCTC   300
CGCTGGTTGT GCAGCGATGG AGAGACCCAA GCCAGAGGAG AAGCGGTTTC TCCTGGAAGA   360
GCCCATGCCC TTCTTTTACC TCAAGTGTTG TAAAATTCGC TACTGCAATT TAGAGGGGCC   420
ACCTATCAAC TCATCAGTGT TCAAAGAATA TGCTGGGAGC ATGGGTGAGA GCTGTGGTGG   480
GCTGTGGCTG GCCATCCTCC TGCTGCTGGC CTCCATTGCA GCCGGCCTCA GCCTGTCTTG   540
AGCCACGGGA CTGCCACAGA CTGAGCCTTC CGGAGCATGG ACTCGCTCCA GACCGTTGTC   600
ACCTGTTGCA TTAAACTTGT TTTCTGTTGA TTACCTCTTG GTTTGACTTC CCAGGGTCTT   660
GGGATGGGAG AGTGGGGATC AGGTGCAGTT GGCTCTTAAC CCTCAAGGGT TCTTTAACTC   720
ACATTCAGAG GAAGTCCAGA TCTCCTGAGT AGTGATTTTG GTGACAAGTT TTTCTCTTTG   780
AAATCAAACC TTGTAACTCA TTTATTGCTG ATGGCCACTC TTTTCCTTGA CTCCCCTCTG   840
CCTCTGAGGG CTTCAGTATT GATGGGGAGG GAGGCCTAAG TACCACTCAT GGAGAGTATG   900
TGCTGAGATG CTTCCGACCT TTCAGGTGAC GCAGGAACAC TGGGGGAGTC TGAATGATTG   960
GGGTGAAGAC ATCCCTGGAG TGAAGGACTC CTCAGCATGG GGGGCAGTGG GGCACACGTT  1020
AGGGCTGCCC CCATTCCAGT GGTGGAGGCG CTGTGGATGG CTGCTTTTCC TCAACCTTTC  1080
CTACCAGATT CCAGGAGGCA GAAGATAACT AATTGTGTTG AAGAAACTTA GACTTCACCC  1140
ACCAGCTGGC ACAGGTGCAC AGATTCATAA ATTCCCACAC GTGTGTGTTC AACATCTGAA  1200
ACTTAGGCCA AGTAGAGAGC ATCAGGGTAA ATGGCGTTCA TTTCTCTGTT AAGATGCAGC  1260
CATCCATGGG GAGCTGAGAA ATCAGACTCA AAGTTCCACC AAAAACAAAT ACAAGGGGAC  1320
TTCAAAAGTT CACGAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA
```

Seq ID NO: 83 Protein sequence:
Protein Accession #: AAH01291

```
1          11         21         31         41         51
|          |          |          |          |          |
MALLALLLVV ALPRVWTDAN LTARQRDPED SQRTDEGDNR VWCHVCEREN TPECQNPRRC    60
KWTEPYCVIA AVKIFPRFFM VAKQCSAGCA AMERPKPEEK RFLLEEPMPF FYLKCCKIRY   120
CNLEGPPINS SVFKEYAGSM GESCGGLWLA ILLLLASIAA GLSLS
```

Seq ID NO: 84 DNA sequence
Nucleic Acid Accession #: NM_022893.1
Coding sequence: 229-2726

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1          11         21         31         41         51
|          |          |          |          |          |
TTTTTTTTTT TTTTTTGCTT AAAAAAAAGC CATGACGGCT CTCCCACAAT TCATCTTCCC    60
TGCGCCATCT TTGTATTATT TCTAATTTAT TTTGGATGTC AAAAGGCACT GATGAAGATA   120
TTTTCTCTGG AGTCTCCTTC TTTCTAACCC GGCTCTCCCG ATGTGAACCG AGCCGTCGTC   180
CGCCCGCCGC CGCCGCCGCC GCCGCCGCCG CCCGCCCCGC AGCCCACCAT GTCTCGCCGC   240
AAGCAAGGCA AACCCCAGCA CTTAAGCAAA CGGGAATTCT CGCCCGAGCC TCTTGAAGCC   300
ATTCTTACAG ATGATGAACC AGACCACGGC CCGTTGGGAG CTCCAGAAGG GGATCATGAC   360
CTCCTCACCT GTGGGCAGTG CCAGATGAAC TTCCCATTGG GGGACATTCT TATTTTTATC   420
GAGCACAAAC GGAAACAATG CAATGGCAGC CTCTGCTTAG AAAAAGCTGT GGATAAGCCA   480
CCTTCCCCTT CACCAATCGA GATGAAAAAA GCATCCAATC CCGTGGAGGT TGGCATCCAG   540
GTCACGCCAG AAGATGACGA TTGTTTATCA ACGTCATCTA GAAGAATTTG CCCCAAACAG   600
GAACACATAG CAGATAAACT TCTGCACTGG AGGGGCCTCT CCTCCCCTCG TTCTGCACAT   660
GGAGCTCTAA TCCCCACGCC TGGGATGAGT GCAGAATATG CCCCGCAGGG TATTTGTAAA   720
GATGAGCCCA GCAGCTACAC ATGTACAACT TGCAAACAGC CATTCACCAG TGCATGGTTT   780
CTCTTGCAAC ACGCACAGAA CACTCATGGA TTAAGAATCT ACTTAGAAAG CGAACACGGA   840
AGTCCCCTGA CCCCGCGGGT TGGTATCCCT TCAGGACTAG GTGCAGAATG TCCTTCCCAG   900
CCACCTCTCC ATGGGATTCA TATTGCAGAC AATAACCCCT TTAACCTGCT AAGAATACCA   960
GGATCAGTAT CGAGAGAGGC TTCCGGCCTG GCAGAAGGGC GCTTTCCACC CACTCCCCCC  1020
CTGTTTAGTC CACCACCGAG ACATCACTTG GACCCCCACC GCATAGAGCG CCTGGGGGCG  1080
GAAGAAATGG CCCTGGCCAC CCATCACCCG AGTGCCTTTG ACAGGGTGCT GCGGTTGAAT  1140
CCAATGGCTA TGGAGCCTCC CGCCATGGAT TTCTCTAGGA GACTTAGAGA GCTGGCAGGG  1200
AACACGTCTA GCCCACCGCT GTCCCCAGGC CGGCCCAGCC CTATGCAAAG GTTACTGCAA  1260
CCATTCCAGC CAGGTAGCAA GCCGCCCTTC CTGGCGACGC CCCCCCTCCC TCCTCTGCAA  1320
TCCGCCCCTC CTCCCTCCCA GCCCCCGGTC AAGTCCAAGT CATGCGAGTT CTGCGGCAAG  1380
ACGTTCAAAT TTCAGAGCAA CCTGGTGGTG CACCGGCGCA GCCACACGGG CGAGAAGCCC  1440
TACAAGTGCA ACCTGTGCGA CCACGCGTGC ACCCAGGCCA GCAAGCTGAA GCGCCACATG  1500
AAGACGCACA TGCACAAATC GTCCCCCATG ACGGTCAAGT CCGACGACGG TCTCTCCACC  1560
GCCAGCTCCC CGGAACCCGG CACCAGCGAC TTGGTGGGCA GCGCCAGCAG CGCGCTCAAG  1620
TCCGTGGTGG CCAAGTTCAA GAGCGAGAAC GACCCCAACC TGATCCCGGA GAACGGGGAC  1680
GAGGAGGAAG AGGAGGACGA CGAGGAAGAG GAAGAAGAGG AGGAAGAGGA GGAGGAGGAG  1740
CTGACGGAGA GCGAGAGGGT GGACTACGGC TTCGGGCTGA GCCTGGAGGC GGCGCGCCAC  1800
CACGAGAACA GCTCGCGGGG CGCGGTCGTG GGCGTGGGCG ACGAGAGCCG CGCCCTGCCC  1860
GACGTCATGC AGGGCATGGT GCTCAGCTCC ATGCAGCACT TCAGCGAGGC CTTCCACCAG  1920
GTCCTGGGCG AGAAGCATAA GCGCGGCCAC CTGGCCGAGG CCGAGGGCCA CAGGGACACT  1980
TGCGACGAAG ACTCGGTGGC CGGCGAGTCG GACCGCATAG ACGATGGCAC TGTTAATGGC  2040
CGCGGCTGCT CCCCGGGCGA GTCGGCCTCG GGGGGCCTGT CCAAAAAGCT GCTGCTGGGC  2100
AGCCCCAGCT CGCTGAGCCC CTTCTCTAAG CGCATCAAGC TCGAGAAGGA GTTCGACCTG  2160
CCCCCGGCCA CGATGCCCAA CACGGAGAAC GTGTACTCGC AGTGGCTCGC CGGCTACGCG  2220
GCCTCCAGGC AGCTCAAAGA TCCCTTCCTT AGCTTCGGAG ACTCCAGACA ATCGCCTTTT  2280
GCCTCCTCGT CGGAGCACTC CTCGGAGAAC GGGAGCTTGC GCTTCTCCAC ACCGCCCGGG  2340
GAGCTGGACG GAGGGATCTC GGGGCGCAGC GGCACGGGAA GTGGAGGGAG CACGCCCCAT  2400
ATTAGTGGTC CGGGCACGGG CAGGCCCAGC TCAAAAGAGG GCAGACGCAG CGACACTTGT  2460
GAGTACTGTG GGAAAGTCTT CAAGAACTGT AGCAATCTCA CTGTCCACAG GAGAAGCCAC  2520
ACGGGCGAAA GGCCTTATAA ATGCGAGCTG TGCAACTATG CCTGTGCCCA GAGTAGCAAG  2580
CTCACCAGGC ACATGAAAAC GCATGGCCAG GTGGGGAAGG ACGTTTACAA ATGTGAAATT  2640
TGTAAGATGC CTTTTAGCGT GTACAGTACC CTGGAGAAAC ACATGAAAAA ATGGCACAGT  2700
GATCGAGTGT TGAATAATGA TATAAAAACT GAATAGAGGT ATATTAATAC CCCTCCCTCA  2760
CTCCCACCTG ACACCCCCTT TTTCACCACT CCCTTTCCCC ATCGCCCTCC AGCCCCACTC  2820
CCTGTAGGAT TTTTTTCTAG TCCCATGTGA TTTAAACAAA CAAACAAACA AACAGAAGTA  2880
ACGAAGCTAA GAATATGAGA GTGCTTGTCA CCAGCACACC TGTTTTTTTT CTTTTTCTTT  2940
TTCTTTTTTC TTTTTCCTTT TTTTTTTTTT TCCTTTATGT TCTCACCGTT TGAATGCATG  3000
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ATCTGTATGG GGCAATACTA TTGCATTTTA CGCAAACTTT GAGCCTTTCT CTTGTGCAAT 3060
AATTTACATG TTGTGTATGT TTTTTTTTAA ACTTAGACAG CATGTATGGT ATGTTATGGC 3120
TATTTTAAAT TGTCCCTAAT TCGTTGCTGA GCAAACATGT TGCTGTTTCC AGTTCCGTTC 3180
TGAGAGAAAA AGAGAGAGAG AGAGAAAAAG ACCATGCTGC ATACATTCTG TAATACATAT 3240
CATGTACAGT TTTATTTTAT AACGTGAGGA GGAAAAAACAG TCTTTGGATT AACCCTCTAT 3300
AGACAGAATA GATAGCACTG AAAAAAAATC TCTATGAGCT AAATGTCTGT CTCTAAAGGG 3360
TTAAATGTAT CAATTGGAAA GGAAGAAAAA AGGCCTTGAA TTGACAAATT AACAGAAAAA 3420
CAGAACAAGT TTATTCTATC ATTTGGTTTT AAAATATGAG TGCCTTGGAT CTATTAAAAC 3480
CACATCGATG GTTCTTTCTA CTTGTTATAA ACTTGTAGCT TAATTCAGCA TTGGGTGAGG 3540
TAATAAACCT TAGGAACTAG CATATAATTC TATATTGTAT TTCTCACAAC AATGGCTACC 3600
TAAAAAGATG ACCCATTATG TCCTAGTTAA TCATCATTTT TCCTTTAGTT TAATTTTATA 3660
AACAAAACTG ATTATACCAG TATAAAAGCT ACTTTGCTCC TGGTGAGAGC TTAAAAGAAA 3720
TGGGCTGTTT TGCCCAAAGT TTTATTTTTT TTAAACAATG ATTAAATTGA ATGTGTAATG 3780
TGCAAAAGCC CTGGAACGCA ATTAAATACA CTAGTAAGGA GTTCATTTTA TGAAGATATT 3840
TGCTTTAATA ATGTCTTTTT AAAAATACTG GCACCAAAAG AAATAGATCC AGATCTACTT 3900
GGTTGTCAAG TGGACAATCA AATGATAAAC TTTAAGACCT TGTATACCAT ATTGAAAGGA 3960
AGAGGCTGAC AATAAGGTTT GACAGAGGGG AACAGAAGAA AATAATATGA TTTATTAGCA 4020
CAACGTGGTA CTATTTGCCA TTTAAAACTA GAACAGGTAT ATAAGCTAAT ATTGATACAA 4080
TGATGATTAA CTATGAATTC TTAAGACTTG CATTTAAATG TGACATTCTT AAAAAAAGAA 4140
GAGAAAGAAT TTTAAGAGTA GCAGTATATA TGTCTGTGCT CCCTAAAAGT TGTACTTCAT 4200
TTCTTTTCCA TACACTGTGT GCTATTTGTG TTAACATGGA AGAGGATTCA TTGTTTTTAT 4260
TTTTATTTTT TTAATTTTTT CTTTTTTATT AAGCTAGCAT CTGCCCCAGT TGGTGTTCAA 4320
ATAGCACTTG ACTCTGCCTG TGATATCTGT ATCTTTTCTC TAATCAGAGA TACAGAGGTT 4380
GAGTATAAAA TAAACCTGCT CAGATAGGAC AATTAAGTGC ACTGTACAAT TTTCCCAGTT 4440
TACAGGTCTA TACTTAAGGG AAAAGTTGCA AGAATGCTGA AAAAAAATTG AACACAATCT 4500
CATTGAGGAG CATTTTTTAA AAACTAAAAA AAAAAAAACT TTGCCAGCCA TTTACTTGAC 4560
TATTGAGCTT ACTTACTTGG ACGCAACATT GCAAGCGCTG TGAATGGAAA CAGAATACAC 4620
TTAACATAGA AATGAATGAT TGCTTTCGCT TCTACAGTGC AAGGATTTTT TTGTACAAAA 4680
CTTTTTTAAA TATAAATGTT AAGAAAAATT TTTTTTAAAA AACACTTCAT TATGTTTAGG 4740
GGGGAACTGC ATTTTAGGGT TCCATTGTCT TGGTGGTGTT ACAAGACTTG TTATCCATTT 4800
AAAAATGGTA GTGGAAATTC TATGCCTTGG ATACACACCG CTCTTCAGGT TGTAAAAAAA 4860
AAAAACATAC ATTGGGGAAA GGTTTAAGAT TATATAGTAC TTAAATATAG GAAAATGCAC 4920
ACTCATGTTG ATTCCTATGC TAAAATACAT TTATGGTCTT TTTTCTGTAT TTCTAGAATG 4980
GTATTTGAAT TAAATGTTCA TCTAGTGTTA GGCACTATAG TATTTATATT GAAGCTTGTA 5040
TTTTTAACTG TTGCTTGTTC TCTTAAAAGG TATCAATGTA CCTTTTTTGG TAGTGGAAAA 5100
AAAAAAGACA GGCTGCCACA GTATATTTTT TTAATTTGGC AGGATAATAT AGTGCAAATT 5160
ATTTGTATGC TTCAAAAAAA AAAAAAAGAG AGAAACAAAA AAGTGTGACA TTACAGATGA 5220
GAAGCCATAT AATGGCGGTT TGGGGGAGCC TGCTAGAATG TCACATGGAT GGCTGTCATA 5280
GGGGTTGTAC ATATCCTTTT TTGTTCCTTT TTCCTGCTGC CATACTGTAT GCAGTACTGC 5340
AAGCTAATAA CGTTGGTTTG TTATGTAGTG TGCTTTTTGT CCCTTTCCTT CTATCACCCT 5400
ACATTCCAGC ATCTTACCTT CATATGCAGT AAAAGAAAGA AAGAAAAAAA AAGGAAAAAA 5460
AAAAAAAAAC CAATGTTTTG CAGTTTTTTT CATTGCCAAA AACTAAATGG TGCTTTATAT 5520
TTAGATTGGA AAGAATTTCA TATGCAAAGC ATATTAAAGA GAAAGCCCGC TTTAGTCAAT 5580
ACTTTTTTGT AAATGGCAAT GCAGAATATT TTGTTATTGG CCTTTTCTAT TCCTGTAATG 5640
AAAGCTGTTT GTCGTAACTT GAAATTTTAT CTTTTACTAT GGGAGTCACT ATTTATTATT 5700
GCTTATGTGC CCTGTTCAAA ACAGAGGCAC TTAATTTGAT CTTTTATTTT TCTTTGTTTT 5760
TATTTTTTTT TTTATTTAGA TGACCAAAGG TCATTACAAC CTGGCTTTTT ATTGTATTTG 5820
TTTCTGGTCT TTGTTAAGTT CTATTGGAAA AACCACTGTC TGTGTTTTTT TGGCAGTTGT 5880
CTGCATTAAC CTGTTCATAC ACCCATTTTG TCCCTTTATT GAAAAAATAA AAAAAATTAA 5940
A

Seq ID NO: 85 Protein sequence:
Protein Accession #: NP_075044.1

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1          11         21         31         41         51
|          |          |          |          |          |
MSRRKQGKPQ HLSKREFSPE PLEAILTDDE PDHGPLGAPE GDHDLLTCGQ CQMNFPLGDI    60
LIFIEHKRKQ CNGSLCLEKA VDKPPSPSPI EMKKASNPVE VGIQVTPEDD DCLSTSSRRI   120
CPKQEHIADK LLHWRGLSSP RSAHGALIPT PGMSAEYAPQ GICKDEPSSY TCTTCKQPFT   180
SAWFLLQHAQ NTHGLRIYLE SEHGSPLTPR VGIPSGLGAE CPSQPPLHGI HIADNNPFNL   240
LRIPGSVSRE ASGLAEGRFP PTPPLFSPPP RHHLDPHRIE RLGAEEMALA THHPSAFDRV   300
LRLNPMAMEP PAMDFSRRLR ELAGNTSSPP LSPGRPSPMQ RLLQPFQPGS KPPFLATPPL   360
PPLQSAPPPS QPPVKSKSCE FCGKTFKFQS NLVVHRRSHT GEKPYKCNLC DHACTQASKL   420
KRHMKTHMHK SSPMTVKSDD GLSTASSPEP GTSDLVGSAS SALKSVVAKF KSENDPNLIP   480
ENGDEEEEED DEEEEEEEEE EEEELTESER VDYGFGLSLE AARHHENSSR GAVVGVGDES   540
RALPDVMQGM VLSSMQHFSE AFHQVLGEKH KRGHLAEAEG HRDTCDEDSV AGESDRIDDG   600
TVNGRGCSPG ESASGGLSKK LLLGSPSSLS PFSKRIKLEK EFDLPPATMP NTENVYSQWL   660
AGYAASRQLK DPFLSFGDSR QSPFASSSEH SSENGSLRFS TPPGELDGGI SGRSGTGSGG   720
STPHISGPGT GRPSSKEGRR SDTCEYCGKV FKNCSNLTVH RRSHTGERPY KCELCNYACA   780
QSSKLTRHMK THGQVGKDVY KCEICKMPFS VYSTLEKHMK KWHSDRVLNN DIKTE
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Seq ID NO: 86 DNA sequence
Nucleic Acid Accession #: XM_035292.2
Coding sequence: 53-1576

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1          11         21         31         41         51
|          |          |          |          |          |
GCTCGCTGGG CCGCGGCTCC CGGGTGTCCC AGGCCCGGCC GGTGCGCAGA GCATGGCGGG    60
TGCGGGCCCG AAGCGGCGCG CGCTAGCGGC GCCGGCGGCC GAGGAGAAGG AAGAGGCGCG   120
GGAGAAGATG CTGGCCGCCA AGAGCGCGGA CGGCTCGGCG CCGGCAGGCG AGGGCGAGGG   180
CGTGACCCTG CAGCGGAACA TCACGCTGCT CAACGGCGTG GCCATCATCG TGGGGACCAT   240
TATCGGCTCG GGCATCTTCG TGACGCCCAC GGGCGTGCTC AAGGAGGCAG GCTCGCCGGG   300
GCTGGCGCTG GTGGTGTGGG CCGCGTGCGG CGTCTTCTCC ATCGTGGGCG CGCTCTGCTA   360
CGCGGAGCTC GGCACCACCA TCTCCAAATC GGGCGGCGAC TACGCCTACA TGCTGGAGGT   420
CTACGGCTCG CTGCCCGCCT TCCTCAAGCT CTGGATCGAG CTGCTCATCA TCCGGCCTTC   480
ATCGCAGTAC ATCGTGGCCC TGGTCTTCGC CACCTACCTG CTCAAGCCGC TCTTCCCCAC   540
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CTGCCCGGTG CCCGAGGAGG CAGCCAAGCT CGTGGCCTGC CTCTGCGTGC TGCTGCTCAC   600
GGCCGTGAAC TGCTACAGCG TGAAGGCCGC CACCCGGGTC CAGGATGCCT TTGCCGCCGC   660
CAAGCTCCTG GCCCTGGCCC TGATCATCCT GCTGGGCTTC GTCCAGATCG GGAAGGGTGA   720
TGTGTCCAAT CTAGATCCCA ACTTCTCATT TGAAGGCACC AAACTGGATG TGGGGAACAT   780
TGTGCTGGCA TTATACAGCG GCCTCTTTGC CTATGGAGGA TGGAATTACT TGAATTTCGT   840
CACAGAGGAA ATGATCAACC CCTACAGAAA CCTGCCCCTG GCCATCATCA TCTCCCTGCC   900
CATCGTGACG CTGGTGTACG TGCTGACCAA CCTGGCCTAC TTCACCACCC TGTCCACCGA   960
GCAGATGCTG TCGTCCGAGG CCGTGGCCGT GGACTTCGGG AACTATCACC TGGGCGTCAT  1020
GTCCTGGATC ATCCCCGTCT TCGTGGGCCT GTCCTGCTTC GGCTCCGTCA ATGGGTCCCT  1080
GTTCACATCC TCCAGGCTCT TCTTCGTGGG GTCCCGGGAA GGCCACCTGC CCTCCATCCT  1140
CTCCATGATC CACCCACAGC TCCTCACCCC CGTGCCGTCC CTCGTGTTCA CGTGTGTGAT  1200
GACGCTGCTC TACGCCTTCT CCAAGGACAT CTTCTCCGTC ATCAACTTCT TCAGCTTCTT  1260
CAACTGGCTC TGCGTGGCCC TGGCCATCAT CGGCATGATC TGGCTGCGCC ACAGAAAGCC  1320
TGAGCTTGAG CGGCCCATCA AGGTGAACCT GGCCCTGCCT GTGTTCTTCA TCCTGGCCTG  1380
CCTCTTCCTG ATCGCCGTCT CCTTCTGGAA GACACCCGTG GAGTGTGGCA TCGGCTTCAC  1440
CATCATCCTC AGCGGGCTGC CCGTCTACTT CTTCGGGGTC TGGTGGAAAA ACAAGCCCAA  1500
GTGGCTCCTC CAGGGCATCT TCTCCACGAC CGTCCTGTGT CAGAAGCTCA TGCAGGTGGT  1560
CCCCCAGGAG ACATAGCCAG GAGGCCGAGT GGCTGCCGGA GGAGCATGC
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Seq ID NO: 87 Protein sequence:
Protein Accession #: XP_035292.2

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1          11         21         31         41         51
|          |          |          |          |          |
MAGAGPKRRA LAAPAAEEKE EAREKMLAAK SADGSAPAGE GEGVTLQRNI TLLNGVAIIV    60
GTIIGSGIFV TPTGVLKEAG SPGLALVVWA ACGVFSIVGA LCYAELGTTI SKSGGDYAYM   120
LEVYGSLPAF LKLWIELLII RPSSQYIVAL VFATYLLKPL FPTCPVPEEA AKLVACLCVL   180
LLTAVNCYSV KAATRVQDAF AAAKLLALAL IILLGFVQIG KGDVSNLDPN FSFEGTKLDV   240
GNIVLALYSG LFAYGGWNYL NFVTEEMINP YRNLPLAIII SLPIVTLVYV LTNLAYFTTL   300
STEQMLSSEA VAVDFGNYHL GVMSWIIPVF VGLSCFGSVN GSLFTSSRLF FVGSREGHLP   360
SILSMIHPQL LTPVPSLVFT CVMTLLYAFS KDIFSVINFF SFFNWLCVAL AIIGMIWLRH   420
RKPELERPIK VNLALPVFFI LACLFLIAVS FWKTPVECGI GFTIILSGLP VYFFGVWWKN   480
KPKWLLQGIF STTVLCQKLM QVVPQET
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Seq ID NO: 88 DNA sequence
Nucleic Acid Accession #: NM_005268.1
Coding sequence: 168-989

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1          11         21         31         41         51
|          |          |          |          |          |
TAAAAAGCAA AAGAATTCGC GGCCGCGTCG ACACGGGCTT CCCCGAAAAC CTTCCCCGCT    60
TCTGGATATG AAATTCAAGC TGCTTGCTGA GTCCTATTGC CGGCTGCTGG GAGCCAGGAG   120
AGCCCTGAGG AGTAGTCACT CAGTAGCAGC TGACGCGTGG GTCCACCATG AACTGGAGTA   180
TCTTTGAGGG ACTCCTGAGT GGGGTCAACA AGTACTCCAC AGCCTTTGGG CGCATCTGGC   240
TGTCTCTGGT CTTCATCTTC CGCGTGCTGG TGTACCTGGT GACGGCCGAG CGTGTGTGGA   300
GTGATGACCA CAAGGACTTC GACTGCAATA CTCGCCAGCC CGGCTGCTCC AACGTCTGCT   360
TTGATGAGTT CTTCCCTGTG TCCCATGTGC GCCTCTGGGC CCTGCAGCTT ATCCTGGTGA   420
CATGCCCCTC ACTGCTCGTG GTCATGCACG TGGCCTACCG GGAGGTTCAG GAGAAGAGGC   480
ACCGAGAAGC CCATGGGGAG AACAGTGGGC GCCTCTACCT GAACCCCGGC AAGAAGCGGG   540
GTGGGCTCTG GTGGACATAT GTCTGCAGCC TAGTGTTCAA GGCGAGCGTG GACATCGCCT   600
TTCTCTATGT GTTCCACTCA TTCTACCCCA AATATATCCT CCCTCCTGTG GTCAAGTGCC   660
ACGCAGATCC ATGTCCCAAT ATAGTGGACT GCTTCATCTC CAAGCCCTCA GAGAAGAACA   720
TTTTCACCCT CTTCATGGTG GCCACAGCTG CCATCTGCAT CCTGCTCAAC CTCGTGGAGC   780
TCATCTACCT GGTGAGCAAG AGATGCCACG AGTGCCTGGC AGCAAGGAAA GCTCAAGCCA   840
TGTGCACAGG TCATCACCCC CACGGTACCA CCTCTTCCTG CAAACAAGAC GACCTCCTTT   900
CGGGTGACCT CATCTTTCTG GGCTCAGACA GTCATCCTCC TCTCTTACCA GACCGCCCCC   960
GAGACCATGT GAAGAAAACC ATCTTGTGAG GGGCTGCCTG GACTGGTCTG GCAGGTTGGG  1020
CCTGGATGGG GAGGCTCTAG CATCTCTCAT AGGTGCAACC TGAGAGTGGG GGAGCTAAGC  1080
CATGAGGTAG GGGCAGGCAA GAGAGAGGAT TCAGACGCTC TGGGAGCCAG TTCCTAGTCC  1140
TCAACTCCAG CCACCTGCCC CAGCTCGACG GCACTGGGCC AGTTCCCCCT CTGCTCTGCA  1200
GCTCGGTTTC CTTTTCTAGA ATGGAAATAG TGAGGGCCAA TGC
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Seq ID NO: 89 Protein sequence:
Protein Accession #: NP_005259.1

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1          11         21         31         41         51
|          |          |          |          |          |
MNWSIFEGLL SGVNKYSTAF GRIWLSLVFI FRVLVYLVTA ERVWSDDHKD FDCNTRQPGC    60
SNVCFDEFFP VSHVRLWALQ LILVTCPSLL VVMHVAYREV QEKRHREAHG ENSGRLYLNP   120
GKKRGGLWWT YVCSLVFKAS VDIAFLYVFH SFYPKYILPP VVKCHADPCP NIVDCFISKP   180
SEKNIFTLFM VATAAICILL NLVELIYLVS KRCHECLAAR KAQAMCTGHH PHGTTSSCKQ   240
DDLLSGDLIF LGSDSHPPLL PDRPRDHVKK TIL
```

Seq ID NO: 90 DNA sequence
Nucleic Acid Accession #: NM_002391.1
Coding sequence: 26-457

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1          11         21         31         41         51
|          |          |          |          |          |
CGGGCGAAGC AGCGCGGGCA GCGAGATGCA GCACCGAGGC TTCCTCCTCC TCACCCTCCT    60
CGCCCTGCTG GCGCTCACCT CCGCGGTCGC CAAAAAGAAA GATAAGGTGA AGAAGGGCGG   120
CCCGGGGAGC GAGTGCGCTG AGTGGGCCTG GGGGCCCTGC ACCCCCAGCA GCAAGGATTG   180
CGGCGTGGGT TTCCGCGAGG GCACCTGCGG GGCCCAGACC CAGCGCATCC GGTGCAGGGT   240
GCCCTGCAAC TGGAAGAAGG AGTTTGGAGC CGACTGCAAG TACAAGTTTG AGAACTGGGG   300
TGCGTGTGAT GGGGGCACAG GCACCAAAGT CCGCCAAGGC ACCCTGAAGA AGGCGCGCTA   360
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CAATGCTCAG TGCCAGGAGA CCATCCGCGT CACCAAGCCC TGCACCCCCA AGACCAAAGC    420
AAAGGCCAAA GCCAAGAAAG GGAAGGGAAA GGACTAGACG CCAAGCCTGG ATGCCAAGGA    480
GCCCCTGGTG TCACATGGGG CCTGGCCACG CCCTCCCTCT CCCAGGCCCG AGATGTGACC    540
CACCAGTGCC TTCTGTCTGC TCGTTAGCTT TAATCAATCA TGCCCTGCCT TGTCCCTCTC    600
ACTCCCCAGC CCCACCCCTA AGTGCCCAAA GTGGGGAGGG ACAAGGGATT CTGGGAAGCT    660
TGAGCCTCCC CCAAAGCAAT GTGAGTCCCA GAGCCCGCTT TTGTTCTTCC CCACAATTCC    720
ATTACTAAGA AACACATCAA ATAAACTGAC TTTTTCCCCC CAATAAAAGC TCTTCTTTTT    780
TAATAT
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Seq ID NO: 91 Protein sequence:
Protein Accession #: NP_002382.1

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1          11         21         31         41         51
|          |          |          |          |          |
MQHRGFLLLT LLALLALTSA VAKKKDKVKK GGPGSECAEW AWGPCTPSSK DCGVGFREGT     60
CGAQTQRIRC RVPCNWKKEF GADCKYKFEN WGACDGGTGT KVRQGTLKKA RYNAQCQETI    120
RVTKPCTPKT KAKAKAKKGK GKD
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Seq ID NO: 92 DNA sequence
Nucleic Acid Accession #: NM_005130.1
Coding sequence: 98-802

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1          11         21         31         41         51
|          |          |          |          |          |
CTCTACCTGA CACAGCTGCA GCCTGCAATT CACTCCCACT GCCTGGGATT GCACTGGATC     60
CGTGTGCTCA GAACAAGGTG AACGCCCAGC TGCAGCCATG AAGATCTGTA GCCTCACCCT    120
GCTCTCCTTC CTCCTACTGG CTGCTCAGGT GCTCCTGGTG GAGGGGAAAA AAAAAGTGAA    180
GAATGGACTT CACAGCAAAG TGGTCTCAGA ACAAAAGGAC ACTCTGGGCA ACACCCAGAT    240
TAAGCAGAAA AGCAGGCCCG GGAACAAAGG CAAGTTTGTC ACCAAAGACC AAGCCAACTG    300
CAGATGGGCT GCTACTGAGC AGGAGGAGGG CATCTCTCTC AAGGTTGAGT GCACTCAATT    360
GGACCATGAA TTTTCCTGTG TCTTTGCTGG CAATCCAACC TCATGCCTAA AGCTCAAGGA    420
TGAGAGAGTC TATTGGAAAC AAGTTGCCCG GAATCTGCGC TCACAGAAAG ACATCTGTAG    480
ATATTCCAAG ACAGCTGTGA AAACCAGAGT GTGCAGAAAG GATTTTCCAG AATCCAGTCT    540
TAAGCTAGTC AGCTCCACTC TATTTGGGAA CACAAAGCCC AGGAAGGAGA AAACAGAGAT    600
GTCCCCCAGG GAGCACATCA AGGGCAAAGA GACCACCCCC TCTAGCCTAG CAGTGACCCA    660
GACCATGGCC ACCAAAGCTC CCGAGTGTGT GGAGGACCCA GATATGGCAA ACCAGAGGAA    720
GACTGCCCTG GAGTTCTGTG GAGAGACTTG GAGCTCTCTC TGCACATTCT TCCTCAGCAT    780
AGTGCAGGAC ACGTCATGCT AATGAGGTCA AAAGAGAACG GGTTCCTTTA AGAGATGTCA    840
TGTCGTAAGT CCCTCTGTAT ACTTTAAAGC TCTCTACAGT CCCCCCAAAA TATGAACTTT    900
TGTGCTTAGT GAGTGCAACG AAATATTTAA ACAAGTTTTG TATTTTTTGC TTTTGTGTTT    960
TGGAATTTGC CTTATTTTTC TTGGATGCGA TGTTCAGAGG CTGTTTCCTG CAGCATGTAT   1020
TTCCATGGCC CACACAGCTA TGTGTTTGAG CAGCGAAGAG TCTTTGAGCT GAATGAGCCA   1080
GAGTGATAAT TTCAGTGCAA CGAACTTTCT GCTGAATTAA TGGTAATAAA ACTCTGGGTG   1140
TTTTTCAAAA AAAAAAAAAA AAA
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Seq ID NO: 93 Protein sequence:
Protein Accession #: NP_005121.1

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1          11         21         31         41         51
|          |          |          |          |          |
MKICSLTLLS FLLLAAQVLL VEGKKKVKNG LHSKVVSEQK DTLGNTQIKQ KSRPGNKGKF     60
VTKDQANCRW AATEQEEGIS LKVECTQLDH EFSCVFAGNP TSCLKLKDER VYWKQVARNL    120
RSQKDICRYS KTAVKTRVCR KDFPESSLKL VSSTLFGNTK PRKEKTEMSP REHIKGKETT    180
PSSLAVTQTM ATKAPECVED PDMANQRKTA LEFCGETWSS LCTFFLSIVQ DTSC
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Seq ID NO: 94 DNA sequence
Nucleic Acid Accession #: NM_012101
Coding sequence: 125-1891

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1          11         21         31         41         51
|          |          |          |          |          |
CTCCTCACAG GTGTGTCTCT AGTCCTCGTG GTTGCCTGCC CCACTCCCTG CCGAGACGCC     60
TGCCAGAAAG GTCACCTATC CTGAACCCCA GCAAGCCTGA AACAGCTCAG CCAAGCACCC    120
TGCGATGGAA GCTGCAGATG CCTCCAGGAG CAACGGGTCG AGCCCAGAAG CCAGGGATGC    180
CCGGAGCCCG TCGGGCCCCA GTGGCAGCCT GGAGAATGGC ACCAAGGCTG ACGGCAAGGA    240
TGCCAAGACC ACCAACGGGC ACGGCGGGGA GGCAGCTGAG GGCAAGAGCC TGGGCAGCGC    300
CCTGAAGCCA GGGGAAGGTA GGAGCGCCCT GTTCGCGGGC AATGAGTGGC GGCGACCCAT    360
CATCCAGTTT GTCGAGTCCG GGGACGACAA GAACTCCAAC TACTTCAGCA TGGACTCTAT    420
GGAAGGCAAG AGGTCGCCGT ACGCAGGGCT CCAGCTGGGG GCTGCCAAGA AGCCACCCGT    480
TACCTTTGCC GAAAAGGGCG ACGTGCGCAA GTCCATTTTC TCGGAGTCCC GGAAGCCCAC    540
GGTGTCCATC ATGGAGCCCG GGGAGACCCG GCGGAACAGC TACCCCCGGG CCGACACGGG    600
CCTTTTTTCA CGGTCCAAGT CCGGCTCCGA GGAGGTGCTG TGCGACTCCT GCATCGGCAA    660
CAAGCAGAAG GCGGTCAAGT CCTGCCTGGT GTGCCAGGCC TCCTTCTGCG AGCTGCATCT    720
CAAGCCCCAC CTGGAGGGCG CCGCCTTCCG AGACCACCAG CTGCTCGAGC CCATCCGGGA    780
CTTTGAGGCC CGCAAGTGTC CCGTGCATGG CAAGACGATG GAGCTCTTCT GCCAGACCGA    840
CCAGACCTGC ATCTGCTACC TTTGCATGTT CCAGGAGCAC AAGAATCATA GCACCGTGAC    900
AGTGGAGGAG GCCAAGGCCG AGAAGGAGAC GGAGCTGTCA CTGCAAAAGG AGCAGCTGCA    960
GCTCAAGATC ATTGAGATTG AGGATGAAGC TGAGAAGTGG CAGAAGGAGA AGGACCGCAT   1020
CAAGAGCTTC ACCACCAATG AGAAGGCCAT CCTGGAGCAG AACTTCCGGG ACCTGGTGCG   1080
GGACCTGGAG AAGCAAAAGG AGGAAGTGAG GGCTGCGCTG GAGCAGCGGG AGCAGGATGC   1140
TGTGGACCAA GTGAAGGTGA TCATGGATGC TCTGGATGAG AGAGCCAAGG TGCTGCATGA   1200
GGACAAGCAG ACCCGGGAGC AGCTGCATAG CATCAGCGAC TCTGTGTTGT TTCTGCAGGA   1260
ATTTGGTGCA TTGATGAGCA ATTACTCTCT CCCCCCACCC CTGCCCACCT ATCATGTCCT   1320
GCTGGAGGGG GAGGGCCTGG GACAGTCACT AGGCAACTTC AAGGACGACC TGCTCAATGT   1380
ATGCATGCGC CACGTTGAGA AGATGTGCAA GGCGGACCTG AGCCGTAACT TCATTGAGAG   1440
GAACCACATG GAGAACGGTG GTGACCATCG CTATGTGAAC AACTACACGA ACAGCTTCGG   1500
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GGGTGAGTGG AGTGCACCGG ACACCATGAA GAGATACTCC ATGTACCTGA CACCCAAAGG  1560
TGGGGTCCGG ACATCATACC AGCCCTCGTC TCCTGGCCGC TTCACCAAGG AGACCACCCA  1620
GAAGAATTTC AACAATCTCT ATGGCACCAA AGGTAACTAC ACCTCCCGGG TCTGGGAGTA  1680
CTCCTCCAGC ATTCAGAACT CTGACAATGA CCTGCCCGTC GTCCAAGGCA GCTCCTCCTT  1740
CTCCCTGAAA GGCTATCCCT CCCTCATGCG GAGCCAAAGC CCCAAGGCCC AGCCCCAGAC  1800
TTGGAAATCT GGCAAGCAGA CTATGCTGTC TCACTACCGG CCATTCTACG TCAACAAAGG  1860
CAACGGGATT GGGTCCAACG AAGCCCCATG AGCTCCTGGC GGAAGGAACG AGGCGCCACA  1920
CCCCTGCTCT TCCTCCTGAC CCTGCTGCTC TTGCCTTCTA AGCTACTGTG CTTGTCTGGG  1980
TGGGAGGGAG CCTGGTCCTG CACCTGCCCT CTGCAGCCCT CTGCCAGCCT CTTGGGGGCA  2040
GTTCCGGCCT CTCCGACTTC CCCACTGGCC ACACTCCATT CAGACTCCTT TCCTGCCTTG  2100
TGACCTCAGA TGGTCACCAT CATTCCTGTG CTCAGAGGCC AACCCATCAC AGGGGTGAGA  2160
TAGGTTGGGG CCTGCCCTAA CCCGCCAGCC TCCTCCTCTC GGGCTGGATC TGGGGGCTAG  2220
CAGTGAGTAC CCGCATGGTA TCAGCCTGCC TCTCCCGCCC ACGCCCTGCT GTCTCCAGGC  2280
CTATAGACGT TTCTCTCCAA GGCCCTATCC CCCAATGTTG TCAGCAGATG CCTGGACAGC  2340
ACAGCCACCC ATCTCCCATT CACATGGCCC ACCTCCTGCT TCCCAGAGGA CTGGCCCTAC  2400
GTGCTCTCTC TCGTCCTACC TATCAATGCC CAGCATGGCA GAACCTGCAG TGGCCAAGGG  2460
CTGCAGATGG AAACCTCTCA GTGTCTTGAC ATCACCCTAC CCAGGCGGTG GGTCTCCACC  2520
ACAGCCACTT TGAGTCTGTG GTCCCTGGAG GGTGGCTTCT CCTGACTGGC AGGATGACCT  2580
TAGCCAAGAT ATTCCTCTGT TCCCTCTGCT GAGATAAAGA ATTCCCTTAA CATGATATAA  2640
TCCACCCATG CAAATAGCTA CTGGCCCAGC TACCATTTAC CATTTGCCTA CAGAATTTCA  2700
TTCAGTCTAC ACTTTGGCAT TCTCTCTGGC GATGGAGTGT GGCTGGGCTG ACCGCAAAAG  2760
GTGCCTTACA CACTGCCCCC ACCCTCAGCC GTTGCCCCAT CAGAGGCTGC CTCCTCCTTC  2820
TGATTACCCC CCATGTTGCA TATCAGGGTG CTCAAGGATT GGAGAGGAGA CAAAACCAGG  2880
AGCAGCACAG TGGGGACATC TCCCGTCTCA ACAGCCCCAG GCCTATGGGG GCTCTGGAAG  2940
GATGGGCCAG CTTGCAGGGG TTGGGGAGGG AGACATCCAG CTTGGGCTTT CCCCTTTGGA  3000
ATAAACCATT GGTCTGTC
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Seq ID NO: 95 Protein sequence:
Protein Accession #: NP_036233.1

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1          11         21         31         41         51
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MEAADASRSN GSSPEARDAR SPSGPSGSLE NGTKADGKDA KTTNGHGGEA AEGKSLGSAL    60
KPGEGRSALF AGNEWRRPII QFVESGDDKN SNYFSMDSME GKRSPYAGLQ LGAAKKPPVT   120
FAEKGDVRKS IFSESRKPTV SIMEPGETRR NSYPRADTGL FSRSKSGSEE VLCDSCIGNK   180
QKAVKSCLVC QASFCELHLK PHLEGAAFRD HQLLEPIRDF EARKCPVHGK TMELFCQTDQ   240
TCICYLCMFQ EHKNHSTVTV EEAKAEKETE LSLQKEQLQL KIIEIEDEAE KWQKEKDRIK   300
SFTTNEKAIL EQNFRDLVRD LEKQKEEVRA ALEQREQDAV DQVKVIMDAL DERAKVLHED   360
KQTREQLHSI SDSVLFLQEF GALMSNYSLP PPLPTYHVLL EGEGLGQSLG NFKDDLLNVC   420
MRHVEKMCKA DLSRNFIERN HMENGGDHRY VNNYTNSFGG EWSAPDTMKR YSMYLTPKGG   480
VRTSYQPSSP GRFTKETTQK NFNNLYGTKG NYTSRVWEYS SSIQNSDNDL PVVQGSSSFS   540
LKGYPSLMRS QSPKAQPQTW KSGKQTMLSH YRPFYVNKGN GIGSNEAP
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Seq ID NO: 96 DNA sequence
Nucleic Acid Accession #: NM_080668.1
Coding sequence: 83-841

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1          11         21         31         41         51
|          |          |          |          |          |
GGCACGAGGG CAGCGAGTGG CCTTCCCGGT TGGCGCGCGC CCGGGGCGGC GGCGCTGGAG    60
GAGCTCGAGA CGGAGCCTAG TTATGTCTGG GAGGCGAACG CGGTCCGGAG GAGCCGCTCA   120
GCGCTCCGGG CCAAGGGCCC CATCTCCTAC TAAGCCTCTG CGGAGGTCCC AGCGGAAATC   180
AGGCTCTGAA CTCCCGAGCA TCCTCCCTGA AATCTGGCCG AAGACACCCA GTGCGGCTGC   240
AGTCAGAAAG CCCATCGTCT TAAAGAGGAT CGTGGCCCAT GCTGTAGAGG TCCCAGCTGT   300
CCAATCACCT CGCAGGAGCC CTAGGATTTC CTTTTTCTTG GAGAAAGAAA ACGAGCCCCC   360
TGGCAGGGAG CTTACTAAGG AGGACCTTTT CAAGACACAC AGCGTCCCTG CCACCCCCAC   420
CAGCACTCCT GTGCCGAACC CTGAGGCCGA GTCCAGCTCC AAGGAAGGAG AGCTGGACGC   480
CAGAGACTTG GAAATGTCTA AGAAAGTCAG GCGTTCCTAC AGCCGGCTGG AGACCCTGGG   540
CTCTGCCTCT ACCTCCACCC CAGGCCGCCG GTCCTGCTTT GGCTTCGAGG GGCTGCTGGG   600
GGCAGAAGAC TTGTCCGGAG TCTCGCCAGT GGTGTGCTCC AAACTCACCG AGGTCCCCAG   660
GGTTTGTGCA AAGCCCTGGG CCCCAGACAT GACTCTCCCT GGAATCTCCC CACCACCCGA   720
GAAACAGAAA CGTAAGAAGA AGAAAATGCC AGAGATCTTG AAAACGGAGC TGGATGAGTG   780
GGCTGCGGCC ATGAATGCCG AGTTTGAAGC TGCTGAGCAG TTTGATCTCC TGGTTGAATG   840
AGATGCAGTG GGGGGTGCAC CTGGCCAGAC TCTCCCTCCT GTCCTGTACA TAGCCACCTC   900
CCTGTGGAGA GGACACTTAG GGTCCCCTCC CCTGGTCTTG TTACCTGTGT GTGTGCTGGT   960
GCTGCGCATG AGGACTGTCT GCCTTTGAGG GCTTGGGCAG CAGCGGCAGC CATCTTGGTT  1020
TTAGGAAATG GGCCGCCTG GCCCAGCCAC TCACTGGTGT CCTGTCTCTT GTCGTCCTGT  1080
CCTTCCTATC TCCCCAAAGT ACCATAGCCA GTTTCCAGAT GGGCCACAGA CTGGGGAGGA  1140
GAATCAGTGG CCCAGCCAGA AGTTAAAGGG CTGAGGGTTG AGGTGAGAGG CACCTCTGCT  1200
CTTGTTGGGA GGGGTGGCTG CTTGGAAATA GGCCCAGGGG CTCTGCCAGC CTCGGCCTCT  1260
CCCTCCTGAG TTGCCTTCTG TTGGTGGCTT TCTTCTTGAA CCCACCTGTG TAAAGAGGTT  1320
TTCAGTTCCG TGGGTTTCCC CTTTGATTCT GTAAATAGTC CCAGAGAGAA TTCGTGGGCT  1380
GAGGGCAATT CTGTCTTGGA GGAAGAAGCT GGACATTCAG CCTGTGGAGT CTGAGTTTTG  1440
AAGGATGTAG GGAGCCTTAG TTGGGTCTCA GACCATAAGT GTGTACTACA CAGAAGCTGT  1500
GTTTTCTAGT TCTGGTCTGC TGTTGAGATG TTTGGTAAAT GCCAGGTTGA TAGGGCGCTG  1560
GCTGCTTGGA GCAAAGGGTG CATTTCAGGG TGTGGCCACC AGGTGCTGTG AGTTTCTGTG  1620
GCTCATGGCC TCTGGGCTGG TCCCTTGCAC AGGGCCCACG CTGGAGTCTT ACCACTCTGC  1680
TGCAGGGGTG GAAGGTGGCC CCTCTTGTCA CCCATACCCA TTTCTTACAA AATAAGTTAC  1740
ACCGAGTCTA CTTGGCCCTA GAAGAGAAAG TTGAAGAGTC CCAGACCTAC TAGCATTTTG  1800
CAACTATGCT TGTAAAGTCC TCGGAAAGTT TCCTCGCGTA CCAGACAGCG GCGGGGGCTG  1860
ATAGCAATTT TAGTTTTTGG CCTCCCTATC CTCTCACATG AGAACACTGC CTGGATGCAT  1920
CTCATGATCT CTGGAGAATT TCCCCATCTT TCTCTTCTTT CCATCGTGTG GATTCAATAG  1980
TTTGGATTTG AAGGCTGCCC TGCCCCCGAC TCTCCTGCCG CACCCCTGGC CATTGTACCT  2040
TTTGATGTTT AGAAGTTCGT GGAAGTAGAC GCTGAGGTGT GCAGAGGAGC TGGTGGATAA  2100
CAGAGAATGC CAGGGAAGAT GAGTGCTGGG TCAGGGTACT TGGATGAAAC GGTGCAGGCC  2160
AGGCGGGCCC TAATAAAACC CTCTGCCAGG TCTGGGAGTC CCAGGCCATC TGCTCAACGC  2220
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TCTGTGGTTT GTCAGACCTG CAAGCAAGCC CCCTGCTGGG GAAGCCTAGG TGTCCTTGAG  2280
CTGAACCGCA CTGAAGAACT CTTGTCCTCA CTGGCTGATG CAGCAGAACT CTTGGGAAAT  2340
GTCTTAGTCC TGCAGAATCA GGAGTCACCA GATGATGCAG AGTTGAGATC ATCATTGCAA  2400
AGTTCTCTGT TCCTGAGGAA CTAAATTTAA GGAAAAAATG GGATTTTGTT TTAGAGTTGG  2460
AAAAAAAGCC TGATTAAAGA GTTTCTGCCT GTTAAAAAAA AAAAAAAAAA AAAAAA
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Seq ID NO: 97 Protein sequence:
Protein Accession #: NP_542399.1

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1          11         21         31         41         51
|          |          |          |          |          |
MSGRRTRSGG AAQRSGPRAP SPTKPLRRSQ RKSGSELPSI LPEIWPKTPS AAAVRKPIVL   60
KRIVAHAVEV PAVQSPRRSP RISFFLEKEN EPPGRELTKE DLFKTHSVPA TPTSTPVPNP  120
EAESSSKEGE LDARDLEMSK KVRRSYSRLE TLGSASTSTP GRRSCFGFEG LLGAEDLSGV  180
SPVVCSKLTE VPRVCAKPWA PDMTLPGISP PPEKQKRKKK KMPEILKTEL DEWAAAMNAE  240
FEAAEQFDLL VE
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Seq ID NO: 98 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 58-12444

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1          11         21         31         41         51
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GGGGCATTTC CGGGTCCGGG CCGAGCGGGC GCACGCGCGG GAGCGGGACT CGGCGGCATG    60
GCGGGCTCCG GAGCCGGTGT GCGTTGCTCC CTGCTGCGGC TGCAGGAGAC CTTGTCCGCT   120
GCGGACCGCT GCGGTGCTGC CCTGGCCGGT CATCAACTGA TCCGCGGCCT GGGGCAGGAA   180
TGCGTCCTGA GCAGCAGCCC CGCGGTGCTG GCATTACAGA CATCTTTAGT TTTTTCCAGA   240
GATTTCGGTT TGCTTGTATT TGTCCGGAAG TCACTCAACA GTATTGAATT TCGTGAATGT   300
AGAGAAGAAA TCCTAAAGTT TTTATGTATT TTCTTAGAAA AAATGGGCCA GAAGATCGCA   360
CCTTACTCTG TTGAAATTAA GAACACTTGT ACCAGTGTTT ATACAAAAGA TAGAGCTGCT   420
AAATGTAAAA TTCCAGCCCT GGACCTTCTT ATTAAGTTAC TTCAGACTTT TAGAAGTTCT   480
AGACTCATGG ATGAATTTAA AATTGGAGAA TTATTTAGTA AATTCTATGG AGAACTTGCA   540
TTGAAAAAAA AAATACCAGA TACAGTTTTA GAAAAAGTAT ATGAGCTCCT AGGATTATTG   600
GGTGAAGTTC ATCCTAGTGA GATGATAAAT AATGCAGAAA ACCTGTTCCG CGCTTTTCTG   660
GGTGAACTTA AGACCCAGAT GACATCAGCA GTAAGAGAGC CCAAACTACC TGTTCTGGCA   720
GGATGTCTGA AGGGGTTGTC CTCACTTCTG TGCAACTTCA CTAAGTCCAT GGAAGAAGAT   780
CCCCAGACTT CAAGGGAGAT TTTTAATTTT GTACTAAAGG CAATTCGTCC TCAGATTGAT   840
CTGAAGAGAT ATGCTGTGCC CTCAGCTGGC TTGCGCCTAT TTGCCCTGCA TGCATCTCAG   900
TTTAGCACCT GCCTTCTGGA CAACTACGTG TCTCTATTTG AAGTCTTGTT AAAGTGGTGT   960
GCCCACACAA ATGTAGAATT GAAAAAAGCT GCACTTTCAG CCCTGGAATC CTTTCTGAAA  1020
CAGGTTTCTA ATATGGTGGC GAAAAATGCA GAAATGCATA AAAATAAACT GCAGTACTTT  1080
ATGGAGCAGT TTTATGGAAT CATCAGAAAT GTGGATTCGA ACAACAAGGA GTTATCTATT  1140
GCTATCCGTG GATATGGACT TTTTGCAGGA CCGTGCAAGG TTATAAACGC AAAAGATGTT  1200
GACTTCATGT ACGTTGAGCT CATTCAGCGC TGCAAGCAGA TGTTCCTCAC CCAGACAGAC  1260
ACTGGTGACG ACCGTGTTTA TCAGATGCCA AGCTTCCTCC AGTCTGTTGC AAGCGTCTTG  1320
CTGTACCTTG ACACAGTTCC TGAGGTGTAT ACTCCAGTTC TGGAGCACCT CGTGGTGATG  1380
CAGATAGACA GTTTCCCACA GTACAGTCCA AAAATGCAGC TGGTGTGTTG CAGAGCCATA  1440
GTGAAGGTGT TCCTAGCTTT GGCAGCAAAA GGGCCAGTTC TCAGGAATTG CATTAGTACT  1500
GTGGTGCATC AGGGTTTAAT CAGAATATGT TCTAAACCAG TGGTCCTTCC AAAGGGGCCT  1560
GAGTCTGAAT CTGAAGACCA CCGTGCTTCA GGGGAAGTCA GAACTGGCAA ATGGAAGGTG  1620
CCCACATACA AAGACTACGT GGATCTCTTC AGACATCTCC TGAGCTCTGA CCAGATGATG  1680
GATTCTATTT TAGCAGATGA AGCATTTTTC TCTGTGAATT CCTCCAGTGA AAGTCTGAAT  1740
CATTTACTTT ATGATGAATT TGTAAAATCC GTTTTGAAGA TTGTTGAGAA ATTGGATCTT  1800
ACACTTGAAA TACAGACTGT TGGGGAACAA GAGAATGGAG ATGAGGCGCC TGGTGTTTGG  1860
ATGATCCCAA CTTCAGATCC AGCGGCTAAC TTGCATCCAG CTAAACCTAA AGATTTTTCG  1920
GCTTTCATTA ACCTGGTGGA ATTTTGCAGA GAGATTCTCC CTGAGAAACA AGCAGAATTT  1980
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CTCATCAGTG GTTTCTACAA ATTGCTTTCT ATTACAGTAA GAAATGCCAA GAAAATAAAA  2100
TATTTCGAGG GAGTTAGTCC AAAGAGTCTG AAACACTCTC CTGAAGACCC AGAAAAGTAT  2160
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AAAGATGAAC TTTTGGCCTC TTGTTTGACC TTTCTTCTGT CCTTGCCACA CAACATCATT  2280
GAACTCGATG TTAGAGCCTA CGTTCCTGCA CTGCAGATGG CTTTCAAACT GGGCCTGAGC  2340
TATACCCCCT TGGCAGAAGT AGGCCTGAAT GCTCTAGAAG AATGGTCAAT TTATATTGAC  2400
AGACATGTAA TGCAGCCTTA TTACAAAGAC ATTCTCCCCT GCCTGGATGG ATACCTGAAG  2460
ACTTCAGCCT TGTCAGATGA GACCAAGAAT AACTGGGAAG TGTCAGCTCT TTCTCGGGCT  2520
GCCCAGAAAG GATTTAATAA AGTGGTGTTA AAGCATCTGA AGAAGACAAA GAACCTTTCA  2580
TCAAACGAAG CAATATCCTT AGAAGAAATA AGAATTAGAG TAGTACAAAT GCTTGGATCT  2640
CTAGGAGGAC AAATAAACAA AAATCTTCTG ACAGTCACGT CCTCAGATGA GATGATGAAG  2700
AGCTATGTGG CCTGGGACAG AGAGAAGCGG CTGAGCTTTG CAGTGCCCTT TAGAGAGATG  2760
AAACCTGTCA TTTTCCTGGA TGTGTTCCTG CCTCGAGTCA CAGAATTAGC GCTCACAGCC  2820
AGTGACAGAC AAACTAAAGT TGCAGCCTGT GAACTTTTAC ATAGCATGGT TATGTTTATG  2880
TTGGGCAAAG CCACGCAGAT GCCAGAAGGG GGACAGGGAG CCCCACCCAT GTACCAGCTC  2940
TATAAGCGGA CGTTTCCTGT GCTGCTTCGA CTTGCGTGTG ATGTTGATCA GGTGACAAGG  3000
CAACTGTATG AGCCACTAGT TATGCAGCTG ATTCACTGGT TCACTAACAA CAAGAAATTT  3060
GAAAGTCAGG ATACTGTTGC CTTACTAGAA GCTATATTGG ATGGAATTGT GGACCCTGTT  3120
GACAGTACTT TAAGAGATTT TTGTGGTCGG TGTATTCGAG AATTCCTTAA ATGGTCCATT  3180
AAGCAAATAA CACCACAGCA GCAGGAGAAG AGTCCAGTAA ACACCAAATC GCTTTTCAAG  3240
CGACTTTATA GCCTTGCGCT TCACCCCAAT GCTTTCAAGA GGCTGGGAGC ATCACTTGCC  3300
TTTAATAATA TCTACAGGGA ATTCAGGGAA GAAGAGTCTC TGGTGGAACA GTTTGTGTTT  3360
GAAGCCTTGG TGATATACAT GGAGAGTCTG GCCTTAGCAC ATGCAGATGA GAAGTCCTTA  3420
GGTACAATTC AACAGTGTTG TGATGCCATT GATCACCTAT GCCGCATCAT TGAAAAGAAG  3480
CATGTTTCTT TAAATAAAGC AAAGAAACGA CGTTTGCCGC GAGGATTTCC ACCTTCCGCA  3540
TCATTGTGTT TATTGGATCT GGTCAAGTGG CTTTTAGCTC ATTGTGGGAG GCCCCAGACA  3600
GAATGTCGAC ACAAATCCAT TGAACTCTTT TATAAATTCG TTCCTTTATT GCCAGGCAAC  3660
AGATCCCCTA ATTTGTGGCT GAAAGATGTT CTCAAGGAAG AAGGTGTCTC TTTTCTCATC  3720
AACACCTTTG AGGGGGGTGG CTGTGGCCAG CCCTCGGGCA TCCTGGCCCA GCCCACCCTC  3780
TTGTACCTTC GGGGGCCATT CAGCCTGCAG GCCACGCTAT GCTGGCTGGA CCTGCTCCTG  3840
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GCCGCGTTGG AGTGCTACAA CACGTTCATT GGCGAGAGAA CTGTAGGAGC GCTCCAGGTC 3900
CTAGGTACTG AAGCCCAGTC TTCACTTTTG AAAGCAGTGG CTTTCTTCTT AGAAAGCATT 3960
GCCATGCATG ACATTATAGC AGCAGAAAAG TGCTTTGGCA CTGGGGCAGC AGGTAACAGA 4020
ACAAGCCCAC AAGAGGGAGA AAGGTACAAC TACAGCAAAT GCACCGTTGT GGTCCGGATT 4080
ATGGAGTTTA CCACGACTCT GCTAAACACC TCCCCGGAAG GATGGAAGCT CCTGAAGAAG 4140
GACTTGTGTA ATACACACCT GATGAGAGTC CTGGTGCAGA CGCTGTGTGA GCCCGCAAGC 4200
ATAGGTTTCA ACATCGGAGA CGTCCAGGTT ATGGCTCATC TTCCTGATGT TTGTGTGAAT 4260
CTGATGAAAG CTCTAAAGAT GTCCCCATAC AAAGATATCC TAGAGACCCA TCTGAGAGAG 4320
AAAATAACAG CACAGAGCAT TGAGGAGCTT TGTGCCGTCA ACTTGTATGG CCCTGACGCG 4380
CAAGTGGACA GGAGCAGGCT GGCTGCTGTT GTGTCTGCCT GTAAACAGCT TCACAGAGCT 4440
GGGCTTCTGC ATAATATATT ACCGTCTCAG TCCACAGATT TGCATCATTC TGTTGGCACA 4500
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CACCAGATTT ACATGCAAGG GCAAACCAGT ACACCACTTC ATGAACACCA GTACATTTAC   540
CGAGTACACA GTGGTGGATG AATCTTCTGT TGCTAAGATT GATGATGCAG CTCCTCCTGA   600
GAAAGTCTGT TTAATTGGCT GTGGGTTTTC CACTGGATAT GGCGCTGCTG TTAAAACTGG   660
CAAGGTCAAA CCTGGTTCCA CTTGCGTCGT CTTTGGCCTG GGAGGAGTTG GCCTGTCAGT   720
CATCATGGGC TGTAAGTCAG CTGGTGCATC TAGGATCATT GGGATTGACC TCAACAAAGA   780
CAAATTTGAG AAGGCCATGG CTGTAGGTGC CACTGAGTGT ATCAGTCCCA AGGACTCTAC   840
CAAACCCATC AGTGAGGTGC TGTCAGAAAT GACAGGCAAC AACGTGGGAT ACACCTTTGA   900
AGTTATTGGG CATCTTGAAA CCATGATTGA TGCCCTGGCA TCCTGCCACA TGAACTATGG   960
GACCAGCGTG GTTGTAGGAG TTCCTCCATC AGCCAAGATG CTCACCTATG ACCCGATGTT  1020
```

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GCTCTTCACT GGACGCACAT GGAAGGGATG TGTCTTTGGA GGTTTGAAAA GCAGAGATGA  1080
TGTCCCAAAA CTAGTGACTG AGTTCCTGGC AAAGAAATTT GACCTGGACC AGTTGATAAC  1140
TCATGTTTTA CCATTTAAAA AAATCAGTGA AGGATTTGAG CTGCTCAATT CAGGACAAAG  1200
CATTCGAACG GTCCTGACGT TTTGAGATCC AAAGTGGCAG GAGGTCTGTG TTGTCATGGT  1260
GAACTGGAGT TTCTCTTGTG AGAGTTCCCT CATCTGAAAT CATGTATCTG TCTCACAAAT  1320
ACAAGCATAA GTAGAAGATT TGTTGAAGAC ATAGAACCCT TATAAAGAAT TATTAACCTT  1380
TATAAACATT TAAAGTCTTG TGAGCACCTG GGAATTAGTA TAATAACAAT GTTAATATTT  1440
TTGATTTACA TTTTGTAAGG CTATAATTGT ATCTTTTAAG AAAACATACA CTTGGATTTC  1500
TATGTTGAAA TGGAGATTTT TAAGAGTTTT AACCAGCTGC TGCAGATATA TAACTCAAAA  1560
CAGATATAGC GTATAAAGAT ATAGTAAATG CATCTCCCAG AGTAATATTC ACTTAACACA  1620
TTGAAACTAT TATTTTTTAG ATTTGAATAT AAATGTATTT TTTAAACACT TGTTATGAGT  1680
TAACTTGGAT TACATTTTGA AATCAGTTCA TTCCATGATG CATATTACTG GATTAGATTA  1740
AGAAAGACAG AAAAGATTAA GGGACGGGCA CATTTTTCAA CGATTAAGAA TCATCATTAC  1800
ATAACTTGGT GAAACTGAAA AAGTATATCA TATGGGTACA CAAGGCTATT TGCCAGCATA  1860
TATTAATATT TTAGAAAATA TTCCTTTTGT AATACTGAAT ATAAACATAG AGCTAGAGTC  1920
ATATTATCAT ACTTATCATA ATGTTCAATT TGATACAGTA GAATTGCAAG TCCCTAAGTC  1980
CCTATTCACT GTGCTTAGTA GTGACTCCAT TTAATAAAAA GTGTTTTTAG TTTTTAACAA  2040
CTAAACCG
```

Seq ID NO: 101 Protein sequence:
Protein Accession #: NP_000664

```
1          11         21         31         41         51
|          |          |          |          |          |
MGTAGKVIKC KAAVLWEQKQ PFSIEEIEVA PPKTKEVRIK ILATGICRTD DHVIKGTMVS    60
KFPVIVGHEA TGIVESIGEG VTTVKPGDKV IPLFLPQCRE CNACRNPDGN LCIRSDITGR   120
GVLADGTTRF TCKGKPVHHF MNTSTFTEYT VVDESSVAKI DDAAPPEKVC LIGCGFSTGY   180
GAAVKTGKVK PGSTCVVFGL GGVGLSVIMG CKSAGASRII GIDLNKDKFE KAMAVGATEC   240
ISPKDSTKPI SEVLSEMTGN NVGYTFEVIG HLETMIDALA SCHMNYGTSV VVGVPPSAKM   300
LTYDPMLLFT GRTWKGCVFG GLKSRDDVPK LVTEFLAKKF DLDQLITHVL PFKKISEGFE   360
LLNSGQSIRT VLTF
```

Seq ID NO: 102 DNA sequence
Nucleic Acid Accession #: NM_006783.1
Coding sequence: 1..786

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGGATTGGG GGACGCTGCA CACTTTCATC GGGGGTGTCA ACAAACACTC CACCAGCATC    60
GGGAAGGTGT GGATCACAGT CATCTTTATT TTCCGAGTCA TGATCCTAGT GGTGGCTGCC   120
CAGGAAGTGT GGGGTGACGA GCAAGAGGAC TTCGTCTGCA ACACACTGCA ACCGGGATGC   180
AAAAATGTGT GCTATGACCA CTTTTTCCCG GTGTCCCACA TCCGGCTGTG GGCCCTCCAG   240
CTGATCTTCG TCTCCACCCC AGCGCTGCTG GTGGCCATGC ATGTGGCCTA CTACAGGCAC   300
GAAACCACTC GCAAGTTCAG GCGAGGAGAG AAGAGGAATG ATTTCAAAGA CATAGAGGAC   360
ATTAAAAAGC ACAAGGTTCG GATAGAGGGG TCGCTGTGGT GGACGTACAC CAGCAGCATC   420
TTTTTCCGAA TCATCTTTGA AGCAGCCTTT ATGTATGTGT TTTACTTCCT TTACAATGGG   480
TACCACCTGC CCTGGGTGTT GAAATGTGGG ATTGACCCCT GCCCCAACCT TGTTGACTGC   540
TTTATTTCTA GGCCAACAGA GAAGACCGTG TTTACCATTT TTATGATTTC TGCGTCTGTG   600
ATTTGCATGC TGCTTAACGT GGCAGAGTTG TGCTACCTGC TGCTGAAAGT GTGTTTTAGG   660
AGATCAAAGA GAGCACAGAC GCAAAAAAAT CACCCCAATC ATGCCCTAAA GGAGAGTAAG   720
CAGAATGAAA TGAATGAGCT GATTTCAGAT AGTGGTCAAA ATGCAATCAC AGGTTTCCCA   780
AGCTAA
```

Seq ID NO: 103 Protein sequence:
Protein Accession #: NP_006774.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MDWGTLHTFI GGVNKHSTSI GKVWITVIFI FRVMILVVAA QEVWGDEQED FVCNTLQPGC    60
KNVCYDHFFP VSHIRLWALQ LIFVSTPALL VAMHVAYYRH ETTRKFRRGE KRNDFKDIED   120
IKKHKVRIEG SLWWTYTSSI FFRIIFEAAF MYVFYFLYNG YHLPWVLKCG IDPCPNLVDC   180
FISRPTEKTV FTIFMISASV ICMLLNVAEL CYLLLKVCFR RSKRAQTQKN HPNHALKESK   240
QNEMNELISD SGQNAITGFP S
```

Seq ID NO: 104 DNA sequence
Nucleic Acid Accession #: NM_020411
Coding sequence: 86-526

```
1          11         21         31         41         51
|          |          |          |          |          |
GGACCTGGGA AGGAGCATAG GACAGGGCAA GGCGGGATAA GGAGGGGCAC CACAGCCCTT    60
AAGGCACGAG GGAACCTCAC TGCGCATGCT CCTTTGGTGC CCACCTCAGT GCGCATGTTC   120
ACTGGGCGTC TTCCCATCGG CCCCTTCGCC AGTGTGGGGA ACGCGGCGGA GCTGTGAGCC   180
GGCGACTCGG GTCCCTGAGG TCTGGATTCT TTCTCCGCTA CTGAGACACG GCGGACACAC   240
ACAAACACAG AACCACACAG CCAGTCCCAG GAGCCCAGTA ATGGAGAGCC CCAAAAAGAA   300
GAACCAGCAG CTGAAAGTCG GGATCCTACA CCTGGGCAGC AGACAGAAGA AGATCAGGAT   360
ACAGCTGAGA TCCCAGTGCG CGACATGGAA GGTGATCTGC AAGAGCTGCA TCAGTCAAAC   420
ACCGGGGATA AATCTGGATT TGGGTTCCGG CGTCAAGGTG AAGATAATAC CTAAAGAGGA   480
ACACTGTAAA ATGCCAGAAG CAGGTGAAGA GCAACCACAA GTTTAAATGA AGACAAGCTG   540
AAACAACGCA AGCTGGTTTT ATATTAGATA TTTGACTTAA ACTATCTCAA TAAAGTTTTG   600
CAGCTTTCAC CAAAAAAAAA AAAAAA
```

Seq ID NO: 105 Protein sequence:
Protein Accession #: NP_065144.1

```
1          11         21         31         41         51
```

```
|          |          |          |          |          |
MLLWCPPQCA CSLGVFPSAP SPVWGTRRSC EPATRVPEVW ILSPLLRHGG HTQTQNHTAS    60
PRSPVMESPK KKNQQLKVGI LHLGSRQKKI RIQLRSQCAT WKVICKSCIS QTPGINLDLG   120
SGVKVKIIPK EEHCKMPEAG EEQPQV
```

Seq ID NO: 106 DNA sequence
Nucleic Acid Accession #: J04129
Coding sequence: 99-587

```
1          11         21         31         41         51
|          |          |          |          |          |
CATCCCTCTG GCTCCAGAGC TCAGAGCCAC CCACAGCCGC AGCCATGCTG TGCCTCCTGC    60
TCACCCTGGG CGTGGCCCTG GTCTGTGGTG TCCCGGCCAT GGACATCCCC CAGACCAAGC   120
AGGACCTGGA GCTCCCAAAG TTGGCAGGGA CCTGGCACTC CATGGCCATG GCGACCAACA   180
ACATCTCCCT CATGGCGACA CTGAAGGCCC CTCTGAGGGT CCACATCACC TCACTGTTGC   240
CCACCCCCGA GGACAACCTG GAGATCGTTC TGCACAGATG GGAGAACAAC AGCTGTGTTG   300
AGAAGAAGGT CCTTGGAGAG AAGACTGGGA ATCCAAAGAA GTTCAAGATC AACTATACGG   360
TGGCGAACGA GGCCACGCTG CTCGATACTG ACTACGACAA TTTCCTGTTT CTCTGCCTAC   420
AGGACACCAC CACCCCCATC CAGAGCATGA TGTGCCAGTA CCTGGCCAGA GTCCTGGTGG   480
AGGACGATGA GATCATGCAG GGATTCATCA GGGCTTTCAG GCCCCTGCCC AGGCACCTAT   540
GGTACTTGCT GGACTTGAAA CAGATGGAAG AGCCGTGCCG TTTCTAGCTC ACCTCCGCCT   600
CCAGGAAGAC CAGACTCCCA CCCTTCCACA CCTCCAGAGC AGTGGGACTT CCTCCTGCCC   660
TTTCAAAGAA TAACCACAGC TCAGAAGACG ATGACGTGGT CATCTGTGTC GCCATCCCCT   720
TCCTGCTGCA CACCTGCACC ATTGCCATGG GGAGGCTGCT CCCTGGGGGC AGAGTCTCTG   780
GCAGAGGTTA TTAATAAACC CTTGGAGCAT G
```

Seq ID NO: 107 Protein sequence:
Protein Accession #: AAA60147

```
1          11         21         31         41         51
|          |          |          |          |          |
MDIPQTKQDL ELPKLAGTWH SMAMATNNIS LMATLKAPLR VHITSLLPTP EDNLEIVLHR    60
WENNSCVEKK VLGEKTGNPK KFKINYTVAN EATLLDTDYD NFLFLCLQDT TTPIQSMMCQ   120
YLARVLVEDD EIMQGFIRAF RPLPRHLWYL LDLKQMEEPC RF
```

Seq ID NO: 108 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 48-794

```
1          11         21         31         41         51
|          |          |          |          |          |
TCCCAGGCAG CAGTTAGCCC GCCGCCCGCC TGTGTGTCCC CAGAGCCATG GAGAGAGCCA    60
GTCTGATCCA GAAGGCCAAG CTGGCAGAGC AGGCCGAACG CTATGAGGAC ATGGCAGCCT   120
TCATGAAAGG CGCCGTGGAG AAGGGCGAGG AGCTCTCCTG CGAAGAGCGA AACCTGCTCT   180
CAGTAGCCTA TAAGAACGTG GTGGGCGGCC AGAGGGCTGC CTGGAGGGTG CTGTCCAGTA   240
TTGAGCAGAA AAGCAACGAG GAGGGCTCGG AGGAGAAGGG GCCCGAGGTG CGTGAGTACC   300
GGGAGAAGGT GGAGACTGAG CTCCAGGGCG TGTGCGACAC CGTGCTGGGC CTGCTGGACA   360
GCCACCTCAT CAAGGAGGCC GGGGACGCCG AGAGCCGGGT CTTCTACCTG AAGATGAAGG   420
GTGACTACTA CCGCTACCTG GCCGAGGTGG CCACCGGTGA CGACAAGAAG CGCATCATTG   480
ACTCAGCCCG GTCAGCCTAC CAGGAGGCCA TGGACATCAG CAAGAAGGAG ATGCCGCCCA   540
CCAACCCCAT CCGCCTGGGC CTGGCCCTGA ACTTTTCCGT CTTCCACTAC GAGATCGCCA   600
ACAGCCCCGA GGAGGCCATC TCTCTGGCCA AGACCACTTT CGACGAGGCC ATGGCTGATC   660
TGCACACCCT CAGCGAGGAC TCCTACAAAG ACAGCACCCT CATCATGCAG CTGCTGCGAG   720
ACAACCTGAC ACTGTGGACG GCCGACAACG CCGGGGAAGA GGGGGGCGAG GCTCCCCAGG   780
AGCCCCAGAG CTGAGTGTTG CCCGCCACCG CCCCGCCCTG CCCCCTCCAG TCCCCCACCC   840
TGCCGAGAGG ACTAGTATGG GGTGGGAGGC CCCACCCTTC TCCCCTAGGC GCTGTTCTTG   900
CTCCAAAGGG CTCCGTGGAG AGGGACTGGC AGAGCTGAGG CCACCTGGGG CTGGGGATCC   960
CACTCTTCTT GCAGCTGTTG AGCGCACCTA ACCACTGGTC ATGCCCCCAC CCCTGCTCTC  1020
CGCACCCGCT TCCTCCCGAC CCCAGGACCA GGCTACTTCT CCCCTCCTCT TGCCTCCCTC  1080
CTGCCCCTGC TGCCTCTGAT CGTAGGAATT GAGGAGTGTC CCGCCTTGTG GCTGAGAACT  1140
GGACAGTGGC AGGGGCTGGA GATGGGTGTG TGTGTGTGTG TGTGTGTGTG TGTGTGTGTG  1200
CGCGCGCGCC AGTGCAAGAC CGAGATTGAG GGAAAGCATG TCTGCTGGGT GTGACCATGT  1260
TTCCTCTCAA TAAAGTTCCC CTGTGACACT C
```

Seq ID NO: 109 Protein sequence:
Protein Accession #: NP_006133.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MERASLIQKA KLAEQAERYE DMAAFMKGAV EKGEELSCEE RNLLSVAYKN VVGGQRAAWR    60
VLSSIEQKSN EEGSEEKGPE VREYREKVET ELQGVCDTVL GLLDSHLIKE AGDAESRVFY   120
LKMKGDYYRY LAEVATGDDK KRIIDSARSA YQEAMDISKK EMPPTNPIRL GLALNFSVFH   180
YEIANSPEEA ISLAKTTFDE AMADLHTLSE DSYKDSTLIM QLLRDNLTLW TADNAGEEGG   240
EAPQEPQS
```

Seq ID NO: 110 DNA sequence
Nucleic Acid Accession #: NM_000695
Coding sequence: 407-1564

```
1          11         21         31         41         51
|          |          |          |          |          |
CACGAGTTGG TTTGGGAGCT GCCAGTCTCC TGGGAGGATC GCAGTCAGCA GAGCAGGGCT    60
GAGGCCTGGG GGTAGGAGCA GAGCCTGCGC ATCTGGAGGC AGCATGTCCA AGAAAGGGAG   120
TGGAGGTGCA GCGAAGGACC CAGGGGCAGA GCCCACGCTG GGGATGGACC CCTTCGAGGA   180
CACACTGCGG CGGCTGCGTG AGGCCTTCAA CTGAGGGCGC ACGCGGCCGG CCGAGTTCCG   240
GGCTGCGCAG CTCCAGGGCC TGGGCCACTT CCTTCAAGAA AACAAGCAGC TTCTGCGCGA   300
```

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CGTGCTGGCC CAGGACCTGC ATAAGCCAGC TTTCGAGGCA GACATATCTG AGCTCATCCT   360
TTGCCAGAAC GAGGTTGACT ACGCTCTCAA GAACCTTCAG GCCTGGATGA AGGATGAACC   420
ACGGTCCACG AACCTGTTCA TGAAGCTGGA CTCGGTCTTC ATCTGGAAGG AACCCTTTGG   480
CCTGGTCCTC ATCATCGCAC CCTGGAACTA CCCATTGAAC CTGACCCTGG TGCTCCTGGT   540
GGGCACCCTC CCCGCAGGGA ATTGCGTGGT GCTGAAGCCG TCAGAAATCA GCCAGGGCAC   600
AGAGAAGGTC CTGGCTGAGG TGCTGCCCCA GTACCTGGAC CAGAGCTGCT TTGCCGTGGT   660
GCTGGGCGGA CCCCAGGAGA CAGGGCAGCT GCTAGAGCAC AAGTTGGACT ACATCTTCTT   720
CACAGGGAGC CCTCGTGTGG GCAAGATTGT CATGACTGCT GCCACCAAGC ACCTGACGCC   780
TGTCACCCTG GAGCTGGGGG GCAAGAACCC CTGCTACGTG GACGACAACT GCGACCCCCA   840
GACCGTGGCC AACCGCGTGG CCTGGTTCTG CTACTTCAAT GCCGGCCAGA CCTGCGTGGC   900
CCCTGACTAC GTCCTGTGCA GCCCCGAGAT GCAGGAGAGG CTGCTGCCCG CCCTGCAGAG   960
CACCATCACC CGTTTCTATG GCGACGACCC CCAGAGCTCC CCAAACCTGG GCCGCATCAT  1020
CAACCAGAAA CAGTTCCAGC GGCTGCGGGC ATTGCTGGGC TGCGGCCGCG TGGCCATTGG  1080
GGGCCAGAGC AACGAGAGCG ATCGCTACAT CGCCCCCACG GTGCTGGTGG ACGTGCAGGA  1140
GACGGAGCCT GTGATGCAGG AGGAGATCTT CGGGCCCATC CTGCCCATCG TGAACGTGCA  1200
GAGCGTGGAC GAGGCCATCA AGTTCATCAA CCGGCAGGAG AAGCCCCTGG CCCTGTACGC  1260
CTTCTCCAAC AGCAGACAGG TTGTGAACCA GATGCTGGAG CGGACCAGCA GCGGCAGCTT  1320
TGGAGGCAAT GAGGGCTTCA CCTACATATC TCTGCTGTCC GTGCCATTCG GGGGAGTCGG  1380
CCACAGTGGG ATGGGCCGGT ACCACGGCAA GTTCACCTTC GACACCTTCT CCCACCACCG  1440
CACCTGCCTG CTCGCCCCCT CCGGCCTGGA GAAATTAAAG GAGATCCGCT ACCCACCCTA  1500
TACCGACTGG AACCAGCAGC TGTTACGCTG GGGCATGGGC TCCCAGAGCT GCACCCTCCT  1560
GTGAGCGTCC CACCCGCCTC CAACGGGTCA CACAGAGAAA CCTGAGTCTA GCCATGAGGG  1620
GCTTATGCTC CCAACTCACA TTGTTCCTCC AGACCGCAGG CTCCCCCAGC CTCAGGTTGC  1680
TGGAGCTGTC ACATGACTGC ATCCTGCCTG CCAGGGCTGC AAAGCAAGGT CTTGCTTCTA  1740
TCTGGGGGAC GCTGCTCGAG AGAGGCCGAG AGGCCGCAGA ACATGCCAGG TGTCCTCACT  1800
CACCCCACCC TCCCCAATTC CAGCCCTTTG CCCTCTCGGT CAGGGTTGGC CAGGCCCAGT  1860
CACAGGGGCA GTGTCACCCT GGAAAATACA GTGCCCTGCC TTCTTAGGGG CATCAGCCCT  1920
GAACGGTTGA GAGCGTGGAG CCCTCCAGGC CTTTGCTCTC CCCTCTAGGC ACACGCGCAC  1980
TTCCACCTCT GCCCCATCCC AACTGCACCA GCACTGCCTC CCCCAGGGAT CCTCTCACAT  2040
CCCACACTGG TCTCTGCACC ACCCCTCTGG TTCACACCGC ACCCTGCACT CACCCACAGC  2100
AGCTCCATCC ACTGGGAAAA CTGGGGTTTG CATCACTCCA CTGCACAGTG TTAGTGGGAC  2160
CTGGGGGCAA GTCCCTTGAC TTCTCTGAGC CTCAGTTTCC TTATGTGAAA GTTGCTGGAA  2220
CCAAAATGGA GTCACTTATG CCAAACTCTA ATAAAATGGA GTCGGGGGGG CACATAGAAG  2280
CCCTCACACA CACATGCCCG TAACAGGATT TATCACCAAG ACACGCCTGC ATGTAAGACC  2340
AGACACAGGG CGTATGGAAA AGCACGTCCT CAAAGACTGT AGTATTCCAG ATGAGCTGCA  2400
GATGCTTACC TACCACGGCC GTCTCCACCA GAAAACCATC GCCAACTCCT GCGATCAGCT  2460
TGTGACTTAC AAACCTTGTT TAAAAGCTGC TTACATGGAC TTCTGTCCTT TAAAACGTTC  2520
CCCTTGGCTG TGGCCCTCTG TGTATGCCTG GGATCCTTCC AAGCACTCAT AGCCCAGATA  2580
GGAATCCTCT GCTCCTCCCA AATAAATTCA TCTGTTC
```

Seq ID NO: 111 Protein sequence:
Protein Accession #: NP_000686

```
1          11         21         31         41         51
|          |          |          |          |          |
MKDEPRSTNL FMKLDSVFIW KEPFGLVLII APWNYPLNLT LVLLVGTLPA GNCVVLKPSE    60
ISQGTEKVLA EVLPQYLDQS CFAVVLGGPQ ETGQLLEHKL DYIFFTGSPR VGKIVMTAAT   120
KHLTPVTLEL GGKNPCYVDD NCDPQTVANR VAWFCYFNAG QTCVAPDYVL CSPEMQERLL   180
PALQSTITRF YGDDPQSSPN LGRIINQKQF QRLRALLGCG RVAIGGQSNE SDRYIAPTVL   240
VDVQETEPVM QEEIFGPILP IVNVQSVDEA IKFINRQEKP LALYAFSNSR QVVNQMLERT   300
SSGSFGGNEG FTYISLLSVP FGGVGHSGMG RYHGKFTFDT FSHHRTCLLA PSGLEKLKEI   360
RYPPYTDWNQ QLLRWGMGSQ SCTLL
```

Seq ID NO: 112 DNA sequence
Nucleic Acid Accession #: NM_004456
Coding sequence: 58-2298

```
1          11         21         31         41         51
|          |          |          |          |          |
GAATTCCGGG CGACGCGCGG GAACAACGCG AGTCGGCGCG CGGGACGAAG AATAATCATG    60
GGCCAGACTG GGAAGAAATC TGAGAAGGGA CCAGTTTGTT GGCGGAAGCG TGTAAAATCA   120
GAGTACATGC GACTGAGACA GCTCAAGAGG TTCAGACGAG CTGATGAAGT AAAGAGTATG   180
TTTAGTTCCA ATCGTCAGAA AATTTTGGAA AGAACGGAAA TCTTAAACCA AGAATGGAAA   240
CAGCGAAGGA TACAGCCTGT GCACATCCTG ACTTCTGTGA GCTCATTGCG CGGGACTAGG   300
GAGTGTTCGG TGACCAGTGA CTTGGATTTT CCAACACAAG TCATCCCATT AAAGACTCTG   360
AATGCAGTTG CTTCAGTACC CATAATGTAT TCTTGGTCTC CCCTACAGCA GAATTTTATG   420
GTGGAAGATG AAACTGTTTT ACATAACATT CCTTATATGG GAGATGAAGT TTTAGATCAG   480
GATGGTACTT TCATTGAAGA ACTAATAAAA AATTATGATG GGAAAGTACA CGGGGATAGA   540
GAATGTGGGT TTATAAATGA TGAAATTTTT GTGGAGTTGG TGAATGCCCT TGGTCAATAT   600
AATGATGATG ACGATGATGA TGATGGAGAC GATCCTGAAG AAAGAGAAGA AAAGCAGAAA   660
GATCTGGAGG ATCACCGAGA TGATAAAGAA AGCCGCCCAC CTCGGAAATT TCCTTCTGAT   720
AAAATTTTGG AGGCCATTTC CTCAATGTTT CCAGATAAGG GCACAGCAGA AGAACTAAAG   780
GAAAAATATA AAGAACTCAC CGAACAGCAG CTCCCAGGCG CACTTCCTCC TGAATGTACC   840
CCCAACATAG ATGGACCAAA TGCTAAATCT GTTCAGAGAG AGCAAAGCTT ACACTCCTTT   900
CATACGCTTT TCTGTAGGCG ATGTTTTAAA TATGACTGCT TCCTACATCC TTTTCATGCA   960
ACACCCAACA CTTATAAGCG GAAGAACACA GAAACAGCTC TAGACAACAA ACCTTGTGGA  1020
CCACAGTGTT ACCAGCATTT GGAGGGAGCA AAGGAGTTTG CTGCTGCTCT CACCGCTGAG  1080
CGGATAAAGA CCCCACCAAA ACGTCCAGGA GGCCGCAGAA GAGGACGGCT TCCCAATAAC  1140
AGTAGCAGGC CCAGCACCCC CACCATTAAT GTGCTGGAAT CAAAGGATAC AGACAGTGAT  1200
AGGGAAGCAG GGACTGAAAC GGGGGGAGAG AACAATGATA AAGAAGAAGA AGAGAAGAAA  1260
GATGAAACTT CGAGCTCCTC TGAAGCAAAT TCTCGGTGTC AAACACCAAT AAAGATGAAG  1320
CCAAATATTG AACCTCCTGA GAATGTGGAG TGGAGTGGTG CTGAAGCCTC AATGTTTAGA  1380
GTCCTCATTG GCACTTACTA TGACAATTTC TGTGCCATTG CTAGGTTAAT TGGGACCAAA  1440
ACATGTAGAC AGGTGTATGA GTTTAGAGTC AAAGAATCTA GCATCATAGC TCCAGCTCCC  1500
GCTGAGGATG TGGATACTCC TCCAAGGAAA AAGAAGAGGA AACACCGGTT GTGGGCTGCA  1560
CACTGCAGAA AGATACAGCT GAAAAAGGAC GGCTCCTCTA ACCATGTTTA CAACTATCAA  1620
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CCCTGTGATC ATCCACGGCA GCCTTGTGAC AGTTCGTGCC CTTGTGTGAT AGCACAAAAT  1680
TTTTGTGAAA AGTTTTGTCA ATGTAGTTCA GAGTGTCAAA ACCGCTTTCC GGGATGCCGC  1740
TGCAAAGCAC AGTGCAACAC CAAGCAGTGC CCGTGCTACC TGGCTGTCCG AGAGTGTGAC  1800
CCTGACCTCT GTCTTACTTG TGGAGCCGCT GACCATTGGG ACAGTAAAAA TGTGTCCTGC  1860
AAGAACTGCA GTATTCAGCG GGGCTCCAAA AAGCATCTAT TGCTGGCACC ATCTGACGTG  1920
GCAGGCTGGG GGATTTTTAT CAAAGATCCT GTGCAGAAAA ATGAATTCAT CTCAGAATAC  1980
TGTGGAGAGA TTATTTCTCA AGATGAAGCT GACAGAAGAG GGAAAGTGTA TGATAAATAC  2040
ATGTGCAGCT TTCTGTTCAA CTTGAACAAT GATTTTGTGG TGGATGCAAC CCGCAAGGGT  2100
AACAAAATTC GTTTTGCAAA TCATTCGGTA AATCCAAACT GCTATGCAAA AGTTATGATG  2160
GTTAACGGTG ATCACAGGAT AGGTATTTTT GCCAAGAGAG CCATCCAGAC TGGCGAAGAG  2220
CTGTTTGTTG ATTACAGATA CAGCCAGGCT GATGCCCTGA AGTATGTCGG CATCGAAAGA  2280
GAAATGGAAA TCCCTTGACA TCTGCTACCT CCTCCCCCTC CTCTGAAACA GCTGCCTTAG  2340
CTTCAGGAAC CTCGAGTACT GTGGGCAATT TAGAAAAAGA ACATGCAGTT TGAAATTCTG  2400
AATTTGCAAA GTACTGTAAG AATAATTTAT AGTAATGAGT TTAAAAATCA ACTTTTTATT  2460
GCCTTCTCAC CAGCTGCAAA GTGTTTTGTA CCAGTGAATT TTTGCAATAA TGCAGTATGG  2520
TACATTTTTC AACTTTGAAT AAAGAATACT TGAACTTGAA AAAAAAAAAA AAAAAA
```

Seq ID NO: 113 Protein sequence:
Protein Accession #: NP_004447

```
1          11         21         31         41         51
|          |          |          |          |          |
MGQTGKKSEK GPVCWRKRVK SEYMRLRQLK RFRRADEVKS MFSSNRQKIL ERTEILNQEW    60
KQRRIQPVHI LTSVSSLRGT RECSVTSDLD FPTQVIPLKT LNAVASVPIM YSWSPLQQNF   120
MVEDETVLHN IPYMGDEVLD QDGTFIEELI KNYDGKVHGD RECGFINDEI FVELVNALGQ   180
YNDDDDDDDG DDPEEREEKQ KDLEDHRDDK ESRPPRKFPS DKILEAISSM FPDKGTAEEL   240
KEKYKELTEQ QLPGALPPEC TPNIDGPNAK SVQREQSLHS FHTLFCRRCF KYDCFLHPFH   300
ATPNTYKRKN TETALDNKPC GPQCYQHLEG AKEFAAALTA ERIKTPPKRP GGRRRGRLPN   360
NSSRPSTPTI NVLESKDTDS DREAGTETGG ENNDKEEEEK KDETSSSSEA NSRCQTPIKM   420
KPNIEPPENV EWSGAEASMF RVLIGTYYDN FCAIARLIGT KTCRQVYEFR VKESSIIAPA   480
PAEDVDTPPR KKKRKHRLWA AHCRKIQLKK DGSSNHVYNY QPCDHPRQPC DSSCPCVIAQ   540
NFCEKFCQCS SECQNRFPGC RCKAQCNTKQ CPCYLAVREC DPDLCLTCGA ADHWDSKNVS   600
CKNCSIQRGS KKHLLLAPSD VAGWGIFIKD PVQKNEFISE YCGEIISQDE ADRRGKVYDK   660
YMCSFLFNLN NDFVVDATRK GNKIRFANHS VNPNCYAKVM MVNGDHRIGI FAKRAIQTGE   720
ELFVDYRYSQ ADALKYVGIE REMEIP
```

Seq ID NO: 114 DNA sequence
Nucleic Acid Accession #: NM_001827
Coding sequence: 96-335

```
1          11         21         31         41         51
|          |          |          |          |          |
AGTCTCCGGC GAGTTGTTGC CTGGGCTGGA CGTGGTTTTG TCTGCTGCGC CCGCTCTTCG    60
CGCTCTCGTT TCATTTTCTG CAGCGCGCCA CGAGGATGGC CCACAAGCAG ATCTACTACT   120
CGGACAAGTA CTTCGACGAA CACTACGAGT ACCGGCATGT TATGTTACCC AGAGAACTTT   180
CCAAACAAGT ACCTAAAACT CATCTGATGT CTGAAGAGGA GTGGAGGAGA CTTGGTGTCC   240
AACAGAGTCT AGGCTGGGTT CATTACATGA TTCATGAGCC AGAACCACAT ATTCTTCTCT   300
TTAGACGACC TCTTCCAAAA GATCAACAAA AATGAAGTTT ATCTGGGGAT CGTCAAATCT   360
TTTTCAAATT TAATGTATAT GTGTATATAA GGTAGTATTC AGTGAATACT TGAGAAATGT   420
ACAAATCTTT CATCCATACC TGTGCATGAG CTGTATTCTT CACAGCAACA GAGCTCAGTT   480
AAATGCAACT GCAAGTAGGT TACTGTAAGA TGTTTAAGAT AAAAGTTCTT CCAGTCAGTT   540
TTTCTCTTAA GTGCCTGTTT GAGTTTACTG AAACAGTTTA CTTTTGTTCA ATAAAGTTTG   600
TATGTTGCAT TTAAAAAAAA AAAAAAA
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Seq ID NO: 115 Protein sequence:
Protein Accession #: NP_001818

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1          11         21         31         41         51
|          |          |          |          |          |
MAHKQIYYSD KYFDEHYEYR HVMLPRELSK QVPKTHLMSE EEWRRLGVQQ SLGWVHYMIH    60
EPEPHILLFR RPLPKDQQK
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Seq ID NO: 116 DNA sequence
Nucleic Acid Accession #: CAT cluster

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1          11         21         31         41         51
|          |          |          |          |          |
TCAGACCTCA TGAGTCACTT GGACTCTTGA GCCACCTCTG GGGGTGGAGT CTCTCTCCTG    60
GCATCTGGAC CCTTGGTGCT ATCGACGAAG CTTGGGTGGG GCTCTTAGCT GCTATGTGCA   120
AGAGGTGTGT TCCAGGGAAA GCCCCTATCT CTCTGCAGAG GTCAAGTGAA AGCGACGGCC   180
GCAGCCAACA GAGTTCAAAA TGCAGGCTTG GAAAGTACAG GGGGCTCTGT GGAGGATGGG   240
AAGGACTGAT CCACATTCCC ACCAGGAAGT TTAGCAGAAC CCCCGCGTGC CAACTGGACC   300
CCTTGGAAGG ACCTGGCTCA GGCTGGACCA CCTCTTGAGA GGGAGGAGCT CTGGATTTGA   360
TCAAGAATTC TTTGCTGAGC ATGGTGCCTC ATGCCTATAA TACCAACACT TTGGGAGGCC   420
AGTGTGGGAG GATCTCTTGA GCCCAGGAGT TCAAGACTAG CCTGGGCAAC ACAGAGAGAA   480
CCCATCTCTA AAATAATAAT AATAATAAAA TAAAAAATTA GCAGGGCATG GTGGCATGTG   540
CCTGTAGTTC CAGCTACCCA GGAGGCTGAG GCAAGAGGAT GGCTGGAGCC TGGGATGTTG   600
AGGCTGCAAT GAACTGTGAT TACCCCACTG CACTCCAGCC TGGGCAAAAG AGCGAGAGAA   660
CCTGTCTCAA ATAATAATAA TAATAATAAT CTTATTTTGG AGAATAAAGA GACCTCTGGA   720
TTTGAGGTGC CATTTGGGTA GAAAGAAAAG ACGTTTACAC CGAGAAATAG TCTGTGTTGC   780
CCTGAAGGAG CAGAGGGATG CATCGCTGGA GGTGACCTAC AGTTGAAGAA GACTCATTAT   840
GACAGACCTT GTCCTTCTTC CTTGTGGAAA GTGTTTCCTC TGCTGCTACT GCTCATGAGA   900
CTCTTCCCCC TCCCTGTCCC AGGGAACCAA AGGGCTTTCT ACCACACCCT TTCTTGCCCC   960
CCGCCTCCCA TGTCTGCTGT GCCTTTGTAC TCAGCAATTC TTGTTTGCTC CATTATCTTC  1020
CAGCCGGATA CAGAGTGAAT AGTTAACCAC ACTTAGGTCA AATAGGATCT AAATTTTTGT  1080
TCCTGCTCCG TGTAAAGAGG CCAGTGTTTG TGTGTTGCAA GCAGCCTTGG AATAGTAACT  1140
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CTTCTCATTT GTTTGGGATC TGGCCACCAA GTTCCAGAAT GATACACGGA TCAGTGCAGA  1200
AGTTCATCAG GCTCTCGGAC CTTAGGGCTG TTGGAGAAGG CTTCAGCAGC AGAACTGATG  1260
GTGAAGGCTC GTGTTCTCCA TCCTCAACTT TCTTTGCTTC GATCATACAC AAGAATACAT  1320
TTGGAAGGGC AAAAAATGAA CACTGTCGTT CATTGCAGCC GTGTTTTGTG ACACAGATGC  1380
ACAGTCTGCT GTGAAGACCT TCTCTCAAGT GGCATTTGGG AGTCCATGCC AGATCATGGT  1440
GCTTCATGAG AGACTGACAG CTATCAGGGG TTGTGGCACT TAGTGAGGAC TCTCCTCCCC  1500
CAGTGTGTGC TGATGACACA TACACACCTG ACAATAGCTT GAGTCTTCTC TGTTCCTTTT  1560
ACTCTGTAGC CAACATACAC ATGATTTAAA ACCCTTTCTA AATATCTATC ATGGTTCATC  1620
CTTGTCCAAA TGCAGAGTCA GAGCTATTTG TACTTCATTA TTATTTCCAA GGCGAATAGT  1680
TGGCTTTCTT TTTGCAAAAA TAATTAAAGT TTTTGTATGT TGCAAAAAAA AAAAAAAAAA  1740
AAACAAAAAA
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Seq ID NO: 117 DNA sequence
Nucleic Acid Accession #: BC012178.1
Coding sequence: 204-2285

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1          11         21         31         41         51
|          |          |          |          |          |
CTTCTCTCCC GCGGCGCTGG GGCCCGCGCT CCGCTGCTGT TGCTCCATTC GGCGCTTTTC    60
TGGCGGCTGG CTCCTCTCCG CTGCCGGCTG CTCCTCGACC AGGCCTCCTT CTCAACCTCA   120
GCCCGCGGCG CCGACCCTTC CGGCACCCTC CCGCCCCGTC TCGTACTGTC GCCGTCACCG   180
CCGCGGCTCC GGCCCTGGCC CCGATGGCTC TGTGCAACGG AGACTCCAAG CTGGAGAATG   240
CTGGAGGAGA CCTTAAGGAT GGCCACCACC ACTATGAAGG AGCTGTTGTC ATTCTGGATG   300
CTGGTGCTCA GTACGGGAAA GTCATAGACC GAAGAGTGAG GGAACTGTTC GTGCAGTCTG   360
AAATTTTCCC CTTGGAAACA CCAGCATTTG CTATAAAGGA ACAAGGATTC CGTGCTATTA   420
TCATCTCTGG AGGACCTAAT TCTGTGTATG CTGAAGATGC TCCCTGGTTT GATCCAGCAA   480
TATTCACTAT TGGCAAGCCT GTTCTTGGAA TTTGCTATGG TATGCAGATG ATGAATAAGG   540
TATTTGGAGG TACTGTGCAC AAAAAAAGTG TCAGAGAAGA TGGAGTTTTC AACATTAGTG   600
TGGATAATAC ATGTTCATTA TTCAGGGGCC TTCAGAAGGA AGAAGTTGTT TTGCTTACAC   660
ATGGAGATAG TGTAGACAAA GTAGCTGATG GATTCAAGGT TGTGGCACGT TCTGGAAACA   720
TAGTAGCAGG CATAGCAAAT GAATCTAAAA AGTTATATGG AGCACAGTTC CACCCTGAAG   780
TTGGCCTTAC AGAAAATGGA AAAGTAATAC TGAAGAATTT CCTTTATGAT ATAGCTGGAT   840
GCAGTGGAAC CTTCACCGTG CAGAACAGAG AACTTGAGTG TATTCGAGAG ATCAAAGAGA   900
GAGTAGGCAC GTCAAAAGTT TTGGTTTTAC TCAGTGGTGG AGTAGACTCA ACAGTTTGTA   960
CAGCTTTGCT AAATCGTGCT TTGAACCAAG AACAAGTCAT TGCTGTGCAC ATTGATAATG  1020
GCTTTATGAG AAAACGAGAA AGCCAGTCTG TTGAAGAGGC CCTCAAAAAG CTTGGAATTC  1080
AGGTCAAAGT GATAAATGCT GCTCATTCTT TCTACAATGG AACAACAACC CTACCAATAT  1140
CAGATGAAGA TAGAACCCCA CGGAAAAGAA TTAGCAAAAC GTTAAATATG ACCACAAGTC  1200
CTGAAGAGAA AAGAAAAATC ATTGGGGATA CTTTTGTTAA GATTGCCAAT GAAGTAATTG  1260
GAGAAATGAA CTTGAAACCA GAGGAGGTTT TCCTTGCCCA AGGTACTTTA CGGCCTGATC  1320
TAATTGAAAG TGCATCCCTT GTTGCAAGTG GCAAAGCTGA ACTCATCAAA ACCCATCACA  1380
ATGACACAGA GCTCATCAGA AAGTTGAGAG AGGAGGGAAA AGTAATAGAA CCTCTGAAAG  1440
ATTTTCATAA AGATGAAGTG AGAATTTTGG GCAGAGAACT TGGACTTCCA GAAGAGTTAG  1500
TTTCCAGGCA TCCATTTCCA GGTCCTGGCC TGGCAATCAG AGTAATATGT GCTGAAGAAC  1560
CTTATATTTG TAAGGACTTT CCTGAAACCA ACAATATTTT GAAAATAGTA GCTGATTTTT  1620
CTGCAAGTGT TAAAAAGCCA CATACCCTAT TACAGAGAGT CAAAGCCTGC ACAACAGAAG  1680
AGGATCAGGA GAAGCTGATG CAAATTACCA GTCTGCATTC ACTGAATGCC TTCTTGCTGC  1740
CAATTAAAAC TGTAGGTGTG CAGGGTGACT GTCGTTCCTA CAGTTACGTG TGTGGAATCT  1800
CCAGTAAAGA TGAACCTGAC TGGGAATCAC TTATTTTTCT GGCTAGGCTT ATACCTCGCA  1860
TGTGTCACAA CGTTAACAGA GTTGTTTATA TATTTGGCCC ACCAGTTAAA GAACCTCCTA  1920
CAGATGTTAC TCCCACTTTC TTGACAACAG GGGTGCTCAG TACTTTACGC CAAGCTGATT  1980
TTGAGGCCCA TAACATTCTC AGGGAGTCTG GGTATGCTGG GAAAATCAGC CAGATGCCGG  2040
TGATTTTGAC ACCATTACAT TTTGATCGGG ACCCACTTCA AAAGCAGCCT TCATGCCAGA  2100
GATCTGTGGT TATTCGAACC TTTATTACTA GTGACTTCAT GACTGGTATA CCTGCAACAC  2160
CTGGCAATGA GATCCCTGTA GAGGTGGTAT TAAAGATGGT CACTGAGATT AAGAAGATTC  2220
CTGGTATTTC TCGAATTATG TATGACTTAA CATCAAAGCC CCCAGGAACT ACTGAGTGGG  2280
AGTAATAAAC TTCTTGTTCT ATTAAAA
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Seq ID NO: 118 Protein sequence:
Protein Accession #: AAH12178.1

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1          11         21         31         41         51
|          |          |          |          |          |
MALCNGDSKL ENAGGDLKDG HHHYEGAVVI LDAGAQYGKV IDRRVRELFV QSEIFPLETP    60
APAIKEQGFR AIIISGGPNS VYAEDAPWFD PAIFTIGKPV LGICYGMQMM NKVFGGTVHK   120
KSVREDGVFN ISVDNTCSLF RGLQKEEVVL LTHGDSVDKV ADGFKVVARS GNIVAGIANE   180
SKKLYGAQFH PEVGLTENGK VILKNFLYDI AGCSGTFTVQ NRELECIREI KERVGTSKVL   240
VLLSGGVDST VCTALLNRAL NQEQVIAVHI DNGFMRKRES QSVEEALKKL GIQVKVINAA   300
HSFYNGTTTL PISDEDRTPR KRISKTLNMT TSPEEKRKII GDTFVKIANE VIGEMNLKPE   360
EVFLAQGTLR PDLIESASLV ASGKAELIKT HHNDTELIRK LREEGKVIEP LKDFHKDEVR   420
ILGRELGLPE ELVSRHPFPG PGLAIRVICA EEPYICKDFP ETNNILKIVA DFSASVKKPH   480
TLLQRVKACT TEEDQEKLMQ ITSLHSLNAF LLPIKTVGVQ GDCRSYSYVC GISSKDEPDW   540
ESLIFLARLI PRMCHNVNRV VYIFGPPVKE PPTDVTPTFL TTGVLSTLRQ ADFEAHNILR   600
ESGYAGKISQ MPVILTPLHF DRDPLQKQPS CQRSVVIRTF ITSDFMTGIP ATPGNEIPVE   660
VVLKMVTEIK KIPGISRIMY DLTSKPPGTT EWE
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Seq ID NO: 119 DNA sequence
Nucleic Acid Accession #: NM_006500.1
Coding sequence: 27..1967

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1          11         21         31         41         51
|          |          |          |          |          |
ACTTGCGTCT CGCCCTCCGG CCAAGCATGG GGCTTCCCAG GCTGGTCTGC GCCTTCTTGC    60
TCGCCGCCTG CTGCTGCTGT CCTCGCGTCG CGGGTGTGCC CGGAGAGGCT GAGCAGCCTG   120
CGCCTGAGCT GGTGGAGGTG GAAGTGGGCA GCACAGCCCT TCTGAAGTGC GGCCTCTCCC   180
AGTCCCAAGG CAACCTCAGC CATGTCGACT GGTTTTCTGT CCACAAGGAG AAGCGGACGC   240
```

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TCATCTTCCG TGTGCGCCAG GGCCAGGGCC AGAGCGAACC TGGGGAGTAC GAGCAGCGGC   300
TCAGCCTCCA GGACAGAGGG GCTACTCTGG CCCTGACTCA AGTCACCCCC CAAGACGAGC   360
GCATCTTCTT GTGCCAGGGC AAGCGCCCTC GGTCCCAGGA GTACCGCATC CAGCTCCGCG   420
TCTACAAAGC TCCGGAGGAG CCAAACATCC AGGTCAACCC CCTGGGCATC CCTGTGAACA   480
GTAAGGAGCC TGAGGAGGTC GCTACCTGTG TAGGGAGGAA CGGGTACCCC ATTCCTCAAG   540
TCATCTGGTA CAAGAATGGC CGGCCTCTGA AGGAGGAGAA GAACCGGGTC CACATTCAGT   600
CGTCCCAGAC TGTGGAGTCG AGTGGTTTGT ACACCTTGCA GAGTATTCTG AAGGCACAGC   660
TGGTTAAAGA AGACAAAGAT GCCCAGTTTT ACTGTGAGCT CAACTACCGG CTGCCCAGTG   720
GGAACCACAT GAAGGAGTCC AGGGAAGTCA CCGTCCCTGT TTTCTACCCG ACAGAAAAAG   780
TGTGGCTGGA AGTGGAGCCC GTGGGAATGC TGAAGGAAGG GGACCGCGTG GAAATCAGGT   840
GTTTGGCTGA TGGCAACCCT CCACCACACT TCAGCATCAG CAAGCAGAAC CCCAGCACCA   900
GGGAGGCAGA GGAAGAGACA ACCAACGACA ACGGGGTCCT GGTGCTGGAG CCTGCCCGGA   960
AGGAACACAG TGGGCGCTAT GAATGTCAGG CCTGGAACTT GGACACCATG ATATCGCTGC  1020
TGAGTGAACC ACAGGAACTA CTGGTGAACT ATGTGTCTGA CGTCCGAGTG AGTCCCGCAG  1080
CCCCTGAGAG ACAGGAAGGC AGCAGCCTCA CCCTGACCTG TGAGGCAGAG AGTAGCCAGG  1140
ACCTCGAGTT CCAGTGGCTG AGAGAAGAGA CAGACCAGGT GCTGGAAAGG GGGCCTGTGC  1200
TTCAGTTGCA TGACCTGAAA CGGGAGGCAG GAGGCGGCTA TCGCTGCGTG GCGTCTGTGC  1260
CCAGCATACC CGGCCTGAAC CGCACACAGC TGGTCAAGCT GGCCATTTTT GGCCCCCCTT  1320
GGATGGCATT CAAGGAGAGG AAGGTGTGGG TGAAAGAGAA TATGGTGTTG AATCTGTCTT  1380
GTGAAGCGTC AGGGCACCCC CGGCCCACCA TCTCCTGGAA CGTCAACGGC ACGGCAAGTG  1440
AACAAGACCA AGATCCACAG CGAGTCCTGA GCACCCTGAA TGTCCTCGTG ACCCCGGAGC  1500
TGTTGGAGAC AGGTGTTGAA TGCACGGCCT CCAACGACCT GGGCAAAAAC ACCAGCATCC  1560
TCTTCCTGGA GCTGGTCAAT TTAACCACCC TCACACCAGA CTCCAACACA ACCACTGGCC  1620
TCAGCACTTC CACTGCCAGT CCTCATACCA GAGCCAACAG CACCTCCACA GAGAGAAAGC  1680
TGCCGGAGCC GGAGAGCCGG GGCGTGGTCA TCGTGGCTGT GATTGTGTGC ATCCTGGTCC  1740
TGGCGGTGCT GGGCGCTGTC CTCTATTTCC TCTATAAGAA GGGCAAGCTG CCGTGCAGGC  1800
GCTCAGGGAA GCAGGAGATC ACGCTGCCCC CGTCTCGTAA GACCGAACTT GTAGTTGAAG  1860
TTAAGTCAGA TAAGCTCCCA GAAGAGATGG GCCTCCTGCA GGGCAGCAGC GGTGACAAGA  1920
GGGCTCCGGG AGACCAGGGA GAGAAATACA TCGATCTGAG GCATTAGCCC CGAATCACTT  1980
CAGCTCCCTT CCCTGCCTGG ACCATTCCCA GCTCCCTGCT CACTCTTCTC TCAGCCAAAG  2040
CCTCCAAAGG GACTAGAGAG AAGCCTCCTG CTCCCCTCAC CTGCACACCC CCTTTCAGAG  2100
GGCCACTGGG TTAGGACCTG AGGACCTCAC TTGGCCCTGC AAGCCGCTTT TCAGGGACCA  2160
GTCCACCACC ATCTCCTCCA CGTTGAGTGA AGCTCATCCC AAGCAAGGAG CCCCAGTCTC  2220
CCGAGCGGGT AGGAGAGTTT CTTGCAGAAC GTGTTTTTTC TTTACACACA TTATGGCTGT  2280
AAATACCTGG CTCCTGCCAG CAGCTGAGCT GGGTAGCCTC TCTGAGCTGG TTTCCTGCCC  2340
CAAAGGCTGG CTTCCACCAT CCAGGTGCAC CACTGAAGTG AGGACACACC GGAGCCAGGC  2400
GCCTGCTCAT GTTGAAGTGC GCTGTTCACA CCCGCTCCGG AGAGCACCCC AGCGGCATCC  2460
AGAAGCAGCT GCAGTGTTGC TGCCACCACC CTCCTGCTCG CCTCTTCAAA GTCTCCTGTG  2520
ACATTTTTTC TTTGGTCAGA AGCCAGGAAC TGGTGTCATT CCTTAAAAGA TACGTGCCGG  2580
GGCCAGGTGT GGTGGCTCAC GCCTGTAATC CCAGCACTTT GGGAGGCCGA GGCGGGCGGA  2640
TCACAAAGTC AGGACGAGAC CATCCTGGCT AACACGGTGA AACCCTGTCT CTACTAAAAA  2700
TACAAAAAAA AATTAGCTAG GCGTAGTGGT TGGCACCTAT AGTCCCAGCT ACTCGGAAGG  2760
CTGAAGCAGG AGAATGGTAT GAATCCAGGA GGTGGAGCTT GCAGTGAGCC GAGACCGTGC  2820
CACTGCACTC CAGCCTGGGC AACACAGCGA GACTCCGTCT CGAGGAAAAA AAAAGAAAAG  2880
ACGCGTACCT GCGGTGAGGA AGCTGGGCGC TGTTTTCGAG TTCAGGTGAA TTAGCCTCAA  2940
TCCCCGTGTT CACTTGCTCC CATAGCCCTC TTGATGGATC ACGTAAAACT GAAAGGCAGC  3000
GGGGAGCAGA CAAAGATGAG GTCTACACTG TCCTTCATGG GGATTAAAGC TATGGTTATA  3060
TTAGCACCAA ACTTCTACAA ACCAAGCTCA GGGCCCCAAC CCTAGAAGGG CCCAAATGAG  3120
AGAATGGTAC TTAGGGATGG AAAACGGGGC CTGGCTAGAG CTTCGGGTGT GTGTGTCTGT  3180
CTGTGTGTAT GCATACATAT GTGTGTATAT ATGGTTTTGT CAGGTGTGTA AATTTGCAAA  3240
TTGTTTCCTT TATATATGTA TGTATATATA TATATGAAAA TATATATATA TATGAAAAAT  3300
AAAGCTTAAT TGTCCCAGAA AATCATACAT TGCTTTTTTA TTCTACATGG GTACCACAGG  3360
AACCTGGGGG CCTGTGAAAC TACAACCAAA AGGCACACAA AACCGTTTCC AGTTGGCAGC  3420
AGAGATCAGG GGTTACCTCT GCTTCTGAGC AAATGGCTCA AGCTCTACCA GAGCAGACAG  3480
CTACCCTACT TTTCAGCAGC AAAACGTCCC GTATGACGCA GCACGAAGGG CCTGGCAGGC  3540
TGTTAGCAGG AGCTATGTCC CTTCCTATCG TTTCCGTCCA CTT
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Seq ID NO: 120 Protein sequence:
Protein Accession #: NP_006491.1

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1          11         21         31         41         51
|          |          |          |          |          |
MGLPRLVCAF LLAACCCCPR VAGVPGEAEQ PAPELVEVEV GSTALLKCGL SQSQGNLSHV    60
DWFSVHKEKR TLIFRVRQGQ GQSEPGEYEQ RLSLQDRGAT LALTQVTPQD ERIFLCQGKR   120
PRSQEYRIQL RVYKAPEEPN IQVNPLGIPV NSKEPEEVAT CVGRNGYPIP QVIWYKNGRP   180
LKEEKNRVHI QSSQTVESSG LYTLQSILKA QLVKEDKDAQ FYCELNYRLP SGNHMKESRE   240
VTVPVFYPTE KVWLEVEPVG MLKEGDRVEI RCLADGNPPP HFSISKQNPS TREAEEETTN   300
DNGVLVLEPA RKEHSGRYEC QAWNLDTMIS LLSEPQELLV NYVSDVRVSP AAPERQEGSS   360
LTLTCEAESS QDLEFQWLRE ETDQVLERGP VLQLHDLKRE AGGGYRCVAS VPSIPGLNRT   420
QLVKLAIFGP PWMAFKERKV WVKENMVLNL SCEASGHPRP TISWNVNGTA SEQDQDPQRV   480
LSTLNVLVTP ELLETGVECT ASNDLGKNTS ILFLELVNLT TLTPDSNTTT GLSTSTASPH   540
TRANSTSTER KLPEPESRGV VIVAVIVCIL VLAVLGAVLY FLYKKGKLPC RRSGKQEITL   600
PPSRKTELVV EVKSDKLPEE MGLLQGSSGD KRAPGDQGEK YIDLRH
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Seq ID NO: 121 DNA sequence
Nucleic Acid Accession #: NM_018306
Coding sequence: 60-671

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1          11         21         31         41         51
|          |          |          |          |          |
ATAGTCTACA CAGAGCTCCC CTTGCTGCCC AGACAAGCTG AAGGACCACA GGAAAAGCCA    60
TGGAGACTTC AGCATCCTCC TCCCAGCCTC AGGACAACAG TCAAGTCCAC AGAGAAACAG   120
AAGATGTAGA CTATGGAGAG ACAGATTTCC ACAAGCAAGA CGGGAAGGCT GGACTCTTTT   180
CCCAAGAACA ATATGAGAGA AACAAGTCTT CTTCCTCCTC CTTCTCTTCC TCCTCATCCT   240
CCTCATCTTC TTCATCCTCC TCCTCCTCAG GTCCTGGGCA TGGGGAGCCT GACGTTTTGA   300
```

AGGATGAGCT TCAACTCTAT GGAGATGCTC CTGGAGAGGT GGTACCCTCT GGGGAATCAG 360
GACTCCGAAG GAGAGGCTCT GACCCAGCAA GTGGAGAAGT GGAGGCCTCT CAGTTAAGAA 420
GACTGAATAT AAAGAAAGAT GATGAGTTTT TCCATTTCGT CCTCCTGTGC TTTGCCATCG 480
GGGCCTTGCT GGTGTGTTAT CACTATTACG CAGACTGGTT CATGTCTCTT GGGGTCGGCC 540
TGCTCACCTT CGCCTCCCTG GAAACCGTTG GCATCTACTT CGGACTAGTG TACCGTATCC 600
ACAGCGTCCT CCAAGGCTTC ATCCCCCTCT TCCAGAAGTT TAGGCTGACA GGGTTCAGGA 660
AGACTGACTG AGGCCACTTC CAGGTGGGCA GCAGAGGCAG GCCCCAGTGT GACCACCACT 720
GCGACCCCTG AGCCCACAAG GGCAGAGCAG CATTCTGAGA GACGCACAGG AGACCAAGCC 780
AGACCAATAA ACAGAACACT TTTCCTTCCA TGTGGTCTGA ATGTTGGCAC CAGCCCGGGC 840
AGGGGCATCT CATTTGGGCA GTACTGCTGT GCAACCCAGC TGCAAGGATG GAAGGCAGAG 900
GGTGGGTGTG GGGCCTGAGG CTTCACAGTA CCTGGACCAG CAGGAAGATT CTGGGAGGTC 960
ACTGCTCTCA GAGGACAGCA AGGACCCTG AGCTCTGCAA GCTGTGATCT GTCTGGGTTC 1020
ATGGTTTTTC TCAAATCCCA GGCTATCTGC ATGCGCTCTC AGGTGCTACC GAGCCATCCT 1080
GGGAGAGATG GATGGTCCAC TGCTTTGAGG CAGGGAGCCA TCGGGCTGGG GCCCCTTGGT 1140
GAACCTGATG CAGGTAAGAT GCTGAGGACT AAAACCATTT TTTTTGCACC CAAAAAAAAA 1200
GGCAGGAAAA TGATCATCAG AAACTAAATG GCAGCCAGGC ATGGGGGCTC ACGACTGTAA 1260
TCCTCGCACT TTGGGAGGCT CAGGCTAAGG GTCGCTTGAA GCTGAGAGTT CAAGACCAAC 1320
CTGGGCAACA TAGTGAGACC CCCATCTCTA CAATTTTTTT TTAATGACCA AATGTGGCGG 1380
TACATACCTG TACATACCTG CGGTTCCAGC TACTCAAGAG GCTGAGGCAG GAGGACTGCT 1440
TGAGCCCAGG AGTTCAGGGC TGCAGTGAGG TACGATCAAG CCACTGCACT CCAGCCTGGG 1500
CGACAGAGCA AGATCGTTTC TCTAAAATT

Seq ID NO: 122 Protein sequence:
Protein Accession #: NP_060776

1 11 21 31 41 51
MEТSASSSQP QDNSQVHRET EDVDYGETDF HKQDGKAGLF SQEQYERNKS SSSSFSSSSS 60
SSSSSSSSSS GPGHGEPDVL KDELQLYGDA PGEVVPSGES GLRRRGSDPA SGEVEASQLR 120
RLNIKKDDEF FHFVLLCFAI GALLVCYHYY ADWFMSLGVG LLTFASLETV GIYFGLVYRI 180
HSVLQGFIPL FQKFRLTGFR KTD

Seq ID NO: 123 DNA sequence
Nucleic Acid Accession #: BC022542
Coding sequence: 243..896

1 11 21 31 41 51
ACTTGGTCCC AGCCGATAAA TCTGGGGCAG CGCGCGGTAG GAGCTGCGGG CGGCCAGGCC 60
CCTTCCTGCG TCCGCACCTG GCCCCGCGCG CCCCTCTCGG GCGTCCGGCT TCCGGCGTCC 120
TGGCGGCTCG GGTGGCGGCG GTTCGGGCGG CCGCCTGGCT GCTCCTCGGG GCGGCGACGG 180
GGCTCACGCG CGGGCCCGCC ACGGCCTTCA CCGCCGCGCG CTCTGACGCC GGCATAAGGG 240
CCATGTGTTC TGAAATTATT TTGAGGCAAG AAGTTTTGAA AGATGGTTTC CACAGAGACC 300
TTTTAATCAA AGTGAAGTTT GGGGAAAGCA TTGAGGACTT GCACACGTGC CGTCTCTTAA 360
TTAAACAGGA CATTCCTGCA GGACTTTATG TGGATCCGTA TGAGTTGGCT TCATTACGAG 420
AGAGAAACAT AACAGAGGCA GTGATGGTTT CAGAAAATTT TGATATAGAG GCCCCTAACT 480
ATTTGTCCAA GGAGTCTGAA GTTCTCATTT ATGCCAGACG AGATTCACAG TGCATTGACT 540
GTTTTCAAGC CTTTTTGCCT GTGCACTGCC GCTATCATCG GCCGCACAGT GAAGATGGAG 600
AAGCCTCGAT TGTGGTCAAT AACCCAGATT TGTTGATGTT TTGTGACCAA GAGTTCCCGA 660
TTTTGAAATG CTGGGCTCAC TCAGAAGTGG CAGCCCCTTG TGCTTTGGAT AATGAGGATA 720
TATGCCAATG GAACAAGATG AAGTATAAAT CAGTATATAA GAATGTGATT CTACAAGTTC 780
CAGTGGGACT GACTGTACAT ACCTCTCTAG TATGTTCTGT GACTCTGCTC ATTACAATCC 840
TGTGCTCTAC ATTGATCCTT GTAGCAGTTT TCAAATATGG CCATTTTTCC CTATAAGTTT 900
TATGTAGTTA AATGCTTCCT AGAAACCTAA ATAAGATCTA TTAATTTCTG ACGAGAGGTG 960
TTCTTCTAGA ATTAATTACT TTTATCTTTT GTCTTCATTT GTGGCCAAAA TTATGTTTAC 1020
TAGAGGAAAT TTGGGATCAT TCTCAGCTAA TTCCAAAATG TAGTGCTCTA TTGCATGGAT 1080
CCTTGGTAAT CCTCAAGCAT CAGATGCCAT AAGGGGAAAC TTAATTCTGC TAAATTAATG 1140
TTTATTTTGT GAGAAGTGAC TTTATCTTCA TTTGGGGTAG AAAAATTATT TCTTTATGTA 1200
GTAGAGACAA ATTATTCTCA TTTTGCAAGT ACTTTCAATT TAAGCTACAA ATTGAGAAAA 1260
CCGTTATAAA TAAGAATAAA ATAGGCCAGG CACAGTGGCT CACACCTGTA ATCCCAGCAC 1320
TTTGGGAGGC CGAGGTGGGC GGATCACCAG AGGTCAAGAG TTTGAGACCA GCTTGGTGAA 1380
ACCCTGTCTC TACTAAAAAT ACAAAAGTTA GCTGGGGCTG GTGGTGGGCA TCTGTAGTCC 1440
CAGCTAATTG GAAGGGTGAG GCGGGAGGAT CGCTTGAACC TGGGAGGCGG AGGTTCCAGA 1500
GAGCCAAGAT CGCACCACTG CACTACAGCC TGGGCGACAG AACGAGACCC TGTCTCCAAA 1560
GGAAAAACAA AAAAGAAGAA TAAAATAATT TGGATGAAAA TCATGTTTAT TTAAATAGTA 1620
ATGTCATGAG ACTATTAAAG ATGTGCCAGA GTTTCAATGA AAATCATTAA AGTAGGACAG 1680
CTAAGAAATT AATATTAATA TAAAAATTAT TGATAATCTT AAATTATTGA TTATTCCTTA 1740
ACGCACTCCA TTCTCCTTTT ACATTTTATC ATGTTTCTTT TGAATATATG AATTGGCAAA 1800
GGACTTGATG AAACTGAGTA CTAAGATTTG GTACAGAGTA TGTCAGGAAG ACAACTCAGA 1860
TTGCCATTTT AAATAAAGTT GTACATGAAC AAAAAAAAAA AAAAAA

Seq ID NO: 124 Protein sequence:
Protein Accession #: AAH22542

1 11 21 31 41 51
MCSEIILRQE VLKDGFHRDL LIKVKFGESI EDLHTCRLLI KQDIPAGLYV DPYELASLRE 60
RNITEAVMVS ENFDIEAPNY LSKESEVLIY ARRDSQCIDC FQAFLPVHCR YHRPHSEDGE 120
ASIVVNNPDL LMFCDQAGSR RMIRFRFDSF DKTIEFPILK CWAHSEVAAP CALENEDICQ 180
WNKMKYKSVY KNVILQVPVG LTVHTSLVCS VTLLITILCS KKKKK

Seq ID NO: 125 DNA sequence
Nucleic Acid Accession #: NM_004994.1
Coding sequence: 20..2143

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GGGCTGCTGC TTTGCTGCCC CCAGACAGCG CCAGTCCACC CTTGTGCTCT TCCCTGGAGA   120
CCTGAGAACC AATCTCACCG ACAGGCAGCT GGCAGAGGAA TACCTGTACC GCTATGGTTA   180
CACTCGGGTG GCAGAGATGC GTGGAGAGTC GAAATCTCTG GGGCCTGCGC TGCTGCTTCT   240
CCAGAAGCAA CTGTCCCTGC CCGAGACCGG TGAGCTGGAT AGCGCCACGC TGAAGGCCAT   300
GCGAACCCCA CGGTGCGGGG TCCCAGACCT GGGCAGATTC CAAACCTTTG AGGGCGACCT   360
CAAGTGGCAC CACCACAACA TCACCTATTG GATCCAAAAC TACTCGGAAG ACTTGCCGCG   420
GGCGGTGATT GACGACGCCT TTGCCCGCGC CTTCGCACTG TGGAGCGCGG TGACGCCGCT   480
CACCTTCACT CGCGTGTACA GCCGGGACGC AGACATCGTC ATCCAGTTTG GTGTCGCGGA   540
GCACGGAGAC GGGTATCCCT TCGACGGGAA GGACGGGCTC CTGGCACACG CCTTTCCTCC   600
TGGCCCCGGC ATTCAGGGAG ACGCCCATTT CGACGATGAC GAGTTGTGGT CCCTGGGCAA   660
GGGCGTCGTG GTTCCAACTC GGTTTGGAAA CGCAGATGGC GCGGCCTGCC ACTTCCCCTT   720
CATCTTCGAG GGCCGCTCCT ACTCTGCCTG CACCACCGAC GGTCGCTCCG ACGGCTTGCC   780
CTGGTGCAGT ACCACGGCCA ACTACGACAC CGACGACCGG TTTGGCTTCT GCCCCAGCGA   840
GAGACTCTAC ACCCGGGACG GCAATGCTGA TGGGAAACCC TGCCAGTTTC CATTCATCTT   900
CCAAGGCCAA TCCTACTCCG CCTGCACCAC GGACGGTCGC TCCGACGGCT ACCGCTGGTG   960
CGCCACCACC GCCAACTACG ACCGGGACAA GCTCTTCGGC TTCTGCCCGA CCCGAGCTGA  1020
CTCGACGGTG ATGGGGGGCA ACTCGGCGGG GGAGCTGTGC GTCTTCCCCT TCACTTTCCT  1080
GGGTAAGGAG TACTCGACCT GTACCAGCGA GGGCCGCGGA GATGGGCGCC TCTGGTGCGC  1140
TACCACCTCG AACTTTGACA GCGACAAGAA GTGGGGCTTC TGCCCGGACC AAGGATACAG  1200
TTTGTTCCTC GTGGCGGCGC ATGAGTTCGG CCACGCGCTG GGCTTAGATC ATTCCTCAGT  1260
GCCGGAGGCG CTCATGTACC CTATGTACCG CTTCACTGAG GGGCCCCCCT TGCATAAGGA  1320
CGACGTGAAT GGCATCCGGC ACCTCTATGG TCCTCGCCCT GAACCTGAGC CACGGCCTCC  1380
AACCACCACC ACACCGCAGC CCACGGCTCC CCCGACGGTC TGCCCCACCG GACCCCCCAC  1440
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AGGTCCCCCC ACTGCTGGCC CTTCTACGGC CACTACTGTG CCTTTGAGTC CGGTGGACGA  1560
TGCCTGCAAC GTGAACATCT TCGACGCCAT CGCGGAGATT GGGAACCAGC TGTATTTGTT  1620
CAAGGATGGG AAGTACTGGC GATTCTCTGA GGGCAGGGGG AGCCGGCCGC AGGGCCCCTT  1680
CCTTATCGCC GACAAGTGGC CCGCGCTGCC CCGCAAGCTG GACTCGGTCT TTGAGGAGCC  1740
GCTCTCCAAG AAGCTTTTCT TCTTCTCTGG GCGCCAGGTG TGGGTGTACA CAGGCGCGTC  1800
GGTGCTGGGC CCGAGGCGTC TGGACAAGCT GGGCCTGGGA GCCGACGTGG CCCAGGTGAC  1860
CGGGGCCCTC CGGAGTGGCA GGGGGAAGAT GCTGCTGTTC AGCGGGCGGC GCCTCTGGAG  1920
GTTCGACGTG AAGGCGCAGA TGGTGGATCC CCGGAGCGCC AGCGAGGTGG ACCGGATGTT  1980
CCCCGGGGTG CCTTTGGACA CGCACGACGT CTTCCAGTAC CGAGAGAAAG CCTATTTCTG  2040
CCAGGACCGC TTCTACTGGC GCGTGAGTTC CCGGAGTGAG TTGAACCAGG TGGACCAAGT  2100
GGGCTACGTG ACCTATGACA TCCTGCAGTG CCCTGAGGAC TAGGGCTCCC GTCCTGCTTT  2160
GCAGTGCCAT GTAAATCCCC ACTGGGACCA ACCCTGGGGA AGGAGCCAGT TTGCCGGATA  2220
CAAACTGGTA TTCTGTTCTG GAGGAAAGGG AGGAGTGGAG GTGGGCTGGG CCCTCTCTTC  2280
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Seq ID NO: 126 Protein sequence:
Protein Accession #: NP_004985.1

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RGESKSLGPA LLLLQKQLSL PETGELDSAT LKAMRTPRCG VPDLGRFQTF EGDLKWHHHN   120
ITYWIQNYSE DLPRAVIDDA FARAFALWSA VTPLTFTRVY SRDADIVIQF GVAEHGDGYP   180
FDGKDGLLAH AFPPGPGIQG DAHFDDDELW SLGKGVVVPT RFGNADGAAC HFPFIFEGRS   240
YSACTTDGRS DGLPWCSTTA NYDTDDRFGF CPSERLYTRD GNADGKPCQF PFIFQGQSYS   300
ACTTDGRSDG YRWCATTANY DRDKLFGFCP TRADSTVMGG NSAGELCVFP FTFLGKEYST   360
CTSEGRGDGR LWCATTSNFD SDKKWGFCPD QGYSLFLVAA HEFGHALGLD HSSVPEALMY   420
PMYRFTEGPP LHKDDVNGIR HLYGPRPEPE PRPPTTTTPQ PTAPPTVCPT GPPTVHPSER   480
PTAGPTGPPS AGPTGPPTAG PSTATTVPLS PVDDACNVNI FDAIAEIGNQ LYLFKDGKYW   540
RFSEGRGSRP QGPFLIADKW PALPRKLDSV FEEPLSKKLF FFSGRQVWVY TGASVLGPRR   600
LDKLGLGADV AQVTGALRSG RGKMLLFSGR RLWRFDVKAQ MVDPRSASEV DRMFPGVPLD   660
THDVFQYREK AYFCQDRFYW RVSSRSELNQ VDQVGYVTYD ILQCPED
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Seq ID NO: 127 DNA sequence
Nucleic Acid Accession #: NM_004181
Coding sequence: 32-670

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GGTGCCAGCG CCTGCCTGCG CGCTGCTGCT GCTGTTTCCC CTCACGGCCC AGCATGAGAA   180
CTTCAGGAAA AAGCAGATTG AAGAGCTGAA GGGACAAGAA GTTAGTCCTA AAGTGTACTT   240
CATGAAGCAG ACCATTGGGA ATTCCTGTGG CACAATCGGA CTTATTCACG CAGTGGCCAA   300
TAATCAAGAC AAACTGGGAT TTGAGGATGG ATCAGTTCTG AAACAGTTTC TTTCTGAAAC   360
AGAGAAAATG TCCCCTGAAG ACAGAGCAAA ATGCTTTGAA AAGAATGAGG CCATACAGGC   420
AGCCCATGAT GCCGTGGCAC AGGAAGGCCA ATGTCGGGTA GATGACAAGG TGAATTTCCA   480
TTTTATTCTG TTTAACAACG TGGATGGCCA CCTCTATGAA CTTGATGGAC GAATGCCTTT   540
TCCGGTGAAC CATGGCGCCA GTTCAGAGGA CACCCTGCTG AAGGACGCTG CCAAGGTGTG   600
CAGAGAATTC ACCGAGCGTG AGCAAGGAGA AGTCCGCTTC TCTGCCGTGG CTCTCTGCAA   660
GGCAGCCTAA TGCTCTGTGG GAGGGACTTT GCTGATTTCC CCTCTTCCCT TCAACATGAA   720
AATATATACC CCCCATGCAG TCTAAAATGC TTCAGTACTT GTGAAACACA GCTGTTCTTC   780
TGTTCTGCAG ACACGCCTTC CCCTCAGCCA CACCCAGGCA CTTAAGCACA AGCAGAGTGC   840
ACAGCTGTCC ACTGGGCCAT TGTGGTGTGA GCTTCAGATG GTGAAGCATT CTCCCCAGTG   900
TATGTCTTGT ATCCGATATC TAACGCTTTA AATGGCTACT TTGGTTTCTG TCTGTAAGTT   960
AAGACCTTGG ATGTGGTTAT GTTGTCCTAA AGAATAAATT TTGCTGATAG TAGC
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Seq ID NO: 128 Protein sequence:
Protein Accession #: NP_004172

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GQEVSPKVYF MKQTIGNSCG TIGLIHAVAN NQDKLGFEDG SVLKQFLSET EKMSPEDRAK   120
CFEKNEAIQA AHDAVAQEGQ CRVDDKVNFH FILFNNVDGH LYELDGRMPF PVNHGASSED   180
TLLKDAAKVC REFTEREQGE VRFSAVALCK AA
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Seq ID NO: 129 DNA sequence
Nucleic Acid Accession #: NM_000213
Coding sequence: 127-5385

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AAGAGGATGG CAGGGCCACG CCCCAGCCCA TGGGCCAGGC TGCTCCTGGC AGCCTTGATC   180
AGCGTCAGCC TCTCTGGGAC CTTGGCAAAC CGCTGCAAGA AGGCCCCAGT GAAGAGCTGC   240
ACGGAGTGTG TCCGTGTGGA TAAGGACTGC GCCTACTGCA CAGACGAGAT GTTCAGGGAC   300
CGGCGCTGCA ACACCCAGGC GGAGCTGCTG GCCGCGGGCT GCCAGCGGGA GAGCATCGTG   360
GTCATGGAGA GCAGCTTCCA AATCACAGAG GAGACCCAGA TTGACACCAC CCTGCGGCGC   420
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TCGGCGATCC ACCCGGGCCT CTGCGAGGAC CTACGCTCCT GCGTGCAGTG CCAGGCGTGG  2040
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GACGAGCTTA AGAGAGCCGA GGAGGTGGTG GTGCGCTGCT CCTTCCGGGA CGAGGATGAC  2160
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TCCTGGGAGG CATGAAGGGG GCAAGGTCCG TCCTCTGTGG GCCCAAACCT ATTTGTAACC  5580
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ACTG
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Seq ID NO: 130 Protein sequence:
Protein Accession #: NP_000204

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CNTQAELLAA GCQRESIVVM ESSFQITEET QIDTTLRRSQ MSPQGLRVRL RPGEERHFEL   120
EVFEPLESPV DLYILMDFSN SMSDDLDNLK KMGQNLARVL SQLTSDYTIG FGKFVDKVSV   180
PQTDMRPEKL KEPWPNSDPP FSFKNVISLT EDVDEFRNKL QGERISGNLD APEGGFDAIL   240
QTAVCTRDIG WRPDSTHLLV FSTESAFHYE ADGANVLAGI MSRNDERCHL DTTGTYTQYR   300
TQDYPSVPTL VRLLAKHNII PIFAVTNYSY SYYEKLHTYF PVSSLGVLQE DSSNIVELLE   360
EAFNRIRSNL DIRALDSPRG LRTEVTSKMF QKTRTGSFHI RRGEVGIYQV QLRALEHVDG   420
THVCQLPEDQ KGNIHLKPSF SDGLKMDAGI ICDVCTCELQ KEVRSARCSF NGDFVCGQCV   480
CSEGWSGQTC NCSTGSLSDI QPCLREGEDK PCSGRGECQC GHCVCYGEGR YEGQFCEYDN   540
FQCPRTSGFL CNDRGRCSMG QCVCEPGWTG PSCDCPLSNA TCIDSNGGIC NGRGHCECGR   600
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LKRAEEVVVR CSFRDEDDDC TYSYTMEGDG APGPNSTVLV HKKKDCPPGS FWWLIPLLLL   720
LLPLLALLLL LCWKYCACCK ACLALLPCCN RGHMVGFKED HYMLRENLMA SDHLDTPMLR   780
SGNLKGRDVV RWKVTNNMQR PGFATHAASI NPTELVPYGL SLRLARLCTE NLLKPDTREC   840
AQLRQEVEEN LNEVYRQISG VHKLQQTKFR QQPNAGKKQD HTIVDTVLMA PRSAKPALLK   900
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LVEAIDVPAG TATLGRRLVN ITIIKEQARD VVSFEQPEFS VSRGDQVARI PVIRRVLDGG  1020
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Seq ID NO: 131 DNA sequence
Nucleic Acid Accession #: BC004372
Coding sequence: 132..2231

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AGAAAAATGG TCGCTACAGC ATCTCTCGGA CGGAGGCCGC TGACCTCTGC AAGGCTTTCA   300
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GCAGGTATGG GTTCATAGAA GGGCATGTGG TGATTCCCCG GATCCACCCC AACTCCATCT   420
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ATGCCTTTGA TGGACCAATT ACCATAACTA TTGTTAACCG TGATGGCACC CGCTATGTCC   600
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ACGTGAGCAG CGGCTCCTCC AGTGAAAGGA GCAGCACTTC AGGAGGTTAC ATCTTTTACA   720
CCTTTTCTAC TGTACACCCC ATCCCAGACG AAGACAGTCC CTGGATCACC GACAGCACAG   780
ACAGAATCCC TGCTACCAGT ACGTCTTCAA ATACCATCTC AGCAGGCTGG GAGCCAAATG   840
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CAACCACAAG GATGACTGAT GTAGACAGAA ATGGCACCAC TGCTTATGAA GGAAACTGGA  1080
ACCCAGAAGC ACACCCTCCC CTCATTCACC ATGAGCATCA TGAGGAAGAA GAGACCCCAC  1140
ATTCTACAAG CACAATCCAG GCAACTCCTA GTAGTACAAC GGAAGAAACA GCTACCCAGA  1200
AGGAACAGTG GTTTGGCAAC AGATGGCATG AGGGATATCG CCAAACACCC AGAGAAGACT  1260
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CCCATTCGAC AACAGGGACA GCTGCAGCCT CAGCTCATAC CAGCCATCCA ATGCAAGGAA  1320
GGACAACACC AAGCCCAGAG GACAGTTCCT GGACTGATTT CTTCAACCCA ATCTCACACC  1380
CCATGGGACG AGGTCATCAA GCAGGAAGAA GGATGGATAT GGACTCCAGT CATAGTACAA  1440
CGCTTCAGCC TACTGCAAAT CCAAACACAG GTTTGGTGGA AGATTTGGAC AGGACAGGAC  1500
CTCTTTCAAT GACAACGCAG CAGAGTAATT CTCAGAGCTT CTCTACATCA CATGAAGGCT  1560
TGGAAGAAGA TAAAGACCAT CCAACAACTT CTACTCTGAC ATCAAGCAAT AGGAATGATG  1620
TCACAGGTGG AAGAAGAGAC CCAAATCATT CTGAAGGCTC AACTACTTTA CTGGAAGGTT  1680
ATACCTCTCA TTACCCACAC ACGAAGGAAA GCAGGACCTT CATCCCAGTG ACCTCAGCTA  1740
AGACTGGGTC CTTTGGAGTT ACTGCAGTTA CTGTTGGAGA TTCCAACTCT AATGTCAATC  1800
GTTCCTTATC AGGAGACCAA GACACATTCC ACCCCAGTGG GGGGTCCCAT ACCACTCATG  1860
GATCTGAATC AGATGGACAC TCACATGGGA GTCAAGAAGG TGGAGCAAAC ACAACCTCTG  1920
GTCCTATAAG GACACCCCAA ATTCCAGAAT GGCTGATCAT CTTGGCATCC CTCTTGGCCT  1980
TGGCTTTGAT TCTTGCAGTT TGCATTGCAG TCAACAGTCG AAGAAGGTGT GGGCAGAAGA  2040
AAAAGCTAGT GATCAACAGT GGCAATGGAG CTGTGGAGGA CAGAAAGCCA AGTGGACTCA  2100
ACGGAGAGGC CAGCAAGTCT CAGGAAATGG TGCATTTGGT GAACAAGGAG TCGTCAGAAA  2160
CTCCAGACCA GTTTATGACA GCTGATGAGA CAAGGAACCT GCAGAATGTG GACATGAAGA  2220
TTGGGGTGTA ACACCTACAC CATTATCTTG GAAAGAAACA ACCGTTGGAA ACATAACCAT  2280
TACAGGGAGC TGGGACACTT AACAGATGCA ATGTGCTACT GATTGTTTCA TTGCGAATCT  2340
TTTTTAGCAT AAAATTTTCT ACTCTTAAAA AAAAAAAAAA AAAAAAA
```

Seq ID NO: 132 Protein sequence:
Protein Accession #: AAH04372

```
1          11         21         31         41         51
|          |          |          |          |          |
MDKFWWHAAW GLCLVPLSLA QIDLNITCRF AGVFHVEKNG RYSISRTEAA DLCKAFNSTL    60
PTMAQMEKAL SIGFETCRYG FIEGHVVIPR IHPNSICAAN NTGVYILTSN TSQYDTYCFN   120
ASAPPEEDCT SVTDLPNAFD GPITITIVNR DGTRYVQKGE YRTNPEDIYP SNPTDDDVSS   180
GSSSERSSTS GGYIFYTFST VHPIPDEDSP WITDSTDRIP ATSTSSNTIS AGWEPNEENE   240
DERDRHLSFS GSGIDDDEDF ISSTISTTPR AFDHTKQNQD WTQWNPSHSN PEVLLQTTTR   300
MTDVDRNGTT AYEGNWNPEA HPPLIHHEHH EEEETPHSTS TIQATPSSTT EETATQKEQW   360
FGNRWHEGYR QTPREDSHST TGTAAASAHT SHPMQGRTTP SPEDSSWTDF FNPISHPMGR   420
GHQAGRRMDM DSSHSTTLQP TANPNTGLVE DLDRTGPLSM TTQQSNSQSF STSHEGLEED   480
KDHPTTSTLT SSNRNDVTGG RRDPNHSEGS TTLLEGYTSH YPHTKESRTF IPVTSAKTGS   540
FGVTAVTVGD SNSNVNRSLS GDQDTFHPSG GSHTTHGSES DGHSHGSQEG GANTTSGPIR   600
TPQIPEWLII LASLLALALI LAVCIAVNSR RRCGQKKKLV INSGNGAVED RKPSGLNGEA   660
SKSQEMVHLV NKESSETPDQ FMTADETRNL QNVDMKIGV
```

Seq ID NO: 133 DNA sequence
Nucleic Acid Accession #: NM_002882
Coding sequence: 150-755

```
1          11         21         31         41         51
|          |          |          |          |          |
CGAGGTTCGG GTCGTGGGGC GGAGGGAAGA GCGGGCGGGC GGGAGGCGCC GGCGCCAGAC    60
GCGGAGGGAA GGAGCTACGA GTAGCCGCCG AGAGGCCGCG GAGCCAGCGA CGACCGACCC   120
AGCCGAGCCG CCGCCGCCGC CGCGCCCCCA TGGCGGCCGC CAAGGACACT CATGAGGACC   180
ATGATACTTC CACTGAGAAT ACAGACGAGT CCAACCATGA CCCTCAGTTT GAGCCAATAG   240
TTTCTCTTCC TGAGCAAGAA ATTAAAACAC TGGAAGAAGA TGAAGAGGAA CTTTTTAAAA   300
TGCGGGCAAA ACTGTTCCGA TTTGCCTCTG AGAACGATCT CCCAGAATGG AAGGAGCGAG   360
GCACTGGTGA CGTCAAGCTC CTGAAGCACA AGGAGAAAGG GGCCATCCGC CTCCTCATGC   420
GGAGGGACAA GACCCTGAAG ATCTGTGCCA ACCACTACAT CACGCCGATG ATGGAGCTGA   480
AGCCCAACGC AGGTAGCGAC CGTGCCTGGG TCTGGAACAC CCACGCTGAC TTCGCCGACG   540
AGTGCCCCAA GCCAGAGCTG CTGGCCATCC GCTTCCTGAA TGCTGAGAAT GCACAGAAAT   600
TCAAAACAAA GTTTGAAGAA TGCAGGAAAG AGATCGAAGA GAGAGAAAAG AAAGCAGGAT   660
CAGGCAAAAA TGATCATGCC GAAAAAGTGG CGGAAAAGCT AGAAGCTCTC TCGGTGAAGG   720
AGGAGACCAA GGAGGATGCT GAGGAGAAGC AATAAATCGT CTTATTTTAT TTTCTTTTCC   780
TCTCTTTCCT TTCCTTTTTT TAAAAAATTT TACCCTGCCC CTCTTTTTCG GTTTGTTTTT   840
ATTCTTTCAT TTTTACAAGG GACGTTATAT AAAGAACTGA ACTC
```

Seq ID NO: 134 Protein sequence:
Protein Accession #: NP_002873

```
1          11         21         31         41         51
|          |          |          |          |          |
MAAAKDTHED HDTSTENTDE SNHDPQFEPI VSLPEQEIKT LEEDEEELFK MRAKLFRFAS    60
ENDLPEWKER GTGDVKLLKH KEKGAIRLLM RRDKTLKICA NHYITPMMEL KPNAGSDRAW   120
VWNTHADFAD ECPKPELLAI RFLNAENAQK FKTKFEECRK EIEEREKKAG SGKNDHAEKV   180
AEKLEALSVK EETKEDAEEK Q
```

Seq ID NO: 135 DNA sequence
Nucleic Acid Accession #: NM_000077.2
Coding sequence: 277-742

```
1          11         21         31         41         51
|          |          |          |          |          |
CCCAACCTGG GGCGACTTCA GGTGTGCCAC ATTCGCTAAG TGCTCGGAGT TAATAGCACC    60
TCCTCCGAGC ACTCGCTCAC GGCGTCCCCT TGCCTGGAAA GATACCGCGG TCCCTCCAGA   120
GGATTTGAGG GACAGGGTCG GAGGGGGCTC TTCCGCCAGC ACCGGAGGAA GAAAGAGGAG   180
GGGCTGGCTG GTCACCAGAG GGTGGGGCGG ACCGCGTGCG CTCGGCGGCT GCGGAGAGGG   240
GGAGAGCAGG CAGCGGGCGG CGGGGAGCAG CATGGAGCCG GCGGCGGGGA GCAGCATGGA   300
GCCTTCGGCT GACTGGCTGG CCACGGCCGC GGCCCGGGGT CGGGTAGAGG AGGTGCGGGC   360
GCTGCTGGAG GCGGGGGCGC TGCCCAACGC ACCGAATAGT TACGGTCGGA GGCCGATCCA   420
GGTCATGATG ATGGGCAGCG CCCGAGTGGC GGAGCTGCTG CTGCTCCACG GCGCGGAGCC   480
```

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CAACTGCGCC GACCCCGCCA CTCTCACCCG ACCCGTGCAC GACGCTGCCC GGGAGGGCTT   540
CCTGGACACG CTGGTGGTGC TGCACCGGGC CGGGGCGCGG CTGGACGTGC GCGATGCCTG   600
GGGCCGTCTG CCCGTGGACC TGGCTGAGGA GCTGGGCCAT CGCGATGTCG CACGGTACCT   660
GCGCGCGGCT GCGGGGGGCA CCAGAGGCAG TAACCATGCC CGCATAGATG CCGCGGAAGG   720
TCCCTCAGAC ATCCCCGATT GAAAGAACCA GAGAGGCTCT GAGAAACCTC GGGAAACTTA   780
GATCATCAGT CACCGAAGGT CCTACAGGGC CACAACTGCC CCCGCCACAA CCCACCCCGC   840
TTTCGTAGTT TTCATTTAGA AAATAGAGCT TTTAAAAATG TCCTGCCTTT TAACGTAGAT   900
ATATGCCTTC CCCCACTACC GTAAATGTCC ATTTATATCA TTTTTTATAT ATTCTTATAA   960
AAATGTAAAA AAGAAAAACA CCGCTTCTGC CTTTTCACTG TGTTGGAGTT TTCTGGAGTG  1020
AGCACTCACG CCCTAAGCGC ACATTCATGT GGGCATTTCT TGCGAGCCTC GCAGCCTCCG  1080
GAAGCTGTCG ACTTCATGAC AAGCATTTTG TGAACTAGGG AAGCTCAGGG GGTTACTGG   1140
CTTCTCTTGA GTCACACTGC TAGCAAATGG CAGAACCAAA GCTCAAATAA AAATAAAATA  1200
ATTTTCATTC ATTCACTC
```

Seq ID NO: 136 Protein sequence:
Protein Accession #: NP_000068.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MEPAAGSSME PSADWLATAA ARGRVEEVRA LLEAGALPNA PNSYGRRPIQ VMMMGSARVA    60
ELLLLHGAEP NCADPATLTR PVHDAAREGF LDTLVVLHRA GARLDVRDAW GRLPVDLAEE   120
LGHRDVARYL RAAAGGTRGS NHARIDAAEG PSDIPD
```

Seq ID NO: 137 DNA sequence
Nucleic Acid Accession #: NM_058196.1
Coding sequence: 104-421

```
1          11         21         31         41         51
|          |          |          |          |          |
TGTGTGGGGG TCTGCTTGGC GGTGAGGGGG CTCTACACAA GCTTCCTTTC CGTCATGCCG    60
GCCCCCACCC TGGCTCTGAC CATTCTGTTC TCTCTGGCAG GTCATGATGA TGGGCAGCGC   120
CCGAGTGGCG GAGCTGCTGC TGCTCCACGG CGCGGAGCCC AACTGCGCCG ACCCCGCCAC   180
TCTCACCCGA CCCGTGCACG ACGCTGCCCG GGAGGGCTTC CTGGACACGC TGGTGGTGCT   240
GCACCGGGCC GGGGCGCGGC TGGACGTGCG CGATGCCTGG GGCCGTCTGC CCGTGGACCT   300
GGCTGAGGAG CTGGGCCATC GCGATGTCGC ACGGTACCTG CGCGCGGCTG CGGGGGGCAC   360
CAGAGGCAGT AACCATGCCC GCATAGATGC CGCGGAAGGT CCCTCAGACA TCCCCGATTG   420
AAAGAACCAG AGAGGCTCTG AGAAACCTCG GGAAACTTAG ATCATCAGTC ACCGAAGGTC   480
CTACAGGGCC ACAACTGCCC CCGCCACAAC CCACCCCGCT TTCGTAGTTT TCATTTAGAA   540
AATAGAGCTT TTAAAAATGT CCTGCCTTTT AACGTAGATA TAAGCCTTCC CCCACTACCG   600
TAAATGTCCA TTTATATCAT TTTTTATATA TTCTTATAAA AATGTAAAAA AGAAAAACAC   660
CGCTTCTGCC TTTTCACTGT GTTGGAGTTT TCTGGAGTGA GCACTCACGC CCTAAGCGCA   720
CATTCATGTG GGCATTTCTT GCGAGCCTCG CAGCCTCCGG AAGCTGTCGA CTTCATGACA   780
AGCATTTTGT GAACTAGGGA AGCTCAGGGG GGTTACTGGC TTCTCTTGAG TCACACTGCT   840
AGCAAATGGC AGAACCAAAG CTCAAATAAA AATAAAATAA TTTTCATTCA TTCACTC
```

Seq ID NO: 138 Protein sequence:
Protein Accession #: NP_478103.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MMMGSARVAE LLLLHGAEPN CADPATLTRP VHDAAREGFL DTLVVLHRAG ARLDVRDAWG    60
RLPVDLAEEL GHRDVARYLR AAAGGTRGSN HARIDAAEGP SDIPD
```

Seq ID NO: 139 DNA sequence
Nucleic Acid Accession #: NM_058197.1
Coding sequence: 272-684

```
1          11         21         31         41         51
|          |          |          |          |          |
CCCAACCTGG GGCGACTTCA GGTGTGCCAC ATTCGCTAAG TGCTCGGAGT TAATAGCACC    60
TCCTCCGAGC ACTCGCTCAC GGCGTCCCCT TGCCTGGAAA GATACCGCGG TCCCTCCAGA   120
GGATTTGAGG GACAGGGTCG GAGGGGGCTC TTCCGCCAGC ACCGGAGGAA GAAAGAGGAG   180
GGGCTGGCTG GTCACCAGAG GGTGGGGCGG ACCGCGTGCG CTCGGCGGCT GCGGAGAGGG   240
GGAGAGCAGG CAGCGGGCGG CGGGGAGCAG CATGGAGCCG GCGGCGGGGA GCAGCATGGA   300
GCCGGCGGCG GGGAGCAGCA TGGAGCCTTC GGCTGACTGG CTGGCCACGG CCGCGGCCCG   360
GGGTCGGGTA GAGGAGGTGC GGGCGCTGCT GGAGGCGGGG GCGCTGCCCA ACGCACCGAA   420
TAGTTACGGT CGGAGGCCGA TCCAGGTGGG TAGAAGGTCT GCAGCGGGAG CAGGGGATGG   480
CGGGCGACTC TGGAGGACGA AGTTTGCAGG GGAATTGGAA TCAGGTAGCG CTTCGATTCT   540
CCGGAAAAAG GGGAGGCTTC CTGGGGAGTT TTCAGAAGGG GTTTGTAATC ACAGACCTCC   600
TCCTGGCGAC GCCCTGGGGG CTTGGGAAAC CAAGGAAGAG GAATGAGGAG CCACGCGCGT   660
ACAGATCTCT CGAATGCTGA GAAGATCTGA AGGGGGGAAC ATATTTGTAT TAGATGGAAG   720
TCATGATGAT GGGCAGCGCC CGAGTGGCGG AGCTGCTGCT GCTCCACGGC GCGGAGCCCA   780
ACTGCGCCGA CCCCGCCACT CTCACCCGAC CCGTGCACGA CGCTGCCCGG GAGGGCTTCC   840
TGGACACGCT GGTGGTGCTG CACCGGGCCG GGGCGCGGCT GGACGTGCGC GATGCCTGGG   900
GCCGTCTGCC CGTGGACCTG GCTGAGGAGC TGGGCCATCG CGATGTCGCA CGGTACCTGC   960
GCGCGGCTGC GGGGGGCACC AGAGGCAGTA ACCATGCCCG CATAGATGCC GCGGAAGGTC  1020
CCTCAGACAT CCCCGATTGA AAGAACCAGA GAGGCTCTGA GAAACCTCGG GAACTTAGAT  1080
CATCAGTCAC CGAAGGTCCT ACAGGGCCAC AACTGCCCCC GCCACAACCC ACCCCGCTTT  1140
CGTAGTTTTC ATTTAGAAAA TAGAGCTTTT AAAAATGTCC TGCCTTTTAA CGTAGATATA  1200
TGCCTTCCCC CACTACCGTA AATGTCCATT TATATCATTT TTTATATATT CTTATAAAAA  1260
TGTAAAAAAG AAAAACACCG CTTCTGCCTT TTCACTGTGT TGGAGTTTTC TGGAGTGAGC  1320
ACTCACGCCC TAAGCGCACA TTCATGTGGG CATTTCTTGC GAGCCTCGCA GCCTCCGGAA  1380
GCTGTCGACT TCATGACAAG CATTTTGTGA ACTAGGGAAG CTCAGGGGGG TTACTGGCTT  1440
CTCTTGAGTC ACACTGCTAG CAAATGGCAG AACCAAAGCT CAAATAAAAA TAAAATAATT  1500
```

TTCATTCATT CACTC

Seq ID NO: 140 Protein sequence:
Protein Accession #: NP_478104.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MEPAAGSSME PAAGSSMEPS ADWLATAAAR GRVEEVRALL EAGALPNAPN SYGRRPIQVG    60
RRSAAGAGDG GRLWRTKFAG ELESGSASIL RKKGRLPGEP SEGVCNHRPP PGDALGAWET   120
KEEE
```

Seq ID NO: 141 DNA sequence
Nucleic Acid Accession #: NM_058195.1
Coding sequence: 163-684

```
1          11         21         31         41         51
|          |          |          |          |          |
CCTCCCTACG GGCGCCTCCG GCAGCCCTTC CCGCGTGCGC AGGGCTCAGA GCCGTTCCGA    60
GATCTTGGAG GTCCGGGTGG GAGTGGGGGT GGGGTGGGGG TGGGGGTGAA GGTGGGGGGC   120
GGGCGCGCTC AGGGAAGGCG GGTGCGCGCC TGCGGGGCGG AGATGGGCAG GGGGCGGTGC   180
GTGGGTCCCA GTCTGCAGTT AAGGGGGCAG GAGTGGCGCT GCTCACCTCT GGTGCCAAAG   240
GGCGGCGCAG CGGCTGCCGA GCTCGGCCCT GGAGGCGGCG AGAACATGGT GCGCAGGTTC   300
TTGGTGACCC TCCGGATTCG GCGCGCGTGC GGCCCGCCGC GAGTGAGGGT TTTCGTGGTT   360
CACATCCCGC GGCTCACGGG GGAGTGGGCA GCGCCAGGGG CGCCCGCCGC TGTGGCCCTC   420
GTGCTGATGC TACTGAGGAG CCAGCGTCTA GGGCAGCAGC CGCTTCCTAG AAGACCAGGT   480
CATGATGATG GGCAGCGCCC GAGTGGCGGA GCTGCTGCTG CTCCACGGCG CGGAGCCCAA   540
CTGCGCCGAC CCCGCCACTC TCACCCGACC CGTGCACGAC GCTGCCCGGG AGGGCTTCCT   600
GGACACGCTG GTGGTGCTGC ACCGGGCCGG GGCGCGGCTG GACGTGCGCG ATGCCTGGGG   660
CCGTCTGCCC GTGGACCTGG CTGAGGAGCT GGGCCATCGC GATGTCGCAC GGTACCTGCG   720
CGCGGCTGCG GGGGGCACCA GAGGCAGTAA CCATGCCCGC ATAGATGCCG CGGAAGGTCC   780
CTCAGACATC CCCGATTGAA AGAACCAGAG AGGCTCTGAG AAACCTCGGG AAACTTAGAT   840
CATCAGTCAC CGAAGGTCCT ACAGGGCCAC AACTGCCCCC GCCACAACCC ACCCCGCTTT   900
CGTAGTTTTC ATTTAGAAAA TAGAGCTTTT AAAAATGTCC TGCCTTTTAA CGTAGATATA   960
TGCCTTCCCC CACTACCGTA AATGTCCATT TATATCATTT TTTATATATT CTTATAAAAA  1020
TGTAAAAAAG AAAAACACCG CTTCTGCCTT TTCACTGTGT TGGAGTTTTC TGGAGTGAGC  1080
ACTCACGCCC TAAGCGCACA TTCATGTGGG CATTTCTTGC GAGCCTCGCA GCCTCCGGAA  1140
GCTGTCGACT TCATGACAAG CATTTTGTGA ACTAGGGAAG CTCAGGGGGG TTACTGGCTT  1200
CTCTTGAGTC ACACTGCTAG CAAATGGCAG AACCAAAGCT CAAATAAAAA TAAAATAATT  1260
TTCATTCATT CACTC
```

Seq ID NO: 142 Protein sequence:
Protein Accession #: NP_478102.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MGRGRCVGPS LQLRGQEWRC SPLVPKGGAA AAELGPGGGE NMVRRFLVTL RIRRACGPPR    60
VRVFVVHIPR LTGEWAAPGA PAAVALVLML LRSQRLGQQP LPRRPGHDDG QRPSGGAAAA   120
PRRGAQLRRP RHSHPTRARR CPGGLPGHAG GAAPGRGAAG RARCLGPSAR GPG
```

Seq ID NO: 143 DNA sequence
Nucleic Acid Accession #: NM_018131
Coding sequence: 412..1107

```
1          11         21         31         41         51
|          |          |          |          |          |
GAAATTGCAC ACTTAAAGAC ATCAGTGGAT GAAATCACAA GTGGGAAAGG AAAGCTGACT    60
GATAAAGAGA GACAGAGACT TTTGGAGAAA ATTCGAGTCC TTGAGGCTGA GAAGGAGAAG   120
AATGCTTATC AACTCACAGA GAAGGACAAA GAAATACAGC GACTGAGAGA CCAACTGAAG   180
GCCAGATATA GTACTACCGC ATTGCTTGAA CAGCTGGAAG AGACAACGAG AGAAGGAGAA   240
AGGAGGGAGC AGGTGTTGAA AGCCTTATCT GAAGAGAAAG ACGTATTGAA ACAACAGTTG   300
TCTGCTGCAA CCTCACGAAT TGCTGAACTT GAAAGCAAAA CCAATACACT CCGTTTATCA   360
CAGACTGTGG CTCCAAACTG CTTCAACTCA TCAATAAATA ATATTCATGA AATGGAAATA   420
CAGCTGAAAG ATGCTCTGGA GAAAAATCAG CAGTGGCTCG TGTATGATCA GCAGCGGGAA   480
GTCTATGTAA AAGGACTTTT AGCAAAGATC TTTGAGTTGG AAAAGAAAAC GGAAACAGCT   540
GCTCATTCAC TCCCACAGCA GACAAAAAAG CCTGAATCAG AAGGTTATCT TCAAGAAGAG   600
AAGCAGAAAT GTTACAACGA TCTCTTGGCA AGTGCAAAAA AAGATCTTGA GGTTGAACGA   660
CAAACCATAA CTCAGCTGAG TTTTGAACTG AGTGAATTTC GAAGAAAATA TGAAGAAACC   720
CAAAAAGAAG TTCACAATTT AAATCAGCTG TTGTATTCAC AAAGAAGGGC AGATGTGCAA   780
CATCTGGAAG ATGATAGGCA TAAAACAGAG AAGATACAAA AACTCAGGGA AGAGAATGAT   840
ATTGCTAGGG GAAAACTTGA AGAAGAGAAG AAGAGATCCG AAGAGCTCTT ATCTCAGGTC   900
CAGTCTCTTT ACACATCTCT GCTAAAGCAG CAAGAAGAAC AAACAAGGGT AGCTCTGTTG   960
GAACAACAGA TGCAGGCATG TACTTTAGAC TTTGAAAATG AAAAACTCGA CCGTCAACAT  1020
GTGCAGCATC AATTGCATGT AATTCTTAAG GAGCTCCGAA AAGCAAGAAA AAATAACACA  1080
GTTGGAATCC TTGAAACAGC TTCATGAGTT TGCCATCACA GAGCCATTAG TCACTTTCCA  1140
AGGAGAGACT GAAAACAGAG AAAAAGTTGC CGCCTCACCA AAAAGTCCCA CTGCTGCACT  1200
CAATGGAAGC CTGGTGGAAT GTCCCAAGTG CAATATACAG TATCCAGCCA CTGAGCATCG  1260
CGATCTGCTT GTCCATGTGG AATACTGTTC AAAGTAGCAA AATAAGTATT TGTTTTGATA  1320
TTAAAAGATT CAATACTGTA TTTTCTGTTA GCTTGTGGGC ATTTTGAATT ATATATTTCA  1380
CATTTTGCAT AAAACTGCCT ATCTACCTTT GACACTCCAG CATGCTAGTG AATCATGTAT  1440
CTTTTAGGCT GCTGTGCATT TCTCTTGGCA GTGATACCTC CCTGACATGG TTCATCATCA  1500
GGCTGCAATG ACAGAATGTG GTGAGCAGCG TCTACTGAGA TACTAACATT TTGCACTGTC  1560
AAAATACTTG GTGAGGAAAA GATAGCTCAG GTTATTGCTA ATGGGTTAAT GCACCAGCAA  1620
GCAAAATATT TTATGTTTCG GGGGTTTTGA AAAATCAAAG ATAATTAACC AAGGATCTTA  1680
ACTGTGTTCG CATTTTTTAT CCAAGCACTT AGAAAACCTA CAATCCTAAT TTTGATGTCC  1740
ATTGTTAAGA GGTGGTGATA GATACTATTT TTTTTCATA TTGTATAGCG GTTATTAGAA  1800
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AAGTTGGGGA TTTTCTTGAT CTTTATTGCT GCTTACCATT GAAACTTAAC CCAGCTGTGT  1860
TCCCCAACTC TGTTCTGCGC ACGAAACAGT ATCTGTTTGA GGCATAATCT TAAGTGGCCA  1920
CACACAATGT TTTCTCTTAT GTTATCTGGC AGTAACTGTA ACTTGAATTA CATTAGCACA  1980
TTCTGCTTAG CTAAAATTGT TAAAATAAAC TTTAATAAAC CCATGTAGCC CTCTCATTTG  2040
ATTGACAGTA TTTTAGTTAT TTTTGGCATT CTTAAAGCTG GGCAATGTAA TGATCAGATC  2100
TTTGTTTGTC TGAACAGGTA TTTTTATACA TGCTTTTTGT AAACCAAAAA CTTTTAAATT  2160
TCTTCAGGTT TTCTAACATG CTTACCACTG GGCTACTGTA AATGAGAAAA GAATAAAATT  2220
ATTTAATGTT TT
```

Seq ID NO: 144 Protein sequence:
Protein Accession #: NP_060601

```
1          11         21         31         41         51
|          |          |          |          |          |
MEIQLKDALE KNQQWLVYDQ QREVYVKGLL AKIFELEKKT ETAAHSLPQQ TKKPESEGYL   60
QEEKQKCYND LLASAKKDLE VERQTITQLS FELSEFRRKY EETQKEVHNL NQLLYSQRRA  120
DVQHLEDDRH KTEKIQKLRE ENDIARGKLE EEKKRSEELL SQVQSLYTSL LKQQEEQTRV  180
ALLEQQMQAC TLDFENEKLD RQHVQHQLHV ILKELRKARK NNTVGILETA S
```

Seq ID NO: 145 DNA sequence
Nucleic Acid Accession #: NM_001168
Coding sequence: 50..478

```
1          11         21         31         41         51
|          |          |          |          |          |
CCGCCAGATT TGAATCGCGG GACCCGTTGG CAGAGGTGGC GGCGGCGGCA TGGGTGCCCC    60
GACGTTGCCC CCTGCCTGGC AGCCCTTTCT CAAGGACCAC CGCATCTCTA CATTCAAGAA   120
CTGGCCCTTC TTGGAGGGCT GCGCCTGCAC CCCGGAGCGG ATGGCCGAGG CTGGCTTCAT   180
CCACTGCCCC ACTGAGAACG AGCCAGACTT GGCCCAGTGT TTCTTCTGCT TCAAGGAGCT   240
GGAAGGCTGG GAGCCAGATG ACGACCCCAT AGAGGAACAT AAAAAGCATT CGTCCGGTTG   300
CGCTTTCCTT TCTGTCAAGA AGCAGTTTGA AGAATTAACC CTTGGTGAAT TTTTGAAACT   360
GGACAGAGAA AGAGCCAAGA ACAAAATTGC AAAGGAAACC AACAATAAGA AGAAAGAATT   420
TGAGGAAACT GCGAAGAAAG TGCGCCGTGC CATCGAGCAG CTGGCTGCCA TGGATTGAGG   480
CCTCTGGCCG GAGCTGCCTG GTCCCAGAGT GGCTGCACCA CTTCCAGGGT TTATTCCCTG   540
GTGCCACCAG CCTTCCTGTG GGCCCCTTAG CAATGTCTTA GGAAAGGAGA TCAACATTTT   600
CAAATTAGAT GTTTCAACTG TGCTCCTGTT TTGTCTTGAA AGTGGCACCA GAGGTGCTTC   660
TGCCTGTGCA GCGGGTGCTG CTGGTAACAG TGGCTGCTTC TCTCTCTCTC TCTCTTTTTT   720
GGGGGCTCAT TTTTGCTGTT TTGATTCCCG GGCTTACCAG GTGAGAAGTG AGGGAGGAAG   780
AAGGCAGTGT CCCTTTTGCT AGAGCTGACA GCTTTGTTCG CGTGGGCAGA GCCTTCCACA   840
GTGAATGTGT CTGGACCTCA TGTTGTTGAG GCTGTCACAG TCCTGAGTGT GGACTTGGCA   900
GGTGCCTGTT GAATCTGAGC TGCAGGTTCC TTATCTGTCA CACCTGTGCC TCCTCAGAGG   960
ACAGTTTTTT TGTTGTTGTG TTTTTTTGTT TTTTTTTTTT GGTAGATGCA TGACTTGTGT  1020
GTGATGAGAG AATGGAGACA GAGTCCCTGG CTCCTCTACT GTTTAACAAC ATGGCTTTCT  1080
TATTTTGTTT GAATTGTTAA TTCACAGAAT AGCACAAACT ACAATTAAAA CTAAGCACAA  1140
AGCCATTCTA AGTCATTGGG GAAACGGGGT GAACTTCAGG TGGATGAGGA GACAGAATAG  1200
AGTGATAGGA AGCGTCTGGC AGATACTCCT TTTGCCACTG CTGTGTGATT AGACAGGCCC  1260
AGTGAGCCGC GGGGCACATG CTGGCCGCTC CTCCCTCAGA AAAAGGCAGT GGCCTAAATC  1320
CTTTTTAAAT GACTTGGCTC GATGCTGTGG GGGACTGGCT GGGCTGCTGC AGGCCGTGTG  1380
TCTGTCAGCC CAACCTTCAC ATCTGTCACG TTCTCCACAC GGGGGAGAGA CGCAGTCCGC  1440
CCAGGTCCCC GCTTTCTTTG GAGGCAGCAG CTCCCGCAGG GCTGAAGTCT GGCGTAAGAT  1500
GATGGATTTG ATTCGCCCTC CTCCCTGTCA TAGAGCTGCA GGGTGGATTG TTACAGCTTC  1560
GCTGGAAACC TCTGGAGGTC ATCTCGGCTG TTCCTGAGAA ATAAAAAGCC TGTCATTTC
```

Seq ID NO: 146 Protein sequence:
Protein Accession #: NP_001159

```
1          11         21         31         41         51
|          |          |          |          |          |
MGAPTLPPAW QPFLKDHRIS TFKNWPFLEG CACTPERMAE AGFIHCPTEN EPDLAQCFFC   60
FKELEGWEPD DDPIEEHKKH SSGCAFLSVK KQFEELTLGE FLKLDRERAK NKIAKETNNK  120
KKEFEETAKK VRRAIEQLAA MD
```

Seq ID NO: 147 DNA sequence
Nucleic Acid Accession #: NM_014176.1
Coding sequence: 127-720

```
1          11         21         31         41         51
|          |          |          |          |          |
GCGCGCAGCG CTGGTACCCC GTTGGTCCGC GCGTTGCTGC GTTGTGAGGG GTGTCAGCTC   60
AGTGCATCCC AGGCAGCTCT TAGTGTGGAG CAGTGAACTG TGTGTGGTTC CTTCTACTTG  120
GGGATCATGC AGAGAGCTTC ACGTCTGAAG AGAGAGCTGC ACATGTTAGC CACAGAGCCA  180
CCCCCAGGCA TCACATGTTG GCAAGATAAA GACCAAATGG ATGACCTGCG AGCTCAAATA  240
TTAGGTGGAG CCAACACACC TTATGAGAAA GGTGTTTTTA AGCTAGAAGT TATCATTCCT  300
GAGAGGTACC CATTTGAACC TCCTCAGATC CGATTTCTCA CTCCAATTTA TCATCCAAAC  360
ATTGATTCTG CTGGAAGGAT TTGTCTGGAT GTTCTCAAAT TGCCACCAAA AGGTGCTTGG  420
AGACCATCCC TCAACATCGC AACTGTGTTG ACCTCTATTC AGCTGCTCAT GTCAGAACCC  480
AACCCTGATG ACCCGCTCAT GGCTGACATA TCCTCAGAAT TTAAATATAA TAAGCCAGCC  540
TTCCTCAAGA ATGCCAGACA GTGGACAGAG AAGCATGCAA GACAGAAACA AAAGGCTGAT  600
GAGGAAGAGA TGCTTGATAA TCTACCAGAG GCTGGTGACT CCAGAGTACA CAACTCAACA  660
CAGAAAAGGA AGGCCAGTCA GCTAGTAGGC ATAGAAAAGA AATTTCATCC TGATGTTTAG  720
GGGACTTGTC CTGGTTCATC TTAGTTAATG TGTTCTTTGC CAAGGTGATC TAAGTTGCCT  780
ACCTTGAATT TTTTTTTAAA TATATTTGAT GACATAATTT TTGTGTAGTT TATTTATCTT  840
GTACATATGT ATTTTGAAAT CTTTTAAACC TGAAAAATAA ATAGTCATTT AATGTTGAAA  900
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AAAAAAAAAA AAAAAAAAAA AAAAAAAA

Seq ID NO: 148 Protein sequence:
Protein Accession #: NP_054895.1

1          11         21         31         41         51
|          |          |          |          |          |
MQRASRLKRE LHMLATEPPP GITCWQDKDQ MDDLRAQILG GANTPYEKGV FKLEVIIPER    60
YPFEPPQIRF LTPIYHPNID SAGRICLDVL KLPPKGAWRP SLNIATVLTS IQLLMSEPNP   120
DDPLMADISS EFKYNKPAFL KNARQWTEKH ARQKQKADEE EMLDNLPEAG DSRVHNSTQK   180
RKASQLVGIE KKFHPDV

Seq ID NO: 149 DNA sequence
Nucleic Acid Accession #: NM_003812
Coding sequence: 224-2722

1          11         21         31         41         51
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TCCTCTGCGT CCCGCCCCGG GAGTGGCTGC GAGGCTAGGC GAGCCGGGAA AGGGGGCGCC    60
GCCCAGCCCC GAGCCCCGCG CCCCGTGCCC CGAGCCCGGA GCCCCCTGCC CGCGGCGGCA   120
CCATGCGCGC CGAGCCGGCG TGACCGGCTC CGCCCGCGGC CGCCCCGCAG CTAGCCCGGC   180
GCTCTCGCCG GCCACACGGA GCGGCGCCCG GGAGCTATGA GCCATGAAGC CGCCCGGCAG   240
CAGCTCGCGG CAGCCGCCCC TGGCGGGCTG CAGCCTTGCC GGCGCTTCCT GCGGCCCCCA   300
ACGCGGCCCC GCCGGCTCGG TGCCTGCCAG CGCCCCGGCC CGCACGCCGC CCTGCCGCCT   360
GCTTCTCGTC CTTCTCCTGC TGCCTCCGCT CGCCGCCTCG TCCCGGCCCC GCGCCTGGGG   420
GGCTGCTGCG CCCAGCGCTC CGCATTGGAA TGAAACTGCA GAAAAAAATT TGGGAGTCCT   480
GGCAGATGAA GACAATACAT TGCAACAGAA TAGCAGCAGT AATATCAGTT ACAGCAATGC   540
AATGCAGAAA GAAATCACAC TGCCTTCAAG ACTCATATAT TACATCAACC AAGACTCGGA   600
AAGCCCTTAT CACGTTCTTG ACACAAAGGC AAGACACCAG CAAAAACATA ATAAGGCTGT   660
CCATCTGGCC CAGGCAAGCT TCCAGATTGA AGCCTTCGGC TCCAAATTCA TTCTTGACCT   720
CATACTGAAC AATGGTTTGT TGTCTTCTGA TTATGTGGAG ATTCACTACG AAAATGGGAA   780
ACCACAGTAC TCTAAGGGTG GAGAGCACTG TTACTACCAT GGAAGCATCA GAGGCGTCAA   840
AGACTCCAAG GTGGCTCTGT CAACCTGCAA TGGACTTCAT GGCATGTTTG AAGATGATAC   900
CTTCGTGTAT ATGATAGAGC CACTAGAGCT GGTTCATGAT GAGAAAAGCA CAGGTCGACC   960
ACATATAATC CAGAAAACCT TGGCAGGACA GTATTCTAAG CAAATGAAGA ATCTCACTAT  1020
GGAAAGAGGT GACCAGTGGC CCTTTCTCTC TGAATTACAG TGGTTGAAAA GAAGGAAGAG  1080
AGCAGTGAAT CCATCACGTG GTATATTTGA AGAAATGAAA TATTTGGAAC TTATGATTGT  1140
TAATGATCAC AAAACGTATA AGAAGCATCG CTCTTCTCAT GCACATACCA ACAACTTTGC  1200
AAAGTCCGTG GTCAACCTTG TGGATTCTAT TTACAAGGAG CAGCTCAACA CCAGGGTTGT  1260
CCTGGTGGCT GTAGAGACCT GGACTGAGAA GGATCAGATT GACATCACCA CCAACCCTGT  1320
GCAGATGCTC CATGAGTTCT CAAAATACCG GCAGCGCATT AAGCAGCATG CTGATGCTGT  1380
GCACCTCATC TCGCGGGTGA CATTTCACTA TAAGAGAAGC AGTCTGAGTT ACTTTGGAGG  1440
TGTCTGTTCT CGCACAAGAG GAGTTGGTGT GAATGAGTAT GGTCTTCCAA TGGCAGTGGC  1500
ACAAGTATTA TCGCAGAGCC TGGCTCAAAA CCTTGGAATC CAATGGGAAC CTTCTAGCAG  1560
AAAGCCAAAA TGTGACTGCA CAGAATCCTG GGGTGGCTGC ATCATGGAGG AAACAGGGGT  1620
GTCCCATTCT CGAAAATTTT CAAAGTGCAG CATTTTGGAG TATAGAGACT TTTTACAGAG  1680
AGGAGGTGGA GCCTGCCTTT TCAACAGGCC AACAAAGCTA TTTGAGCCCA CGGAATGTGG  1740
AAATGGATAC GTGGAAGCTG GGGAGGAGTG TGATTGTGGT TTTCATGTGG AATGCTATGG  1800
ATTATGCTGT AAGAAATGTT CCCTCTCCAA CGGGGCTCAC TGCAGCGACG GGCCCTGCTG  1860
TAACAATACC TCATGTCTTT TTCAGCCACG AGGGTATGAA TGCCGGGATG CTGTGAACGA  1920
GTGTGATATT ACTGAATATT GTACTGGAGA CTCTGGTCAG TGCCCACCAA ATCTTCATAA  1980
GCAAGACGGA TATGCATGCA ATCAAAATCA GGGCCGCTGC TACAATGGCG AGTGCAAGAC  2040
CAGAGACAAC CAGTGTCAGT ACATCTGGGG AACAAAGGCT GCAGGGTCTG ACAAGTTCTG  2100
CTATGAAAAG CTGAATACAG AAGGCACTGA GAAGGGAAAC TGCGGGAAGG ATGGAGACCG  2160
GTGGATTCAG TGCAGCAAAC ATGATGTGTT CTGTGGATTC TTACTCTGTA CCAATCTTAC  2220
TCGAGCTCCA CGTATTGGTC AACTTCAGGG TGAGATCATT CCAACTTCCT TCTACCATCA  2280
AGGCCGGGTG ATTGACTGCA GTGGTGCCCA TGTAGTTTTA GATGATGATA CGGATGTGGG  2340
CTATGTAGAA GATGGAACGC CATGTGGCCC GTCTATGATG TGTTTAGATC GGAAGTGCCT  2400
ACAAATTCAA GCCCTAAATA TGAGCAGCTG TCCACTCGAT TCCAAGGGTA AAGTCTGTTC  2460
GGGCCATGGG GTGTGTAGTA ATGAAGCCAC CTGCATTTGT GATTTCACCT GGGCAGGGAC  2520
AGATTGCAGT ATCCGGGATC CAGTTAGGAA CCTTCACCCC CCCAAGGATG AAGGACCCAA  2580
GGGTCCTAGT GCCACCAATC TCATAATAGG CTCCATCGCT GGTGCCATCC TGGTAGCAGC  2640
TATTGTCCTT GGGGGCACAG GCTGGGGATT TAAAAATGTC AAGAAGAGAA GGTTCGATCC  2700
TACTCAGCAA GGCCCCATCT GAATCAGCTG CGCTGGATGG ACACCGCCTT GCACTGTTGG  2760
ATTCTGGGTA TGACATACTC GCAGCAGTGT TACTGGAACT ATTAAGTTTG TAAACAAAAC  2820
CTTTGGGTGG TAATGACTAC GGAGCTAAAG TTGGGGTGAC AAGGATGGGG TAAAAGAAAA  2880
CTGTCTCTTT TGGAAATAAT GTCAAAGAAC ACCTTTCACC ACCTGTCAGT AAACGGGGGA  2940
GGGGGCAAAA GACCATGCTA TAAAAAGAAC TGTTCCAGAA TCTTTTTTTT TCCCTAATGG  3000
ACGAAGGAAC AACACACACA CAAAAATTAA ATGCAATAAA GGAATCATTA AAAA

Seq ID NO: 150 Protein sequence:
Protein Accession #: NP_003803

1          11         21         31         41         51
|          |          |          |          |          |
MKPPGSSSRQ PPLAGCSLAG ASCGPQRGPA GSVPASAPAR TPPCRLLLVL LLLPPLAASS    60
RPRAWGAAAP SAPHWNETAE KNLGVLADED NTLQQNSSSN ISYSNAMQKE ITLPSRLIYY   120
INQDSESPYH VLDTKARHQQ KHNKAVHLAQ ASFQIEAFGS KFILDLILNN GLLSSDYVEI   180
HYENGKPQYS KGGEHCYYHG SIRGVKDSKV ALSTCNGLHG MFEDDTFVYM IEPLELVHDE   240
KSTGRPHIIQ KTLAGQYSKQ MKNLTMERGD QWPFLSELQW LKRRKRAVNP SRGIFEEMKY   300
LELMIVNDHK TYKKHRSSHA HTNNFAKSVV NLVDSIYKEQ LNTRVVLVAV ETWTEKDQID   360
ITTNPVQMLH EFSKYRQRIK QHADAVHLIS RVTFHYKRSS LSYFGGVCSR TRGVGVNEYG   420
LPMAVAQVLS QSLAQNLGIQ WEPSSRKPKC DCTESWGGCI MEETGVSHSR KFSKCSILEY   480
RDFLQRGGGA CLFNRPTKLF EPTECGNGYV EAGEECDCGF HVECYGLCCK KCSLSNGAHC   540
SDGPCCNNTS CLFQPRGYEC RDAVNECDIT EYCTGDSGQC PPNLHKQDGY ACNQNQGRCY   600
NGECKTRDNQ CQYIWGTKAA GSDKFCYEKL NTEGTEKGNC GKDGDRWIQC SKHDVFCGFL   660
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LCTNLTRAPR IGQLQGEIIP TSFYHQGRVI DCSGAHVVLD DDTDVGYVED GTPCGPSMMC   720
LDRKCLQIQA LNMSSCPLDS KGKVCSGHGV CSNEATCICD FTWAGTDCSI RDPVRNLHPP   780
KDEGPKGPSA TNLIIGSIAG AILVAAIVLG GTGWGFKNVK KRRFDPTQQG PI
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Seq ID NO: 151 DNA sequence
Nucleic Acid Accession #: NM_023915
Coding sequence: 250-1326

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1          11         21         31         41         51
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GGCACGAGGG TTTCGTTTTC ATGCTTTACC AGAAAATCCA CTTCCCTGCC GACCTTAGTT     60
TCAAAGCTTA TTCTTAATTA GAGACAAGAA ACCTGTTTCA ACTTGAAGAC ACCGTATGAG    120
GTGAATGGAC AGCCAGCCAC CACAATGAAA GAAATCAAAC CAGGAATAAC CTATGCTGAA    180
CCCACGCCTC AATCGTCCCC AAGTGTTTCC TGACACGCAT CTTTGCTTAC AGTGCATCAC    240
AACTGAAGAA TGGGGTTCAA CTTGACGCTT GCAAAATTAC CAAATAACGA GCTGCACGGC    300
CAAGAGAGTC ACAATTCAGG CAACAGGAGC GACGGGCCAG GAAAGAACAC CACCCTTCAC    360
AATGAATTTG ACACAATTGT CTTGCCGGTG CTTTATCTCA TTATATTTGT GGCAAGCATC    420
TTGCTGAATG GTTTAGCAGT GTGGATCTTC TTCCACATTA GGAATAAAAC CAGCTTCATA    480
TTCTATCTCA AAAACATAGT GGTTGCAGAC CTCATAATGA CGCTGACATT TCCATTTCGA    540
ATAGTCCATG ATGCAGGATT TGGACCTTGG TACTTCAAGT TTATTCTCTG CAGATACACT    600
TCAGTTTTGT TTTATGCAAA CATGTATACT TCCATCGTGT TCCTTGGGCT GATAAGCATT    660
GATCGCTATC TGAAGGTGGT CAAGCCATTT GGGGACTCTC GGATGTACAG CATAACCTTC    720
ACGAAGGTTT TATCTGTTTG TGTTTGGGTG ATCATGGCTG TTTTGTCTTT GCCAAACATC    780
ATCCTGACAA ATGGTCAGCC AACAGAGGAC AATATCCATG ACTGCTCAAA ACTTAAAAGT    840
CCTTTGGGGG TCAAATGGCA TACGGCAGTC ACCTATGTGA ACAGCTGCTT GTTTGTGGCC    900
GTGCTGGTGA TTCTGATCGG ATGTTACATA GCCATATCCA GGTACATCCA CAAATCCAGC    960
AGGCAATTCA TAAGTCAGTC AAGCCGAAAG CGAAAACATA ACCAGAGCAT CAGGGTTGTT   1020
GTGGCTGTGT TTTTTACCTG CTTTCTACCA TATCACTTGT GCAGAATTCC TTTTACTTTT   1080
AGTCACTTAG ACAGGCTTTT AGATGAATCT GCACAAAAAA TCCTATATTA CTGCAAAGAA   1140
ATTACACTTT TCTTGTCTGC GTGTAATGTT TGCCTGGATC CAATAATTTA CTTTTTCATG   1200
TGTAGGTCAT TTTCAAGAAG GCTGTTCAAA AAATCAAATA TCAGAACCAG GAGTGAAAGC   1260
ATCAGATCAC TGCAAAGTGT GAGAAGATCG GAAGTTCGCA TATATTATGA TTACACTGAT   1320
GTGTAGGCCT TTTATTGTTT GTTGGAATCG ATATGTACAA AGTGTAAATA AATGTTTCTT   1380
TTCATTATCC TTAAAAAAAA AA
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Seq ID NO: 152 Protein sequence:
Protein Accession #: NP_076404

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1          11         21         31         41         51
|          |          |          |          |          |
MGFNLTLAKL PNNELHGQES HNSGNRSDGP GKNTTLHNEF DTIVLPVLYL IIFVASILLN     60
GLAVWIFFHI RNKTSFIFYL KNIVVADLIM TLTFPFRIVH DAGFGPWYFK FILCRYTSVL    120
FYANMYTSIV FLGLISIDRY LKVVKPFGDS RMYSITFTKV LSVCVWVIMA VLSLPNIILT    180
NGQPTEDNIH DCSKLKSPLG VKWHTAVTYV NSCLFVAVLV ILIGCYIAIS RYIHKSSRQF    240
ISQSSRKRKH NQSIRVVVAV FFTCFLPYHL CRIPFTFSHL DRLLDESAQK ILYYCKEITL    300
FLSACNVCLD PIIYFFMCRS FSRRLFKKSN IRTRSESIRS LQSVRRSEVR IYYDYTDV
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Seq ID NO: 153 DNA sequence
Nucleic Acid Accession #: D80008.1
Coding sequence: 149-739

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1          11         21         31         41         51
|          |          |          |          |          |
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CGAAAGGAGT GAGGCGCCGA GAGCCCAGAT ACCATTTTGG CGTGAGAGCT GGTGGTTGGC    120
AAGGCCGCGG GAGTGGGAAG CGTCCGCCAT GTTCTGCGAA AAAGCCATGG AACTGATCCG    180
CGAGCTGCAT CGCGCGCCCG AAGGGCAACT GCCTGCCTTC AACGAGGATG GACTCAGACA    240
AGTTCTGGAG GAGATGAAAG CTTTGTATGA ACAAAACCAG TCTGATGTGA ATGAAGCAAA    300
GTCAGGTGGA CGAAGTGATT TGATACCAAC TATCAAATTT CGACACTGTT CTCTGTTAAG    360
AAATCGACGC TGCACTGTAG CATACCTGTA TGACCGCTTG CTTCGGATCA GAGCACTCAG    420
ATGGGAATAT GGTAGCGTCT TGCCAAATGC ATTACGATTT CACATGGCTG CTGAAGAAAT    480
GGAGTGGTTT AATAATTATA AAAGATCTCT TGCTACTTAT ATGAGGTCAC TGGGAGGAGA    540
TGAAGGTTTG GACATTACAC AGGATATGAA ACCACCAAAA AGCCTATATA TTGAAGTCCG    600
GTGTCTAAAA GACTATGGAG AATTTGAAGT TGATGATGGC ACTTCAGTCC TATTAAAAAA    660
AAATAGCCAG CACTTTTTAC CTCGATGGAA ATGTGAGCAG CTGATCAGAC AAGGAGTCCT    720
GGAGCACATC CTGTCATGAC CATGCGCCGA GGCACTTCCA GGCTTCACTC AACTCATGGA    780
CTCCTCTGTA CTCACTCTCT CCACCACTCC CTTCACCTCC CTCTTTGATT TTAGAAGCTA    840
TAGACATTGT TTAAGATAAC TAAGAATACT TGGCTAAGAA GTATAATTTG CTAACTATTA    900
AGGACTTTCT TTTTTTAATG TTGTACACTA TTCTTCCTAC TCTTTTTTGG TTTTGGTTTT    960
GTTTTGTAGA GACTGTCTCA CTATGTTGCC CAAGCTGGTC TCAAACTCCT GGCCTCAAGC   1020
AGTCCTCCCA CCTTAGCTTC TCAAAGTGTT GAGATCACAG GCGTGAGCCA CTGCACCCGG   1080
CCCCTACTCC TTTTTCTAAT AAGCTGTATC TGTAATCACA GCATTCCTAC AGTTGTTACA   1140
GTGTGTTTTT TAAATGAAAG TAAACATGGT TACATTTGAA TCTCTTAAAT AAGCAGTCAC   1200
TTGGCTGGAC AGGAAGAAGG TAGATCCTGT GTGTCTTGTT TTCTGGTCAT GTGTATTGTA   1260
CAAGCTAGAG AGCTGAATTT CTGAGATACA CATTTTCAAA TCACATGCAA GTGAAGATGA   1320
TGGTCTGTAG AAATTTTCAG TATATATAAT GTTTAATGAC ATACTAATTT ATCATCTGGC   1380
TATTTGGGAA GGAAGGACAC ACATGGATTT TGCACATTTC CACCATGGTG GCTGGTGTGG   1440
CTTGTGGCTA TGGGGTGATC ACCAGTATCA CCACTTTGGA AGGGGACAGT GAAATTGGGG   1500
CTAGAGAAGG AACTTTGTAC AGTTTTCCCT GAGATTCAGA TTGACTGAAA AGTCACATGA   1560
AGAGTTGATT GTCTTTTAAT GGTATGTTTT AAACAGCTGA CATTTTAAAT TTTGATGAAA   1620
TCCAGTTTAT TCGTTTGTTC TTTTATGCTT TGGGTGTTGC ATCCGAGAAA TCTTTTCCCA   1680
TCCCAAGATC ACAATTTTTT TTCCTTTTTA CTTCTAGAAG TGTTATAATT TTAAGCTTTA   1740
TACTTTGGTC TATGACCCGT TTTTTTTTTT GTTTTGTTTT GTTTTTTCGT TTGTTTCTTT   1800
GTTTTGAGAT GGAGTCTTGT TCTGTCACCC AGGCTGGGGT GCAGTGGCGT GATCTTGGCT   1860
CACTGCAATC TCTATCCCCT GGGTTCAAGT GATTCTCTTG TCTCAGCCTC CCAAGTAGCT   1920
GGGATTACAG GCACAGGCCG CCACGCCTGG CTAATTTTTG TATTTTTAGT AGAGACAGAG   1980
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TTTTACCATG TTGGCCAGGC TGGTTTCAAA CTCCTGACCT CAAGTGACCC ACCTTGGCCT 2040
CCCAAAGTTT TGGGATTACA AGTGTGGGCC ACCGCGGCCA GCCTATGATC CATTTTGAAT 2100
GAATTTTTTA TATGGTGCAA GGTGTCAATC CACCTTCACT TTTTCTTGGG AATATAGATA 2160
TCCAGCTGTT TCACTACCAT TTTTTGAAAG GACTGCCCTT TGCTCTATCA CCTTTGCATT 2220
TTTGTTAAAA AGTAGTTGTC AATGTATATG TGGGTTTATT TCAGGACTCT GTTTTGTTCC 2280
ATTGACCTGT TTTTCTCTCC TGAATGCCAA TACCATATTT GTATGTAGTG TATGTAATTT 2340
TCTAATAATT CTTGAAACAG ATAGTATTAA TGTGTCATAT TTTTGCTGTT GTTTGTATTT 2400
TTTGTAGAGA TGGGGTTTCA CCGTGTTGGC CAGGCTGTGT TGAACTCCTG AGCTAAAGCA 2460
ATACACTTGC CTCGTCCTCC CCATGTGCTG GGATTACAGG CGTGAGCCTT GGTGCTGGCC 2520
CAGTGTACCA CATTTCTTTT TGAGATTTGT TTTGGCTATG TTAAGTCCTT TGCTTTTGAT 2580
GTGAAATTTG GGAACAGGCA GGGTGTGGTG GCTTATGCCT GTAATCCTAG AACTTTGGGA 2640
GGCCTAGATG GGTGGATCAC TTGAGCTCAG GAGTTCCAGA CCAGCCCGGG CCTATGGCAA 2700
AACTCCGTCT CTACAAAAAA TAGAAAAAAT TAGCCAGGTG TGGTGGTGCA TGCCTGTAGT 2760
CACAGTTACA CGGCAGGCTG AGGTGGGAGG ATCACTTGAA CCCCAGAGGT CAAGACTGCA 2820
GTGAGCTGAG ATCACACCAC TGTACTCCAG CCTGGGTGAC AAAGTGAGAC TCTATCTCAA 2880
AAAGAAATTA GGATCAATTT GTCAATTTCT ACAACAACAA CAACAAAAAC CCCTGTTGGG 2940
CACCTTGATT GAGATTGCAT TGAATTTATA TAAAACTGTT GGGAGAATTG ACATCTTAAT 3000
AATATTGAGT CTTCTGGCCT ATAAACAAGG TCTGTCTTCC TAGGTATTAA TGTTTTGTCT 3060
TCTATTTCTC TTAATAATCT TTTGTAGTTT TCAGTGTACA GGTCTACCAT GTCAGCATTT 3120
CATAGTTTTG ATGCTAAATG GTATTTTAAA ATTTCAAATT CTAACCACTT GTTGCTAGTA 3180
AATAGAAATA CAATTGATGT TGAACTTGTA TCCTTCAGCC TTGCTAAACT GTGAGTTCTC 3240
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TTC

Seq ID NO: 154 Protein sequence:
Protein Accession #: BAA11503.1

1 11 21 31 41 51
| | | | | |
MFCEKAMELI RELHRAPEGQ LPAFNEDGLR QVLEEMKALY EQNQSDVNEA KSGGRSDLIP 60
TIKFRHCSLL RNRRCTVAYL YDRLLRIRAL RWEYGSVLPN ALRFHMAAEE MEWFNNYKRS 120
LATYMRSLGG DEGLDITQDM KPPKSLYIEV RCLKDYGEFE VDDGTSVLLK KNSQHFLPRW 180
KCEQLIRQGV LEHILS

Seq ID NO: 155 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 149-709

1 11 21 31 41 51
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AAGGCCGCGG GAGTGGGAAG CGTCCGCCAT GTTCTGCGAA AAAGCCATGG AACTGATCCG 180
CGAGCTGCAT CGCGCGCCCG AAGGGCAACT GCCTGCCTTC AACGAGGATG GACTCAGACA 240
AGTTCTGGAG GAGATGAAAG CTTTGTATGA ACAAAACCAG TCTGATGTGA ATGAAGCAAA 300
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AAATCGACGC TGCACTGTAG CATACCTGTA TGACCGCTTG CTTCGGATCA GAGCACTCAG 420
ATGGGAATAT GGTAGCGTCT TGCCAAATGC ATTACGATTT CACATGGCTG CTGAAGAAAT 480
GGAGTGGTTT AATAATTATA AAAGATCTCT TGCTACTTAT ATGAGGTCAC TGGGAGGAGA 540
TGAAGGTTTG GACATTACAC AGGATATGAA ACCACCAAAA AGCCTATATA TTGAAGCTGG 600
ATGCAGTGGC GCGATCTCGG CTCAACCTGC AACCTCCACC TCCCAGGTTC ACCTCAACTG 660
CAACCTCCAC CTCCCAGGTC CGGTGTCTAA AAGACTATGG AGAATTTGAA GTTGATGATG 720
GCACTTCAGT CCTATTAAAA AAAAATAGCC AGCACTTTTT ACCTCGATGG AAATGTGAGC 780
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CAGGCTTCAC TCAACTCATG GACTCCTCTG TACTCACTCT CTCCACCACT CCCTTCACCT 900
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TCCACCATGG TGGCTGGTGT GGCTTGTGGC TATGGGGTGA TCACCAGTAT CACCACTTTG 1560
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GCATCCGAGA AATCTTTTCC CATCCCAAGA TCACAATTTT TTTTCCTTTT TACTTCTAGA 1800
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TGTCTCAGCC TCCCAAGTAG CTGGGATTAC AGGCACAGGC CGCCACGCCT GGCTAATTTT 2040
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TTGTATGTAG TGTATGTAAT TTTCTAATAA TTCTTGAAAC AGATAGTATT AATGTGTCAT 2460
ATTTTTGCTG TTGTTTGTAT TTTTTGTAGA GATGGGGTTT CACCGTGTTG GCCAGGCTGT 2520
GTTGAACTCC TGAGCTAAAG CAATACACTT GCCTCGTCCT CCCCATGTGC TGGGATTACA 2580
GGCGTGAGCC TTGGTGCTGG CCCAGTGTAC CACATTTCTT TTTGAGATTT GTTTTGGCTA 2640
TGTTAAGTCC TTTGCTTTTG ATGTGAAATT TGGGAACAGG CAGGGTGTGG TGGCTTATGC 2700
CTGTAATCCT AGAACTTTGG GAGGCCTAGA TGGGTGGATC ACTTGAGCTC AGGAGTTCCA 2760
GACCAGCCCG GGCCTATGGC AAAACTCCGT CTCTACAAAA AATAGAAAAA ATTAGCCAGG 2820

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TGTGGTGGTG CATGCCTGTA GTCACAGTTA CACGGCAGGC TGAGGTGGGA GGATCACTTG  2880
AACCCCAGAG GTCAAGACTG CAGTGAGCTG AGATCACACC ACTGTACTCC AGCCTGGGTG  2940
ACAAAGTGAG ACTCTATCTC AAAAAGAAAT TAGGATCAAT TTGTCAATTT CTACAACAAC  3000
AACAACAAAA ACCCCTGTTG GGCACCTTGA TTGAGATTGC ATTGAATTTA TATAAAACTG  3060
TTGGGAGAAT TGACATCTTA ATAATATTGA GTCTTCTGGC CTATAAACAA GGTCTGTCTT  3120
CCTAGGTATT AATGTTTTGT CTTCTATTTC TCTTAATAAT CTTTTGTAGT TTTCAGTGTA  3180
CAGGTCTACC ATGTCAGCAT TTCATAGTTT TGATGCTAAA TGGTATTTTA AAATTTCAAA  3240
TTCTAACCAC TTGTTGCTAG TAAATAGAAA TACAATTGAT GTTGAACTTG TATCCTTCAG  3300
CCTTGCTAAA CTGTGAGTTC TCATGGTGTT TTTGTAAATT ACATCAACAG TCATGTGTTC  3360
TATGAATAAA GAGTTTTACT CCTTC
```

Seq ID NO: 156 Protein sequence:
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MPCEKAMELI RELHRAPEGQ LPAFNEDGLR QVLEEMKALY EQNQSDVNEA KSGGRSDLIP    60
TIKFRHCSLL RNRRCTVAYL YDRLLRIRAL RWEYGSVLPN ALRFHMAAEE MEWFNNYKRS   120
LATYMRSLGG DEGLDITQDM KPPKSLYIEA GCSGAISAQP ATSTSQVHLN CNLHLPGPVS   180
KRLWRI
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Seq ID NO: 157 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 148-621

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1          11         21         31         41         51
|          |          |          |          |          |
TTCGGCGCCA AAGCGCGGAG CGGAGGCCGA GGCGAGAGCC TGGCGCTGTA GGACTAGAAC    60
GAAAGGAGTG AGGCGCCGAG AGCCCAGATA CCATTTTGGC GTGAGAGCTG GTGGTTGGCA   120
AGGCCGCGGG AGTGGGAAGC GTCCGCCATG TTCTGCGAAA AAGCCATGGA ACTGATCCGC   180
GAGCTGCATC GCGCGCCCGA AGGGCAACTG CCTGCCTTCA ACGAGGATGG ACTCAGACAA   240
GTTCTGGAGG AGATGAAAGC TTTGTATGAA CAAAACCAGT CTGATGTGAA TGAAGCAAAG   300
TCAGGTGGAC GAAGTGATTT GATACCAACT ATCAAATTTC GACACTGTTC TCTGTTAAGA   360
AATCGACGCT GCACTGTAGC ATACCTGTAT GACCGCTTGC TTCGGATCAG AGCACTCAGA   420
TGGGAATATG GTAGCGTCTT GCCAAATGCA TTACGATTTC ACATGGCTGC TGAAGAAGTC   480
CGGTGTCTAA AAGACTATGG AGAATTTGAA GTTGATGATG GCACTTCAGT CCTATTAAAA   540
AAAAATAGCC AGCACTTTTT ACCTCGATGG AAATGTGAGC AGCTGATCAG ACAAGGAGTC   600
CTGGAGCACA TCCTGTCATG ACCATGCGCC GAGGCACTTC CAGGCTTCAC TCAACTCATG   660
GACTCCTCTG TACTCACTCT CTCCACCACT CCCTTCACCT CCCTCTTTGA TTTTAGAAGC   720
TATAGACATT GTTTAAGATA ACTAAGAATA CTTGGCTAAG AAGTATAATT TGCTAACTAT   780
TAAGGACTTT CTTTTTTTAA TGTTGTACAC TATTCTTCCT ACTCTTTTTT GGTTTTGGTT   840
TTGTTTTGTA GAGACTGTCT CACTATGTTG CCCAAGCTGG TCTCAAACTC CTGGCCTCAA   900
GCAGTCCTCC CACCTTAGCT TCTCAAAGTG TTGAGATCAC AGGCGTGAGC CACTGCACCC   960
GGCCCCTACT CCTTTTTCTA ATAAGCTGTA TCTGTAATCA CAGCATTCCT ACAGTTGTTA  1020
CAGTGTGTTT TTTAAATGAA AGTAAACATG GTTACATTTG AATCTCTTAA ATAAGCAGTC  1080
ACTTGGCTGG ACAGGAAGAA GGTAGATCCT GTGTGTCTTG TTTTCTGGTC ATGTGTATTG  1140
TACAAGCTAG AGAGCTGAAT TTCTGAGATA CACATTTTCA AATCACATGC AAGTGAAGAT  1200
GATGGTCTGT AGAAATTTTC AGTATATATA ATGTTTAATG ACATACTAAT TTATCATCTG  1260
GCTATTTGGG AAGGAAGGAC ACACATGGAT TTTGCACATT TCCACCATGG TGGCTGGTGT  1320
GGCTTGTGGC TATGGGGTGA TCACCAGTAT CACCACTTTG GAAGGGGACA GTGAAATTGG  1380
GGCTAGAGAA GGAACTTTGT ACAGTTTTCC CTGAGATTCA GATTGACTGA AAAGTCACAT  1440
GAAGAGTTGA TTGTCTTTTA ATGGTATGTT TTAAACAGCT GACATTTTAA ATTTTGATGA  1500
AATCCAGTTT ATTCGTTTGT TCTTTTATGC TTTGGGTGTT GCATCCGAGA AATCTTTTCC  1560
CATCCCAAGA TCACAATTTT TTTTCCTTTT TACTTCTAGA AGTGTTATAA TTTTAAGCTT  1620
TATACTTTGG TCTATGACCC GTTTTTTTTT TTGTTTTGTT TTGTTTTTTC GTTTGTTTCT  1680
TTGTTTTGAG ATGGAGTCTT GTTCTGTCAC CCAGGCTGGG GTGCAGTGGC GTGATCTTGG  1740
CTCACTGCAA TCTCTATCCC CTGGGTTCAA GTGATTCTCT TGTCTCAGCC TCCCAAGTAG  1800
CTGGGATTAC AGGCACAGGC CGCCACGCCT GGCTAATTTT TGTATTTTTA GTAGAGACAG  1860
AGTTTTACCA TGTTGGCCAG GCTGGTTTCA AACTCCTGAC CTCAAGTGAC CCACCTTGGC  1920
CTCCCAAAGT TTTGGGATTA CAAGTGTGGG CCACCGCGGC CAGCCTATGA TCCATTTTGA  1980
ATGAATTTTT TATATGGTGC AAGGTGTCAA TCCACCTTCA CTTTTTCTTG GGAATATAGA  2040
TATCCAGCTG TTTCACTACC ATTTTTTGAA AGGACTGCCC TTTGCTCTAT CACCTTTGCA  2100
TTTTTGTTAA AAAGTAGTTG TCAATGTATA TGTGGGTTTA TTTCAGGACT CTGTTTTGTT  2160
CCATTGACCT GTTTTTCTCT CCTGAATGCC AATACCATAT TTGTATGTAG TGTATGTAAT  2220
TTTCTAATAA TTCTTGAAAC AGATAGTATT AATGTGTCAT ATTTTTGCTG TTGTTTGTAT  2280
TTTTTGTAGA GATGGGGTTT CACCGTGTTG GCCAGGCTGT GTTGAACTCC TGAGCTAAAG  2340
CAATACACTT GCCTCGTCCT CCCCATGTGC TGGGATTACA GGCGTGAGCC TTGGTGCTGG  2400
CCCAGTGTAC CACATTTCTT TTTGAGATTT GTTTTGGCTA TGTTAAGTCC TTTGCTTTTG  2460
ATGTGAAATT TGGGAACAGG CAGGGTGTGG TGGCTTATGC CTGTAATCCT AGAACTTTGG  2520
GAGGCCTAGA TGGGTGGATC ACTTGAGCTC AGGAGTTCCA GACCAGCCCG GGCCTATGGC  2580
AAAACTCCGT CTCTACAAAA AATAGAAAAA ATTAGCCAGG TGTGGTGGTG CATGCCTGTA  2640
GTCACAGTTA CACGGCAGGC TGAGGTGGGA GGATCACTTG AACCCCAGAG GTCAAGACTG  2700
CAGTGAGCTG AGATCACACC ACTGTACTCC AGCCTGGGTG ACAAAGTGAG ACTCTATCTC  2760
AAAAAGAAAT TAGGATCAAT TTGTCAATTT CTACAACAAC AACAACAAAA ACCCCTGTTG  2820
GGCACCTTGA TTGAGATTGC ATTGAATTTA TATAAAACTG TTGGGAGAAT TGACATCTTA  2880
ATAATATTGA GTCTTCTGGC CTATAAACAA GGTCTGTCTT CCTAGGTATT AATGTTTTGT  2940
CTTCTATTTC TCTTAATAAT CTTTTGTAGT TTTCAGTGTA CAGGTCTACC ATGTCAGCAT  3000
TTCATAGTTT TGATGCTAAA TGGTATTTTA AAATTTCAAA TTCTAACCAC TTGTTGCTAG  3060
TAAATAGAAA TACAATTGAT GTTGAACTTG TATCCTTCAG CCTTGCTAAA CTGTGAGTTC  3120
TCATGGTGTT TTTGTAAATT ACATCAACAG TCATGTGTTC TATGAATAAA GAGTTTTACT  3180
CCTTC
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Seq ID NO: 158 Protein sequence:
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
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MFCEKAMELI RELHRAPEGQ LPAFNEDGLR QVLEEMKALY EQNQSDVNEA KSGGRSDLIP    60
TIKFRHCSLL RNRRCTVAYL YDRLLRIRAL RWEYGSVLPN ALRFHMAAEE VRCLKDYGEF   120
EVDDGTSVLL KKNSQHFLPR WKCEQLIRQG VLEHILS
```

Seq ID NO: 159 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 149-229

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1          11         21         31         41         51
|          |          |          |          |          |
GTTCGGCGCC AAAGCGCGGA GCGGAGGCCG AGGCGAGAGC CTGGCGCTGT AGGACTAGAA    60
CGAAAGGAGT GAGGCGCCGA GAGCCCAGAT ACCATTTTGG CGTGAGAGCT GGTGGTTGGC   120
AAGGCCGCGG GAGTGGGAAG CGTCCGCCAT GTTCTGCGAA AAAGCCATGG AACTGATCCG   180
CGAGCTGCAT CGCGCGCCCG AAGGGCAACT GCCTGCCTTC AACAATTAGC TGGGTGTGGT   240
GGCACACACC TGTAGTCCCA GCAACTTAGG AGGCTGAAGT GAGAGGATTG CATGGCTCCA   300
GGAAGTTGAA ACTGCAGTGA ACTGTGGTCA CGCTATTACA CTCCAGCCTG GGTGACAGAC   360
TGAATCCCTG TCTCAAAAAG GAAAAGGAGG ATGGACTCAG ACAAGTTCTG GAGGAGATGA   420
AAGCTTTGTA TGAACAAAAC CAGTCTGATG TGTTCTCTGT TAAGAAATCG ACGCTGCACT   480
GTAGCATACC TGTATGACCG CTTGCTTCGG ATCAGAGCAC TCAGATGG
```

Seq ID NO: 160 Protein sequence:
Protein Accession #: Eos sequence

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGTTCTGCG AAAAAGCCAT GGAACTGATC CGCGAGCTGC ATCGCGCGCC CGAAGGGCAA    60
CTGCCTGCCT TCAACAATTA G
```

Seq ID NO: 161 DNA sequence
Nucleic Acid Accession #: U10694
Coding sequence: 1333-2280

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1          11         21         31         41         51
|          |          |          |          |          |
GGATCCGGCC GGATCTCAGG GAGGTGAGGA CTTTGTTCTC AGAGGGTGTG TGTGGACAAA    60
ACAGGGAGGC CCTGTGTTCG ACAGACACAG TGGTCCCAGG ATTGGAGAGC AGTCCAGGTG   120
AGGAACCTAA GGGAGGATCG AGGGTACCTC CAGGCCAGAG AAACTCTCAG ATCAAGAGAG   180
TTTGCCCTGC CCCTACTGTC ACCCCAGAGA GCCCGGGCAG GGCTGTCTGC TGAGGTCCCT   240
CCTTTATCCT GGGATCACTG GTGTCGGGGA GGGCTGGCCT TGGTCTGAGG GGGCTGCACT   300
CACGTCAGCA GAGGGAGGGT CCCAGGCCCT GCCAGGAGTC CAGGTGCAGA CTGAGGGGAC   360
CCCACTCACC AAACACAGAG GACCTAGCCC CACCCTGCCC CTTGTGTCAG CTGAGGGAAG   420
CCGCTGGGTG GATGGACTCC CCTCACTTCC TCTTCAGGTG TCTCCTGGAG ATAGGGCCTC   480
AGGTCAACAG AGGGAGGGTT CCAGACCCTG CAGGCATCAA GATGAGGACC AGGCAGTATC   540
CTCACCCCAG GACACATGGA CCCCATTGAA TTTAGACATC TCTTACTGTA CTTCCGAGGA   600
AACCCTGGGC AGGTGTGGGC AGATGTTGGT TGGGGCATGT CCTTCTGTTC CATATCAGGG   660
ATGTGAGCTC CTGATCTGAG AGACTCTCAG GCAAGTAGAG GAGTAGAGTC CAGTCCCTGC   720
CAGGAGAAAG GTCAGGGCCC TGAGTGAGCG CAGAGGGGAC CATCCACCCC AAAAGTGTGT   780
AGAACTCAAG AGTGTCCAGC CCGCCCTCTT GACAGCACTG AGGGACCGGG GCTCTGCCTG   840
CAGTCTGCAG CCTAAGGGCC CCTCGATTCC TCTTCCAGGA GCTCCAGGAA GCAGGCAGGC   900
CTTGGTCTGA GACAGTGTCC TCAGGTCGCA GAGCAGAGGA GACCCAGGCA GTGTCAGCAG   960
TGAAGGTGAA GTGTTCACCC TGAATGTGCA CCAAGGGCCC CACCTGCCCC AGCACACATG  1020
GGACCCCATA GCACCTGGCC CCATTCCCCC TACTGTCACT CATAGAGCCT TGATCTCTGC  1080
AGGCTAGCTG CACGCTGAGT AGCCCTCTCA CTTCCTCCCT CAGGTTCTCG GGACAGGCTA  1140
ACCAGGAGGA CAGGAGCCCC AAGAGGCCCC AGAGCAGCAC TGACGAAGAC CTGTAAGTCA  1200
GCCTTTGTTA GAACCTCCAA GGTTCGGTTC TCAGCTGAAG TCTCTCACAC ACTCCCTCTC  1260
TCCCCAGGCC TGTGGGTCTC CATCGCCCAG CTCCTGCCCA CGCTCCTGAC TGCTGCCCTG  1320
ACCAGAGTCA TCATGTCTCT CGAGCAGAGG AGTCCGCACT GCAAGCCTGA TGAAGACCTT  1380
GAAGCCCAAG GAGAGGACTT GGGCCTGATG GGTGCACAGG AACCCACAGG CGAGGAGGAG  1440
GAGACTACCT CCTCCTCTGA CAGCAAGGAG GAGGAGGTGT CTGCTGCTGG GTCATCAAGT  1500
CCTCCCCAGA GTCCTCAGGG AGGCGCTTCC TCCTCCATTT CCGTCTACTA CACTTTATGG  1560
AGCCAATTCG ATGAGGGCTC CAGCAGTCAA GAAGAGGAAG AGCCAAGCTC CTCGGTCGAC  1620
CCAGCTCAGC TGGAGTTCAT GTTCCAAGAA GCACTGAAAT TGAAGGTGGC TGAGTTGGTT  1680
CATTTCCTGC TCCACAAATA TCGAGTCAAG GAGCCGGTCA CAAAGGCAGA AATGCTGGAG  1740
AGCGTCATCA AAAATTACAA GCGCTACTTT CCTGTGATCT TCGGCAAAGC CTCCGAGTTC  1800
ATGCAGGTGA TCTTTGGCAC TGATGTGAAG GAGGTGGACC CCGCCGGCCA CTCCTACATC  1860
CTTGTCACTG CTCTTGGCCT CTCGTGCGAT AGCATGCTGG GTGATGGTCA TAGCATGCCC  1920
AAGGCCGCCC TCCTGATCAT TGTCCTGGGT GTGATCCTAA CCAAAGACAA CTGCGCCCCT  1980
GAAGAGGTTA TCTGGGAAGC GTTGAGTGTG ATGGGGGTGT ATGTTGGGAA GGAGCACATG  2040
TTCTACGGGG AGCCCAGGAA GCTGCTCACC CAAGATTGGG TGCAGGAAAA CTACCTGGAG  2100
TACCGGCAGG TGCCCGGCAG TGATCCTGCG CACTACGAGT TCCTGTGGGG TTCCAAGGCC  2160
CACGCTGAAA CCAGCTATGA GAAGGTCATA AATTATTTGG TCATGCTCAA TGCAAGAGAG  2220
CCCATCTGCT ACCCATCCCT TTATGAAGAG GTTTTGGGAG AGGAGCAAGA GGGAGTCTGA  2280
GCACCAGCCG CAGCCGGGGC CAAAGTTTGT GGGGTCAGGG CCCCATCCAG CAGCTGCCCT  2340
GCCCCATGTG ACATGAGGCC CATTCTTCGC TCTGTGTTTG AAGAGAGCAA TCAGTGTTCT  2400
CAGTGGCAGT GGGTGGAAGT GAGCACACTG TATGTCATCT CTGGGTTCCT TGTCTATTGG  2460
GTGATTTGGA GATTTATCCT TGCTCCCTTT TGGAATTGTT CAAATGTTCT TTTAATGGTC  2520
AGTTTAATGA ACTTCACCAT CGAAGTTAAT GAATGACAGT AGTCACACAT ATTGCTGTTT  2580
ATGTTATTTA GGAGTAAGAT TCTTGCTTTT GAGTCACATG GGAAATCCC TGTTATTTTG  2640
TGAATTGGGA CAAGATAACA TAGCAGAGGA ATTAATAATT TTTTTGAAAC TTGAACTTAG  2700
CAGCAAAATA GAGCTCATAA AGAAATAGTG AAATGAAAAT GTAGTTAATT CTTGCCTTAT  2760
ACCTCTTTCT CTCTCCTGTA AAATTAAAAC ATATACATGT ATACCTGGAT TTGCTTGGCT  2820
TCTTTGAGCA TGTAAGAGAA ATAAAAATTG AAAGAATAAT TTTTCCTGTT CACTGGCTCA  2880
TTTTTTCTTC AGACACGCAC TGAACATCTG TTATTCGGAA CACCCTGGGT T
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Seq ID NO: 162 Protein sequence:
Protein Accession #: AAA68877.1

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1          11         21         31         41         51
|          |          |          |          |          |
MSLEQRSPHC KPDEDLEAQG EDLGLMGAQE PTGEEEETTS SSDSKEEEVS AAGSSSPPQS    60
PQGGASSSIS VYYTLWSQFD EGSSSQEEEE PSSSVDPAQL EFMFQEALKL KVAELVHFLL   120
HKYRVKEPVT KAEMLESVIK NYKRYFPVIF GKASEFMQVI FGTDVKEVDP AGHSYILVTA   180
LGLSCDSMLG DGHSMPKAAL LIIVLGVILT KDNCAPEEVI WEALSVMGVY VGKEHMFYGE   240
PRKLLTQDWV QENYLEYRQV PGSDPAHYEF LWGSKAHAET SYEKVINYLV MLNAREPICY   300
PSLYEEVLGE EQEGV
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Seq ID NO: 163 DNA sequence
Nucleic Acid Accession #: AF292100
Coding sequence: 30-809

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1          11         21         31         41         51
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AAGTTCGTCA GTTTATGATC TTCACACAAT CTAGTGAAAA AACAGCAGTA AGTTGTCTTT   120
CTCAAAATGA CTGGAAGTTA GATGTTGCAA CAGATAATTT TTTCCAAAAT CCTGAACTTT   180
ATATACGAGA GAGTGTAAAA GGATCATTGG ACAGGAAGAA GTTAGAACAG CTGTACAATA   240
GATACAAAGA CCCTCAAGAT GAGAATAAAA TTGGAATAGA TGGCATACAG CAGTTCTGTG   300
ATGACCTGGC ACTCGATCCA GCCAGCATTA GTGTGTTGAT TATTGCGTGG AAGTTCAGAG   360
CAGCAACACA GTGCGAGTTC TCCAAACAGG AGTTCATGGA TGGCATGACA GAATTAGGAT   420
GTGACAGCAT AGAACAACTA AAGGCCCAGA TACCCAAGAT GGAACAAGAA TTGAAAGAAC   480
CAGGACGATT TAAGGATTTT TACCAGTTTA CTTTTAATTT TGCAAAGAAT CCAGGACAAA   540
AAGGATTAGA TCTAGAAATG GCCATTGCCT ACTGGAACTT AGTGCTTAAT GGAAGATTTA   600
AATTCTTAGA CTTATGGAAT AAATTTTTGT TGGAACATCA TAAACGATCA ATACCAAAAG   660
ACACTTGGAA TCTTCTTTTA GACTTCAGTA CGATGATTGC AGATGACATG TCTAATTATG   720
ATGAAGAAGG AGCATGGCCT GTTCTTATTG ATGACTTTGT GGAATTTGCA CGCCCTCAAA   780
TTGCTGGGAC AAAAAGTACA ACAGTGTAGC ACTAAAGGAA CCTTTTAGAA TGTACATAGT   840
CTGTACAATA AATACAACAG AAAATTGCAC AGTCAATTTC TGCTGGCTGG ACTGAACTGA   900
AGATCAATCC TCACAATTCA GACTGAGGGT TGAGACAAAA CTTTAAGGAT ACATCTTGGA   960
CCATATCGTA TTTCATTCTT CTAATGGTGG TTTGGGCTTG TCTTCTAGTC TGGGCCGCTC  1020
TAAACATTTA TAATTCCAAC ATTGTGGATT TCATCTTATA TCTGTGGACC ATCCTAGTTT  1080
ATTCTCCCAT AAGTCTTAGA AGCTTTATGG TGATTATTTT GAGGTTTTCA TTCTCGCATA  1140
AAGCACAATG CTGTCTTCAT CAGAAAACAG TTGGCATAAG AATTAAACAT ATGAACATCA  1200
CAAAACAATT TATAAAAACT TCTTAAATAT ACGCTTTGGG CTAGTTGCAA AGACTATGCT  1260
AATAGCACTT CCAGTGAGAG TGATATATTT AAGTGTACTG GATCTGGAAT GGTGTTTTGG  1320
TTTGGGGGGA ATTTTTTTTT TTTCCTGGCA AATCACATAT GTTGTTGATG TGAGTATCTG  1380
ATGAAAAAAC AATGTCAGAA TAACCGACAT GAAAATTTTT TAGGATAACT TGGTGCCTAC  1440
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CTGCATAATG TTAGATTCTT CTCCTGTCTA CATTATGCAC TACATAATTG GACTTCATTA  1620
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TTTTGGATTG CTACACAATA CAATATTCTA AATTTAGGCA TGAGGGTTTT TTTGTTTTAT  1740
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AAGATAGTAG GAGTTAAATT TTGAAAATGG TTGTGATGAG CCACGAAATT CAATCTTTAT  1860
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AATTACTTTA ACTGCTAATC ACTGTGGTTG CCAAATATTT ACTTCAGAAG CAAAGATTTT  1980
CAAACAAGCA TACACGATGC AAAATACCAG TCTGGCTTCT AGTCTATTTA CTGTTTTGTT  2040
TCACTCAGAT TAGCTCAGTT TTCTCATCAA AGCAGAATGC TATCTTGCGT GTGTGTGTGT  2100
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TTTTTTTTTT TTTTTTTTAA ATTACAAAAG CCATGAGCTG CTTTTATGCT GAAAATGGTC  2220
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TAAGGCAGGC TAGAAATGTA ATACTTCAAA TGTTTGATGA TTATGGTCTT TTGATAGGAA  2340
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AGGAATGTAC TTAGAATAGC AGTACATTTT ATGCAAATAT GGAAATTATT TTAAGAAACA  2460
ATGACATATC AAAACTGCTT TTTACATGAT TTTGAAATAG ACTAGAAAGC TTTCCCTATA  2520
GACATATTAA TATTCCAATC ATAACTTTAA TTCAAGAATG CAGTTTTACC AAAAGAAAAA  2580
TTTGAAAATT TCTATTCAGG CTACTGGAAT TGGTTATTAA AAGAAAAAGG AAAAAGAAGA  2640
ATCTTGCTGC TTTCAGTATT TCCTGATTTT TTTGTAAATA TAAAGAGGAA CTTCAATTAT  2700
GAAAAATTTT TAAAAGATAT ATATATCTAT ATATCTATAT ATATGTACTG TTTTGTTTCC  2760
TGTCTTGAAG ATTTTGAGTT ATGGTTATTG GTTTCAGATT GATTAATTCA CATATGCTGT  2820
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CTGTGAGAGA GCCAGAGAGA GTGAGAGAGA TTGACAGAGA AAGGGAGAGA CACACACACG  3240
CCCCTTGAAT TGCTTTAACT CCTAAGTGTT TCAGTCCTCA TTCCGGTAAA CTCCCCATGC  3300
TGATTCTTTG TTTTAAACTG AACCATAGGT ACAGTTTCCT TTTTGCCAAA TGTCAAAACA  3360
GGTACAAATT TTAAAATGTA ATGCTTTTTA AATAGAAAAA TGTATAAAAT TAGAAGTGCC  3420
CACATATAAA AAATACTTGA GATGAAGATT ATCTTTAGTG AATATCATCT GCATATCTCT  3480
GTAAGTTCAA TTGTGTTTCT TACAGTCCCT GTCATATTAC CAACAGAGGC AATAAAAGCT  3540
GCAGTGAAAT TG
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Seq ID NO: 164 Protein sequence:
Protein Accession #: AAG00606

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1          11         21         31         41         51
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MNKLKSSQKD KVRQFMIFTQ SSEKTAVSCL SQNDWKLDVA TDNFFQNPEL YIRESVKGSL    60
DRKKLEQLYN RYKDPQDENK IGIDGIQQFC DDLALDPASI SVLIIAWKFR AATQCEFSKQ   120
EFMDGMTELG CDSIEQLKAQ IPKMEQELKE PGRFKDFYQF TFNFAKNPGQ KGLDLEMAIA   180
YWNLVLNGRF KPLDLWNKFL LEHHKRSIPK DTWNLLLDFS TMIADDMSNY DEEGAWPVLI   240
DDFVEFARPQ IAGTKSTTV
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Seq ID NO: 165 DNA sequence
Nucleic Acid Accession #: AF256215
Coding sequence: 220-2028

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GCCTACGGGC TGCGGTGGCG GCCGCCGCGG CACCCGGCAG GGCCCGCCAG TCCCCGCTTC   120
CCTGCTCCAG AGCCGCCGCC TGGGCCGGGG CAGGGCGGGC CCGGGGCTCC TCCATGCTGC   180
CAGCCGCCGG GCTGCGGAGC CGACCAAGTG GCTCCTGCGA TGGCGGCGGA AGAGGAGGCT   240
GCGGCGGGAG GTAAAGTGTT GAGAGAGGAG AACCAGTGCA TTGCTCCTGT GGTTTCCAGC   300
CGCGTGAGTC CAGGGACAAG ACCAACAGCT ATGGGGTCTT TCAGCTCACA CATGACAGAG   360
TTTCCACGAA AACGCAAAGG AAGTGATTCA GACCCATCCC AAGTGGAAGA TGGTGAACAC   420
CAAGTTAAAA TGAAGGCCTT CAGAGAAGCT CATAGCCAAA CTGAAAAGCG GAGGAGAGAT   480
AAAATGAATA ACCTGATTGA AGAACTGTCT GCAATGATCC CTCAGTGCAA CCCCATGGCG   540
CGTAAACTGG ACAAACTTAC AGTTTTAAGA ATGGCTGTTC AACACTTGAG ATCTTTAAAA   600
GGCTTGACAA ATTCTTATGT GGGAAGTAAT TATAGACCAT CATTTCTTCA GGATAATGAG   660
CTCAGACATT TAATCCTTAA GACTGCAGAA GGCTTCTTAT TTGTGGTTGG ATGTGAAAGA   720
GGAAAAATTC TCTTCGTTTC TAAGTCAGTC TCCAAAATAC TTAATTATGA TCAGGCTAGT   780
TTGACTGGAC AAAGCTTATT TGACTTCTTA CATCCAAAAG ATGTTGCCAA AGTAAAGGAA   840
CAACTTTCTT CTTTTGATAT TTCACCAAGA GAAAAGCTAA TAGATGCCAA AACTGGTTTG   900
CAAGTTCACA GTAATCTCCA CGCTGGAAGG ACACGTGTGT ATTCTGGCTC AAGACGATCT   960
TTTTTCTGTC GGATAAAGAG TTGTAAAATC TCTGTCAAAG AAGAGCATGG ATGCTTACCC  1020
AACTCAAAGA AGAAAGAGCA CAGAAAATTC TATACTATCC ATTGCACTGG TTACTTGAGA  1080
AGCTGGCCTC CAAATATTGT TGGAATGGAA GAAGAAAGGA ACAGTAAGAA AGACAACAGT  1140
AATTTTACCT GCCTTGTGGC CATTGGAAGA TTACAGCCAT ATATTGTTCC ACAGAACAGT  1200
GGAGAGATTA ATGTGAAACC AACTGAATTT ATAACCCGGT TTGCAGTGAA TGGAAAATTT  1260
GTCTATGTAG ATCAAAGGGC AACAGCGATT TTAGGATATC TGCCTCAGGA ACTTTTGGGA  1320
ACTTCTTGTT ATGAATATTT TCATCAAGAT GACCACAATA ATTTGACTGA CAAGCACAAA  1380
GCAGTTCTAC AGAGTAAGGA GAAAATACTT ACAGATTCCT ACAAATTCAG AGCAAAAGAT  1440
GGCTCTTTTG TAACTTTAAA AAGCCAATGG TTTAGTTTCA CAAATCCTTG GACAAAAGAA  1500
CTGGAATATA TTGTATCTGT CAACACTTTA GTTTTGGGAC ATAGTGAGCC TGGAGAAGCA  1560
TCATTTTTAC CTTGTAGCTC TCAATCATCA GAAGAATCCT CTAGACAGTC CTGTATGAGT  1620
GTACCTGGAA TGTCTACTGG AACAGTACTT GGTGCTGGTA GTATTGGAAC AGATATTGCA  1680
AATGAAATTC TGGATTTACA GAGGTTACAG TCTTCTTCAT ACCTTGATGA TTCGAGTCCA  1740
ACAGGTTTAA TGAAAGATAC TCATACTGTA AACTGCAGGA GTATGTCAAA TAAGGAGTTG  1800
TTTCCACCAA GTCCTTCTGA AATGGGGGAG CTAGAGGCTA CCAGGCAAAA CCAGAGTACT  1860
GTTGCTGTCC ACAGCCATGA GCCACTCCTC AGTGATGGTG CACAGTTGGA TTTCGATGCC  1920
CTATGTGACA ATGATGACAC AGCCATGGCT GCATTTATGA ATTACTTAGA AGCAGAGGGG  1980
GGCCTGGGAG ACCCTGGGGA CTTCAGTGAC ATCCAGTGGA CCCTCTAGCC TTTGATTTTT  2040
AACTCCAAAA ATGAGAAACA TTTTAAAGCA TTATTTACGA AAAAACTGTC TCAACTATTC  2100
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CATATTTTTA TGGTATACAC TATGTTCCTT TTTTCTACTG CGAGTCAATT TTTTGAATTT  4740
TCGTGAGAAA GAATATATCT ACAAATTGCA CGAAAGTATC ATAAAAACAG TACTCTAGAG  4800
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CTCGTCTGTA TATTGGTATT TTTAAATTTT TGTGGTAAAT AATGAAAAGA GTGAAATTAT 6720
ATTTTATAAT TACTCATTTG TAGTTTTTTT TTTTAATTTA ATAAACTTCC TCCAAAAAGT 6780
GCTCCCTTAA AA

Seq ID NO: 166 Protein sequence:
Protein Accession #: AAG34652

1 11 21 31 41 51

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QHLRSLKGLT NSYVGSNYRP SFLQDNELRH LILKTAEGFL FVVGCERGKI LFVSKSVSKI 180
LNYDQASLTG QSLFDFLHPK DVAKVKEQLS SFDISPREKL IDAKTGLQVH SNLHAGRTRV 240
YSGSRRSFFC RIKSCKISVK EEHGCLPNSK KKEHRKFYTI HCTGYLRSWP PNIVGMEEER 300
NSKKDNSNFT CLVAIGRLQP YIVPQNSGEI NVKPTEFITR FAVNGKFVYV DQRATAILGY 360
LPQELLGTSC YEYFHQDDHN NLTDKHKAVL QSKEKILTDS YKFRAKDGSF VTLKSQWFSF 420
TNPWTKELEY IVSVNTLVLG HSEPGEASFL PCSSQSSEES SRQSCMSVPG MSTGTVLGAG 480
SIGTDIANEI LDLQRLQSSS YLDDSSPTGL MKDTHTVNCR SMSNKELFPP SPSEMGELEA 540
TRQNQSTVAV HSHEPLLSDG AQLDFDALCD NDDTAMAAFM NYLEAEGGLG DPGDFSDIQW 600
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Seq ID NO: 167 DNA sequence
Nucleic Acid Accession #: NM_014400
Coding sequence: 86-1126

1 11 21 31 41 51

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GATCTGGACT GCAGGCTGGC TGCTGCTGCT GCTGCTTCGC GGAGGAGCGC AGGCCCTGGA 180
GTGCTACAGC TGCGTGCAGA AAGCAGATGA CGGATGCTCC CCGAACAAGA TGAAGACAGT 240
GAAGTGCGCG CCGGGCGTGG ACGTCTGCAC CGAGGCCGTG GGGGCGGTGG AGACCATCCA 300
CGGACAATTC TCGCTGGCAG TGCSGGGTTG CGGTTCGGGA CTCCCCGGCA AGAATGACCG 360
CGGCCTGGAT CTTCACGGGC TTCTGGCGTT CATCCAGCTG CAGCAATGCG CTCAGGATCG 420
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ATACCCGCCC AACGGCGTGG AGTGCTACAG CTGTGTGGGC CTGAGCCGGG AGGCGTGCCA 540
GGGTACATCG CCGCCGGTCG TGAGCTGCTA CAACGCCAGC GATCATGTCT ACAAGGGCTG 600
CTTCGACGGC AACGTCACCT TGACGGCAGC TAATGTGACT GTGTCCTTGC CTGTCCGGGG 660
CTGTGTCCAG GATGAATTCT GCACTCGGGA TGGAGTAACA GGCCCAGGGT TCACGCTCAG 720
TGGCTCCTGT TGCCAGGGGT CCCGCTGTAA CTCTGACCTC CGCAACAAGA CCTACTTCTC 780
CCCTCGAATC CCACCCCTTG TCCGGCTGCC CCCTCCAGAG CCCACGACTG TGGCCTCAAC 840
CACATCTGTC ACCACTTCTA CCTCGGCCCC AGTGAGACCC ACATCCACCA CCAAACCCAT 900
GCCAGCGCCA ACCAGTCAGA CTCCGAGACA GGGAGTAGAA CACGAGGCCT CCCGGGATGA 960
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TCCTGCAAAA GGGGGGCCCC AGCAGCCCCA TAATAAAGGC TGTGTGGCTC CCACAGCTGG 1080
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GGTGGGACAA TGGCTCCCCA CTCTAAGCAC TGCCTCCCCT ACTCCCCGCA TCTTTGGGGA 1560
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CTTATGTCTG TGTGTGATCA GTTTCTGGCA CATAAATGCC TCAATAAAGA TTTAATTACT 1680

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TTGTATAGTG AAAAAAAA
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Seq ID NO: 168 Protein sequence:
Protein Accession #: NP_055215

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CTEAVGAVET IHGQFSLAVX GCGSGLPGKN DRGLDLHGLL AFIQLQQCAQ DRCNAKLNLT   120
SRALDPAGNE SAYPPNGVEC YSCVGLSREA CQGTSPPVVS CYNASDHVYK GCFDGNVTLT   180
AANVTVSLPV RGCVQDEPCT RDGVTGPGFT LSGSCCQGSR CNSDLRNKTY FSPRIPPLVR   240
LPPPEPTTVA STTSVTTSTS APVRPTSTTK PMPAPTSQTP RQGVEHEASR DEEPRLTGGA   300
AGHQDRSNSG QYPAKGGPQQ PHNKGCVAPT AGLAALLLAV AAGVLL
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Seq ID NO: 169 DNA sequence
Nucleic Acid Accession #: NM_006875
Coding sequence: 186-1190

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CCCGGGCGTC CACGCCCTGC GGGCTTAGCG GGTTCAGTGG GCTCAATCTG CGCAGCGCCA   180
CCTCCATGTT GACCAAGCCT CTACAGGGGC CTCCCGCGCC CCCCGGGACC CCCACGCCGC   240
CGCCAGGAGG CAAGGATCGG GAAGCGTTCG AGGCCGAGTA TCGACTCGGC CCCCTCCTGG   300
GTAAGGGGGG CTTTGGCACC GTCTTCGCAG GACACCGCCT CACAGATCGA CTCCAGGTGG   360
CCATCAAAGT GATTCCCCGG AATCGTGTGC TGGGCTGGTC CCCCTTGTCA GACTCAGTCA   420
CATGCCCACT CGAAGTCGCA CTGCTATGGA AAGTGGGTGC AGGTGGTGGG CACCCTGGCG   480
TGATCCGCCT GCTTGACTGG TTTGAGACAC AGGAAGGCTT CATGCTGGTC CTCGAGCGGC   540
CTTTGCCCGC CCAGGATCTC TTTGACTATA TCACAGAGAA GGGCCCACTG GGTGAAGGCC   600
CAAGCCGCTG CTTCTTTGGC CAAGTAGTGG CAGCCATCCA GCACTGCCAT TCCCGTGGAG   660
TTGTCCATCG TGACATCAAG GATGAGAACA TCCTGATAGA CCTACGCCGT GGCTGTGCCA   720
AACTCATTGA TTTTGGTTCT GGTGCCCTGC TTCATGATGA ACCCTACACT GACTTTGATG   780
GGACAAGGGT GTACAGCCCC CCAGAGTGGA TCTCTCGACA CCAGTACCAT GCACTCCCGG   840
CCACTGTCTG GTCACTGGGC ATCCTCCTCT ATGACATGGT GTGTGGGGAC ATTCCCTTTG   900
AGAGGGACCA GGAGATTCTG GAAGCTGAGC TCCACTTCCC AGCCCATGTC TCCCCAGACT   960
GCTGTGCCCT AATCCGCCGG TGCCTGGCCC CCAAACCTTC TTCCCGACCC TCACTGGAAG  1020
AGATCCTGCT GGACCCCTGG ATGCAAACAC CAGCCGAGGA TGTTACCCCT CAACCCCTCC  1080
AAAGGAGGCC CTGCCCCTTT GGCCTGGTCC TTGCTACCCT AAGCCTGGCC TGGCCTGGCC  1140
TGGCCCCCAA TGGTCAGAAG AGCCATCCCA TGGCCATGTC ACAGGGATAG ATGGACATTT  1200
GTTGACTTGG TTTTACAGGT CATTACCAGT CATTAAAGTC CAGTATTACT AAGGTAAGGG  1260
ATTGAGGATC AGGGGTTAGA AGACATAAAC CAAGTTTGCC CAGTTCCCTT CCCAATCCTA  1320
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CTGAGCCGGG ATTGTCCAAT TACTAAAATG TAAATAATCA CGTATTGTGG GGAGGGGAGT  1980
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Seq ID NO: 170 Protein sequence:
Protein Accession #: NP_006866

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KVIPRNRVLG WSPLSDSVTC PLEVALLWKV GAGGGHPGVI RLLDWFETQE GFMLVLERPL   120
PAQDLFDYIT EKGPLGEGPS RCFFGQVVAA IQHCHSRGVV HRDIKDENIL IDLRRGCAKL   180
IDFGSGALLH DEPYTDFDGT RVYSPPEWIS RHQYHALPAT VWSLGILLYD MVCGDIPFER   240
DQEILEAELH FPAHVSPDCC ALIRRCLAPK PSSRPSLEEI LLDPWMQTPA EDVTPQPLQR   300
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Seq ID NO: 171 DNA sequence
Nucleic Acid Accession #: NM_003646
Coding sequence: 89..2875

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GAGCAGCGAC TCCGAGTCGG CTTCCGCCTC GTCCAGCGGC TCCGAGCGCG ACGCCGGTCC   180
CGAGCCGGAC AAGGCGCCGC GGCGACTCAA CAAGCGGCGC TTCCCGGGGC TGCGGCTCTT   240
CGGGCACAGG AAAGCCATCA CCAAGTCGGG CCTCCAGCAC CTGGCCCCCC CTCCGCCCAC   300
CCCTGGGGCC CCGTGCAGCG AGTCAGAGCG GCAGATCCGG AGTACAGTGG ACTGGAGCGA   360
GTCAGCGACA TATGGGGAGC ACATCTGGTT CGAGACCAAC GTGTCCGGGG ACTTCTGCTA   420
CGTTGGGGAG CAGTACTGTG TAGCCAGGAT GCTGAAGTCA GTGTCTCGAA GAAAGTGCGC   480
AGCCTGCAAG ATTGTGGTGC ACACGCCCTG CATCGAGCAG CTGGAGAAGA TAAATTTCCG   540
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GCACCACTGG GTACACAGAC GACGCCAGGA CGGCAAGTGT CGGCACTGTG GGAAGGGATT   660
CCAGCAGAAG TTCACCTTCC ACAGCAAGGA GATTGTGGCC ATCAGCTGCT CGTGGTGCAA   720
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GCAGGCATAC CACAGCAAGG TGTCCTGCTT CATGCTGCAG CAGATCGAGG AGCCGTGCTC 780
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CCAGAATACT CTGAAAGCAA GCAAGAAGAA GAAGAGGGCA TCCTTCAAGA GGAAGTCCAG 900
CAAGAAAGGG CCTGAGGAGG GCCGCTGGAG ACCCTTCATC ATCAGGCCCA CCCCCTCCCC 960
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CGGGGGCGAC GGCACGGTGG GCTGGATCCT CTCCACCCTG GACCAGCTAC GCCTGAAGCC 1200
GCCACCCCCT GTTGCCATCC TGCCCCTGGG TACTGGCAAC GACTTGGCCC GAACCCTCAA 1260
CTGGGGTGGG GGCTACACAG ATGAGCCTGT GTCCAAGATC CTCTCCCACG TGGAGGAGGG 1320
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ATCCAAGGCC ATCCCGGTGC AGGTGGATGG CGAGCCCTGC AAGCTTGCAG CCTCACGCAT 1920
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CGACACTCCC CGGCAGCGGG CTGAGAAGGC TCAGGACACC GAGCTGGCCG CCTACCTGGA 2820
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Seq ID NO: 172 Protein sequence:
Protein Accession #: NP_003637

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MLKSVSRRKC AACKIVVHTP CIEQLEKINF RCKPSFRESG SRNVREPTFV RHHWVHRRRQ  180
DGKCRHCGKG FQQKFTFHSK EIVAISCSWC KQAYHSKVSC FMLQQIEEPC SLGVHAAVVI  240
PPTWILRARR PQNTLKASKK KKRASFKRKS SKKGPEEGRW RPFIIRPTPS PLMKPLLVFV  300
NPKSGGNQGA KIIQSFLWYL NPRQVFDLSQ GGPKEALEMY RKVHNLRILA CGGDGTVGWI  360
LSTLDQLRLK PPPPVAILPL GTGNDLARTL NWGGGYTDEP VSKILSHVEE GNVVQLDRWD  420
LHAEPNPEAG PEDRDEGATD RLPLDVFNNY FSLGFDAHVT LEFHESREAN PEKFNSRFRN  480
KMFYAGTAFS DFLMGSSKDL AKHIRVVCDG MDLTPKIQDL KPQCVVFLNI PRYCAGTMPW  540
GHPGEHHDFE PQRHDDGYLE VIGFTMTSLA ALQVGGHGER LTQCREVVLT TSKAIPVQVD  600
GEPCKLAASR IRIALRNQAT MVQKAKRRSA APLHSDQQPV PEQLRIQVSR VSMHDYEALH  660
YDKEQLKEAS VPLGTVVVPG DSDLELCRAH IERLQQEPDG AGAKSPTCQK LSPKWCFLDA  720
TTASRFYRID RAQEHLNYVT EIAQDEIYIL DPELLGASAR PDLPTPTSPL PTSPCSPTPR  780
SLQGDAAPPQ GEELIEAAKR NDFCKLQELH RAGGDLMHRD EQSRTLLHHA VSTGSKDVVR  840
YLLDHAPPEI LDAVEENGET CLHQAAALGQ RTICHYIVEA GASLMKTDQQ GDTPRQRAEK  900
AQDTELAAYL ENRQHYQMIQ REDQETAV
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Seq ID NO: 173 DNA sequence
Nucleic Acid Accession #: AF232772
Coding sequence: 1-1662

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CTTTTTGCCT TCCTGGAGCA CCGGCGCATG CGACGTGCCG GCCAGGCCCT GAAGCTGCCC  240
TCCCCGCGGC GGGGCTCGGT GGCACTGTGC ATTGCCGCAT ACCAGGAGGA CCCTGACTAC  300
TTGCGCAAGT GCCTGCGCTC GGCCCAGCGC ATCTCCTTCC CTGACCTCAA GGTGGTCATG  360
GTGGTGGATG GCAACCGCCA GGAGGACGCC TACATGCTGG ACATCTTCCA CGAGGTGCTG  420
GGCGGCACCG AGCAGGCCGG CTTCTTTGTG TGGCGCAGCA ACTTCCATGA GGCAGGCGAG  480
GGTGAGACGG AGGCCAGCCT GCAGGAGGGC ATGGACCGTG TGCGGGATGT GGTGCGGGCC  540
AGCACCTTCT CGTGCATCAT GCAGAAGTGG GGAGGCAAGC GCGAGGTCAT GTACACGGCC  600
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GTCGGGGGAG ATGTCCAGAT CCTCAACAAG TACGACTCAT GGATTTCCTT CCTGAGCAGC  780
GTGCGGTACT GGATGGCCTT CAACGTGGAG CGGGCCTGCC AGTCCTACTT TGGCTGTGTG  840
CAGTGTATTA GTGGGCCCTT GGGCATGTAC CGCAACAGCC TCCTCCAGCA GTTCCTGGAG  900
GACTGGTACC ATCAGAAGTT CCTAGGCAGC AAGTGCAGCT TCGGGGATGA CCGGCACCTC  960
ACCAACCGAG TCCTGAGCCT TGGCTACCGA ACTAAGTATA CCGCGCGCTC CAAGTGCCTC 1020
ACAGAGACCC CCACTAAGTA CCTCCGGTGG CTCAACCAGC AAACCCGCTG GAGCAAGTCT 1080
TACTTCCGGG AGTGGCTCTA CAACTCTCTG TGGTTCCATA AGCACCACCT CTGGATGACC 1140
TACGAGTCAG TGGTCACGGG TTTCTTCCCC TTCTTCCTCA TTGCCACGGT TATACAGCTT 1200
TTCTACCGGG GCCGCATCTG GAACATTCTC CTCTTCCTGC TGACGGTGCA GCTGGTGGGC 1260
ATTATCAAGG CCACCTACGC CTGCTTCCTT CGGGGCAATG CAGAGATGAT CTTCATGTCC 1320
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CTCTACTCCC TCCTCTATAT GTCCAGCCTT CTGCCGGCCA AGATCTTTGC CATTGCTACC  1380
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TGCCAGGACC TGTTCAGTGA GACAGAGCTA GCCTTCCTTG TCTCTGGGGC TATACTGTAT  1560
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GGGAGGAGGG AGTGCTGTGT TTTAGTCTCT TAATGGTCCA AAGGACAAAT CTAAAATGCA  1800
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AGTCCCATTC AGTGGCAACT TGTGATAGGT ACCTGAGTGA CGGCAACCTG CGGAAGGAGG  2040
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GCGCGTGAGA TACAAGGCCC AGAAGCCTGA TCTTTGGGCA TCAGAAAACA GGGTCCAGGA  2220
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CAGGGAGTTA GCACTGAACT GCTTTTAAAA GTGCACATTA AAAAGGAAAG TTTGCCAGGA  2340
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CTCATGCCTC CTGAGGCTGT TTTTGGCTGT TTTCCCTCTG CTGCTTTTGG GGAATGAGGG  3120
GAAGCCATTT TCCAAGTGAC TTGCAATCCA GGCTGTTCTC AGCGTTTTGA GTTTAAAACC  3180
TGGGATCCTG ACTAAGCCTT TGACTTAAGG GTTGCTTGCT TGCCCTCCAA ATGTCCTTTC  3240
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AACAGTTGCC ACATCACACA GACCTCCAGT TTCTGGTAAG ACTGCTGGTT GACATCAGAC  3480
CCAACCCATT GAAGGCTGGA AGGCAGCAGG CATTTGCTAA GGCAGCTGAT CCAGGCAATC  3540
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CAAGTGCAGA GTTCAGACTT CGCTAAGGGC TTGTTTTTCT TCAGCATTTA CTTGAAGATT  3660
AATGTAGGAT GACAGGCTCT CCTGGCTGTC CTACCATCAG CTCTGCCTTG CACTGTGGTC  3720
GTCAACTTTC CTCAAATCAA AAACAGGCAG GTACAGGTAG TGGGCTCACA ACGTTTGACC  3780
TCGACTGGTT TTTCTAAGTT ATTTTGTACA TTTTTCAGCA GCAAAACCAA ACTGGGTCTT  3840
CAGCTTTATC CCCGTTTCTT GCAAGGGAAG AGCCTTTATA CAATTGGACG CATTTTGGTT  3900
TTTCCTCATT GAGAATTCAA ATCCTCTTTT GTATTGTTTC TACAATAATT TGTAAACATA  3960
TTTATTTTTA CCTGCTTTTT TTTTTTTTTT TAATTTTCAG GTCAAGTTTT TTATACTGCA  4020
CTTATTTGTC AAAATAAAGA TTCTCACAT
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Seq ID NO: 174 Protein sequence:
Protein Accession #: AAF36984

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LFAFLEHRRM RRAGQALKLP SPRRGSVALC IAAYQEDPDY LRKCLRSAQR ISFPDLKVVM   120
VVDGNRQEDA YMLDIFHEVL GGTEQAGFFV WRSNFHEAGE GETEASLQEG MDRVRDVVRA   180
STFSCIMQKW GGKREVMYTA FKALGDSVDY IQVCDSDTVL DPACTIEMLR VLEEDPQVGG   240
VGGDVQILNK YDSWISFLSS VRYWMAFNVE RACQSYFGCV QCISGPLGMY RNSLLQQFLE   300
DWYHQKFLGS KCSPGDDRHL TNRVLSLGYR TKYTARSKCL TETPTKYLRW LNQQTRWSKS   360
YFREWLYNSL WFHKHHLWMT YESVVTGFFP FFLIATVIQL FYRGRIWNIL LFLLTVQLVG   420
IIKATYACFL RGNAEMIFMS LYSLLYMSSL LPAKIFAIAT INKSGWGTSG RKTIVVNFIG   480
LIPVSIWVAV LLEGLAYTAY CQDLFSETEL AFLVSGAILY GCYWVALLML YLAIIARRCG   540
KKPEQYSLAF AEV
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Seq ID NO: 175 DNA sequence
Nucleic Acid Accession #: NM_000691
Coding sequence: 43..1404

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TTCCAGCAGC TGGAGGCGCT GCAGCGCCTG ATCCAGGAGC AGGAGCAGGA GCTGGTGGGC   180
GCGCTGGCCG CAGACCTGCA CAAGAATGAA TGGAACGCCT ACTATGAGGA GGTGGTGTAC   240
GTCCTAGAGG AGATCGAGTA CATGATCCAG AAGCTCCCTG AGTGGGCCGC GGATGAGCCC   300
GTGGAGAAGA CGCCCCAGAC TCAGCAGGAC GAGCTCTACA TCCACTCGGA GCCACTGGGC   360
GTGGTCCTCG TCATTGGCAC CTGGAACTAC CCCTTCAACC TCACCATCCA GCCCATGGTG   420
GGCGCCATCG CTGCAGGGAA CGCAGTGGTC CTCAAGCCCT CGGAGCTGAG TGAGAACATG   480
GCGAGCCTGC TGGCTACCAT CATCCCCCAG TACCTGGACA AGGATCTGTA CCCAGTAATC   540
AATGGGGGTG TCCCTGAGAC CACGGAGCTG CTCAAGGAGA GGTTCGACCA TATCCTGTAC   600
ACGGGCAGCA CGGGGGTGGG GAAGATCATC ATGACGGCTG CTGCCAAGCA CCTGACCCCT   660
GTCACGCTGG AGCTGGGAGG GAAGAGTCCC TGCTACGTGG ACAAGAACTG TGACCTGGAC   720
GTGGCCTGCC GACGCATCGC CTGGGGGAAA TTCATGAACA GTGGCCAGAC CTGCGTGGCC   780
CCAGACTACA TCCTCTGTGA CCCCTCGATC CAGAACCAAA TTGTGGAGAA GCTCAAGAAG   840
TCACTGAAAG AGTTCTACGG GGAAGATGCT AAGAAATCCC GGGACTATGG AAGAATCATT   900
AGTGCCCGGC ACTTCCAGAG GGTGATGGGC CTGATTGAGG GCCAGAAGGT GGCTTATGGG   960
GGCACCGGGG ATGCCGCCAC TCGCTACATA GCCCCCACCA TCCTCACGGA CGTGGACCCC  1020
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CAGTCCCCGG TGATGCAAGA GGAGATCTTC GGGCCTGTGC TGCCCATCGT GTGCGTGCGC  1080
AGCCTGGAGG AGGCCATCCA GTTCATCAAC CAGCGTGAGA AGCCCCTGGC CCTCTACATG  1140
TTCTCCAGCA ACGACAAGGT GATTAAGAAG ATGATTGCAG AGACATCCAG TGGTGGGGTG  1200
GCGGCCAACG ATGTCATCGT CCACATCACC TTGCACTCTC TGCCCTTCGG GGGCGTGGGG  1260
AACAGCGGCA TGGGATCCTA CCATGGCAAG AAGAGCTTCG AGACTTTCTC TCACCGCCGC  1320
TCTTGCCTGG TGAGGCCTCT GATGAATGAT GAAGGCCTGA AGGTCAGATA CCCCCCGAGC  1380
CCGGCCAAGA TGACCCAGCA CTGAGGAGGG GTTGCTCCGC CTGGCCTGGC CATACTGTGT  1440
CCCATCGGAG TGCGGACCAC CCTCACTGGC TCTCCTGGCC CTGGAGAATC GCTCCTGCAG  1500
CCCCAGCCCA GCCCCACTCC TCTGCTGACC TGCTGACCTG TGCACACCCC ACTCCCACAT  1560
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CAATTTTCTA ACTCGG
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Seq ID NO: 176 Protein sequence:
Protein Accession #: NP_000682

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YEEVVYVLEE IEYMIQKLPE WAADEPVEKT PQTQQDELYI HSEPLGVVLV IGTWNYPFNL   120
TIQPMVGAIA AGNAVVLKPS ELSENMASLL ATIIPQYLDK DLYPVINGGV PETTELLKER   180
FDHILYTGST GVGKIIMTAA AKHLTPVTLE LGGKSPCYVD KNCDLDVACR RIAWGKFMNS   240
GQTCVAPDYI LCDPSIQNQI VEKLKKSLKE FYGEDAKKSR DYGRIISARH FQRVMGLIEG   300
QKVAYGGTGD AATRYIAPTI LTDVDPQSPV MQEEIFGPVL PIVCVRSLEE AIQFINQREK   360
PLALYMFSSN DKVIKKMIAE TSSGGVAAND VIVHITLHSL PFGGVGNSGM GSYHGKKSFE   420
TFSHRRSCLV RPLMNDEGLK VRYPPSPAKM TQH
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Seq ID NO: 177 DNA sequence
Nucleic Acid Accession #: NM_001067.1
Coding sequence: 108-4703

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CATTGCAGCC TGTAAATGAA AATATGCAAG TCAACAAAAT AAAGAAAAAT GAAGATGCTA   180
AGAAAAGACT GTCTGTTGAA AGAATCTATC AAAAGAAAAC ACAATTGGAA CATATTTTGC   240
TCCGCCCAGA CACCTACATT GGTTCTGTGG AATTAGTGAC CCAGCAAATG TGGGTTTACG   300
ATGAAGATGT TGGCATTAAC TATAGGGAAG TCACTTTTGT TCCTGGTTTG TACAAAATCT   360
TTGATGAGAT TCTAGTTAAT GCTGCGGACA ACAAACAAAG GGACCCAAAA ATGTCTTGTA   420
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TCCTAACTTC TAGTAACTAT GATGATGATG AAAAGAAAGT GACAGGTGGT CGAAATGGCT   600
ATGGAGCCAA ATTGTGTAAC ATATTCAGTA CCAAATTTAC TGTGGAAACA GCCAGTAGAG   660
AATACAAGAA AATGTTCAAA CAGACATGGA TGGATAATAT GGGAAGAGCT GGTGAGATGG   720
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AGTTTAAAAT GCAAAGCCTG GACAAAGATA TTGTTGCACT AATGGTCAGA AGAGCATATG   840
ATATTGCTGG ATCCACCAAA GATGTCAAAG TCTTTCTTAA TGGAAATAAA CTGCCAGTAA   900
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AAAAAGGCTT TCAGCAAATT AGCTTTGTCA ACAGCATTGC TACATCCAAG GGTGGCAGAC  1080
ATGTTGATTA TGTAGCTGAT CAGATTGTGA CTAAACTTGT TGATGTTGTG AAGAAGAAGA  1140
ACAAGGGTGG TGTTGCAGTA AAAGCACATC AGGTGAAAAA TCACATGTGG ATTTTTGTAA  1200
ATGCCTTAAT TGAAAACCCA ACCTTTGACT CTCAGACAAA AGAAAACATG ACTTTACAAC  1260
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GTGGTATTGT AGAAAGCATA CTAAACTGGG TGAAGTTTAA GGCCCAAGTC CAGTTAAACA  1380
AGAAGTGTTC AGCTGTAAAA CATAATAGAA TCAAGGGAAT TCCCAAACTC GATGATGCCA  1440
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CCAAAACTTT GGCTGTTTCA GGCCTTGGTG TGGTTGGGAG AGACAAATAT GGGGTTTTCC  1560
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GTTATATGTG TGTGACTTGA GTAATGTTAT CAACGTTTTT GTAAATATTT ACTATGTTTT 5640
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Seq ID NO: 178 Protein sequence:
Protein Accession #: NP_001058.1

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VQLNKKCSAV KHNRIKGIPK LDDANDAGGR NSTECTLILT EGDSAKTLAV SGLGVVGRDK  480
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DQDQDGSHIK GLLINFIHHN WPSLLRHRFL EEFITPIVKV SKNKQEMAFY SLPEFEEWKS  600
STPNHKKWKV KYYKGLGTST SKEAKEYFAD MKRHRIQFKY SGPEDDAAIS LAFSKKQIDD  660
RKEWLTNFME DRRQRKLLGL PEDYLYGQTT TYLTYNDFIN KELILFSNSD NERSIPSMVD  720
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Seq ID NO: 179 DNA sequence
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Protein Accession #: Eos sequence

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Seq ID NO: 181 DNA sequence
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Coding sequence: 148-4518

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Seq ID NO: 182 Protein sequence:
Protein Accession #: Eos sequence

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Seq ID NO: 183 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 148-4494

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Seq ID NO: 184 Protein sequence:
Protein Accession #: EOS sequence

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Seq ID NO: 185 DNA sequence
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Seq ID NO: 186 Protein sequence:
Protein Accession #: EOS sequence

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Seq ID NO: 187 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 148-4632

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Seq ID NO: 188 Protein sequence:
Protein Accession #: EOS sequence

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Seq ID NO: 191 DNA sequence
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TGCCAGGTGT TCGCCGAGGC GCTGCAGGCC TATGGGGTGC GCTTTACGCG ACTGCCGCTG   540
GAGCGCGGTG TGGGTGGCTG CACTTGGCTG GAGGCCCCCG CGCGTGCCTT CGCCTGCGCC   600
GTGGAGCGCG ACGCCCGGGC GGCCGTGGGC CCCTTCTCCC GCCACGGCCT GCGGTGGACA   660
GACGCCTTCG TGGGCCTGAG CACTTGCGGC CGGCACATGT CCGCTCACCG CGTGTCCGGG   720
GCCCTGGCGC GGGTCCTGGA AGGTACCCTA GCGGGCCACA CCCTGACAGC CGAGCTGATG   780
GCGCACCCCG GCTACCCCAG TGTGCCTCCC ACCGGCGGCT GCGGTGAAGG CCCCGACGCT   840
TTCTCTTGCT CTTGGGAGCG GCTGCATGAG CTGCGCGTCC TCACCGCGCC CACGCTGCGG   900
GCCCAGCTTG CCCAGGATGG CGTGCAGCTT TGCGCCCTCG ACGACCTGGA CTCCAAGAGG   960
CCAGGGGAGG AGGTCCCCTG TGAGCCCACT CTGGAACCCT TCCTGGAACC CTCCCTACTC  1020
TGACCCCCTA CAGACAACCA AGCACTAATC CCCTTAGTAC CAAGAAAGGG GAGCCAGGAT  1080
TTAGTCCTGG CCCAGCCCAG AGCTGGGACC TGGAGCACGA TCTGTTGACT TCCCTGGGTA  1140
GGACACTGCC ACCTCTGGGC TCAGGTCCTC ATGCCTCCAA ATGGCATCTA GAGTTTGAGC  1200
AGCCTTCTTG GCTGCAGGCA GGCCTAGCCT GTGGCAGCGG GCTAGGGCCC GCAGAGCATT  1260
TGGTGCCCCT CCATGTTGCA ATGCAAACAC CTTCACCACT GGGGCAGTGG GGAGAGATGG  1320
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Seq ID NO: 192 Protein sequence:
Protein Accession #: XP_059328

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|          |          |          |          |          |
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GLHANLSEGR PVGPARRGAS SLLGPEGFFL GKMGFREAVA AGDVDLPQVR EELEAQLSCF   120
RELLGRAPTH ADGHQHVHVL PGVCQVFAEA LQAYGVRFTR LPLERGVGGC TWLEAPARAF   180
ACAVERDARA AVGPFSRHGL RWTDAFVGLS TCGRHMSAHR VSGALARVLE GTLAGHTLTA   240
ELMAHPGYPS VPPTGGCGEG PDAFSCSWER LHELRVLTAP TLRAQLAQDG VQLCALDDLD   300
SKRPGEEVPC EPTLEPFLEP SLL
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Seq ID NO: 193 DNA sequence
Nucleic Acid Accession #: NM_005688.1
Coding sequence: 126..4439

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GTGTGAGGGA GAGAACCAGC ACTTCTGGGA CGCACAGAGA CCGTGAAGAT TCCAAGTTCA 240
GGAGAACTCG ACCGTTGGAA TGCCAAGATG CCTTGGAAAC AGCAGCCCGA GCCGAGGGCC 300
TCTCTCTTGA TGCCTCCATG CATTCTCAGC TCAGAATCCT GGATGAGGAG CATCCCAAGG 360
GAAAGTACCA TCATGGCTTG AGTGCTCTGA AGCCCATCCG GACTACTTCC AAACACCAGC 420
ACCCAGTGGA CAATGCTGGG CTTTTTTCCT GTATGACTTT TTCGTGGCTT TCTTCTCTGG 480
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AAGTTGGGCC AGACGCTGCT TCCCTGCGAA GGGTTGTGTG GATCTTCTGC CGCACCAGGC 660
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TCATGGTGAA ACACCTCTTG GAGTATACCC AGGCAACAGA GTCTAACCTG CAGTACAGCT 780
TGTTGTTAGT GCTGGGCCTC CTCCTGACGG AAATCGTGCG GTCTTGGTCG CTTGCACTGA 840
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GCTTCCTGGG ATCAGCTGTT TTTATCCTCT TTTACCCAGC AATGATGTTT GCATCACGGC 1140
TCACAGCATA TTTCAGGAGA AAATGCGTGG CCGCCACGGA TGAACGTGTC CAGAAGATGA 1200
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ACAGCATCGA TCTGGAGATC CAAGAGGGTA AACTGGTTGG AATCTGCGGC AGTGTGGGAA 1920
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GGTTGAGTTA CTGGATCAAG CAAGGAAGCG GGAACACCAC TGTGACTCGA GGGAACGAGA 2820
CCTCGGTGAG TGACAGCATG AAGGACAATC CTCATATGCA GTACTATGCC AGCATCTACG 2880
CCCTCTCCAT GGCAGTCATG CTGATCCTGA AAGCCATTCG AGGAGTTGTC TTTGTCAAGG 2940
GCACGCTGCG AGCTTCCTCC CGGCTGCATG ACGAGCTTTT CCGAAGGATC CTTCGAAGCC 3000
CTATGAAGTT TTTTGACACG ACCCCCACAG GGAGGATTCT CAACAGGTTT TCCAAAGACA 3060
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GGCCCCTTGT CATCCTCTTT TCAGTCCTGC ACATTGTCTC CAGGGTCCTG ATTCGGGAGC 3240
TGAAGCGTCT GGACAATATC ACGCAGTCAC CTTTCCTCTC CCACATCACG TCCAGCATAC 3300
AGGGCCTTGC CACCATCCAC GCCTACAATA AAGGGCAGGA GTTTCTGCAC AGATACCAGG 3360
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CTGTCCTGGT GTCACTTACT GTTTCTGTCA GGAGAGCAGC GGGGCGAAGC CCAGGCCCCT 5160
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TTTCCTGCCT TCTTCTTTTT GCTGTTGTTT CTAAACAAGA ATCAGTCTAT CCACAGAGAG 5280
TCCCACTGCC TCAGGTTCCT ATGGCTGGCC ACTGCACAGA GCTCTCCAGC TCCAAGACCT 5340

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GTTGGTTCCA AGCCCTGGAG CCAACTGCTG CTTTTTGAGG TGGCACTTTT TCATTTGCCT  5400
ATTCCCACAC CTCCACAGTT CAGTGGCAGG GCTCAGGATT TCGTGGGTCT GTTTTCCTTT  5460
CTCACCGCAG TCGTCGCACA GTCTCTCTCT CTCTCTCCCC TCAAAGTCTG CAACTTTAAG  5520
CAGCTCTTGC TAATCAGTGT CTCACACTGG CGTAGAAGTT TTTGTACTGT AAAGAGACCT  5580
ACCTCAGGTT GCTGGTTGCT GTGTGGTTTG GTGTGTTCCC GCAAACCCCC TTTGTGCTGT  5640
GGGGCTGGTA GCTCAGGTGG GCGTGGTCAC TGCTGTCATC AGTTGAATGG TCAGCGTTGC  5700
ATGTCGTGAC CAACTAGACA TTCTGTCGCC TTAGCATGTT TGCTGAACAC CTTGTGGAAG  5760
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AAAAAAAAAA AAAAAAAA
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Seq ID NO: 194 Protein sequence:
Protein Accession #: NP_005679.1

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LDASMHSQLR ILDEEHPKGK YHHGLSALKP IRTTSKHQHP VDNAGLFSCM TFSWLSSLAR   120
VAHKKGELSM EDVWSLSKHE SSDVNCRRLE RLWQEELNEV GPDAASLRRV VWIFCRTRLI   180
LSIVCLMITQ LAGFSGPAFM VKHLLEYTQA TESNLQYSLL LVLGLLLTEI VRSWSLALTW   240
ALNYRTGVRL RGAILTMAFK KILKLKNIKE KSLGELINIC SNDGQRMFEA AAVGSLLAGG   300
PVVAILGMIY NVIILGPTGF LGSAVFILFY PAMMFASRLT AYFRRKCVAA TDERVQKMNE   360
VLTYIKFIKM YAWVKAFSQS VQKIREEERR ILEKAGYFQG ITVGVAPIVV VIASVVTFSV   420
HMTLGFDLTA AQAFTVVTVF NSMTFALKVT PFSVKSLSEA SVAVDRFKSL FLMEEVHMIK   480
NKPASPHIKI EMKNATLAWD SSHSSIQNSP KLTPKMKKDK RASRGKKEKV RQLQRTEHQA   540
VLAEQKGHLL LDSDERPSPE EEEGKHIHLG HLRLQRTLHS IDLEIQEGKL VGICGSVGSG   600
KTSLISAILG QMTLLEGSIA ISGTFAYVAQ QAWILNATLR DNILFGKEYD EERYNSVLNS   660
CCLRPDLAIL PSSDLTEIGE RGANLSGGQR QRISLARALY SDRSIYILDD PLSALDAHVG   720
NHIFNSAIRK HLKSKTVLFV THQLQYLVDC DEVIFMKEGC ITERGTHEEL MNLNGDYATI   780
FNNLLLGETP PVEINSKKET SGSQKKSQDK GPKTGSVKKE KAVKPEEGQL VQLEEKGQGS   840
VPWSVYGVYI QAAGGPLAFL VIMALFMLNV GSTAFSTWWL SYWIKQGSGN TTVTRGNETS   900
VSDSMKDNPH MQYYASIYAL SMAVMLILKA IRGVVFVKGT LRASSRLHDE LFRRILRSPM   960
KFFDTTPTGR ILNRFSKDMD EVDVRLPFQA EMFIQNVILV FFCVGMIAGV FPWFLVAVGP  1020
LVILFSVLHI VSRVLIRELK RLDNITQSPF LSHITSSIQG LATIHAYNKG QEFLHRYQEL  1080
LDDNQAPFFL FTCAMRWLAV RLDLISIALI TTTGLMIVLM HGQIPPAYAG LAISYAVQLT  1140
GLFQFTVRLA SETEARFTSV ERINHYIKTL SLEAPARIKN KAPSPDWPQE GEVTFENAEM  1200
RYRENLPLVL KKVSFTIKPK EKIGIVGRTG SGKSSLGMAL FRLVELSGGC IKIDGVRISD  1260
IGLADLRSKL SIIPQEPVLF SGTVRSNLDP FNQYTEDQIW DALERTHMKE CIAQLPLKLE  1320
SEVMENGDNF SVGERQLLCI ARALLRHCKI LILDEATAAM DTETDLLIQE TIREAFADCT  1380
MLTIAHRLHT VLGSDRIMVL AQGQVVEFDT PSVLLSNDSS RFYAMFAAAE NKVAVKG
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Seq ID NO: 195 DNA sequence
Nucleic Acid Accession #: NM_006470
Coding sequence: 228..1922

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TTGCAGCAGC TGCAATCATC TAGGCGTGGT TCTCTTGTCT GACTTGGGCT GCACAGATCC   180
TGGGCCAAGG GACAGAAGAA AGACAGCCTA GGAGCAGAGC CTCCCAGATG GCTGAGTTGG   240
ATCTAATGGC TCCAGGGCCA CTGCCCAGGG CCACTGCTCA GCCCCCAGCC CCTCTCAGCC   300
CAGACTCTGG GTCACCCAGC CCAGATTCTG GGTCAGCCAG CCCAGTGGAA GAAGAGGACG   360
TGGGCTCCTC GGAGAAGCTT GGCAGGGAGA CGGAGGAACA GGACAGCGAC TCTGCAGAGC   420
AGGGGGATCC TGCTGGTGAG GGGAAAGAGG TCCTGTGTGA CTTCTGCCTT GATGACACCA   480
GAAGAGTGAA GGCAGTGAAG TCCTGTCTAA CCTGCATGGT GAATTACTGT GAAGAGCACT   540
TGCAGCCGCA TCAGGTGAAC ATCAAACTGC AAAGCCACCT GCTGACCGAG CCAGTGAAGG   600
ACCACAACTG GCGATACTGC CCTGCCCACC ACAGCCCACT GTCTGCTTTC TGCTGCCCTG   660
ATCAGCAGTG CATCTGCCAG GACTGTTGCC AGGAGCACAG TGGCCACACC ATAGTCTCCC   720
TGGATGCAGC CCGCAGGGAC AAGGAGGCTG AACTCCAGTG CACCCAGTTA GACTTGGAGC   780
GGAAACTCAA GTTGAATGAA AATGCCATCT CCAGGCTCCA GGCTAACCAA AAGTCTGTTC   840
TGGTGTCGGT GTCAGAGGTC AAAGCGGTGG CTGAAATGCA GTTTGGGGAA CTCCTTGCTG   900
CTGTGAGGAA GGCCCAGGCC AATGTGATGC TCTTCTTAGA GGAGAAGGAG CAAGCTGCGC   960
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GCAAGCAGGA GCTGGAGAGG ATGGCGGCCA TCAGCAACAC TGTCCAGTTC TTGGAGGAGT  1080
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ATAAACTCTC GGGCATCCGC AAAGTTATCA CGGAATCCAC TGTACACTTA ATCCAGTTGC  1200
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CTCAAGTGTC TGCCGTTGTT CAGCGCAAAT ATTGGACTTC CAAACCTGAG CCCAGCACCA  1320
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ACCTGCACAG GTACTATTTT GAGGTGGAGA TCTTCGGGGC AGGCACCTAT GTTGGCCTGA  1560
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TCTCCTGGAG CCTCCAATGG AACGGGAAGG AGTTCACGGC CTGGTACAGT GACATGGAGA  1680
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Seq ID NO: 196 Protein sequence:
Protein Accession #: NP_006461

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DSAEQGDPAG EGKEVLCDFC LDDTRRVKAV KSCLTCMVNY CEEHLQPHQV NIKLQSHLLT  120
EPVKDHNWRY CPAHHSPLSA FCCPDQQCIC QDCCQEHSGH TIVSLDAARR DKEAELQCTQ  180
LDLERKLKLN ENAISRLQAN QKSVLVSVSE VKAVAEMQFG ELLAAVRKAQ ANVMLFLEEK  240
EQAALSQANG IKAHLEYRSA EMEKSKQELE RMAAISNTVQ FLEEYCKFKN TEDITFPSVY  300
VGLKDKLSGI RKVITESTVH LIQLLENYKK KLQEFSKEEE YDIRTQVSAV VQRKYWTSKP  360
EPSTREQFLQ YAYDITFDPD TAHKYLRLQE ENRKVTNTTP WEHPYPDLPS RFLHWRQVLS  420
QQSLYLHRYY FEVEIFGAGT YVGLTCKGID RKGEERNSCI SGNNFSWSLQ WNGKEFTAWY  480
SDMETPLKAG PFRRLGVYID FPGGILSFYG VEYDTMTLVH KFACKFSEPV YAAFWLSKKE  540
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Seq ID NO: 197 DNA sequence
Nucleic Acid Accession #: NM_004316
Coding sequence: 433-1149

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GGAGGAGGGG AGGGAGGAGG AGGCGGCGTG CAGGGAGGAG AAAAAGCATT TTCACCTTTT   240
TTGCTCCCAC TCTAAGAAGT CTCCCGGGGA TTTTGTATAT ATTTTTTAAC TTCCGTCAGG   300
GCTCCCGCTT CATATTTCCT TTTCTTTCCC TCTCTGTTCC TGCACCCAAG TTCTCTCTGT   360
GTCCCCCTCG CGGGCCCCGC ACCTCGCGTC CCGGATCGCT CTGATTCCGC GACTCCTTGG   420
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CAGCAGCAGC AGCAGCAGCA GCAGGCGCCG CAGCTGAGAC CGGCGGCCGA CGGCCAGCCC   660
TCAGGGGGCG GTCACAAGTC AGCGCCCAAG CAAGTCAAGC GACAGCGCTC GTCTTCGCCC   720
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CAGCAGCCGG CCGCCGTGGC GCGCCGCAAC GAGCGCGAGC GCAACCGCGT CAAGTTGGTC   840
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AGTAAGGTGG AGACACTGCG CTCGGCGGTC GAGTACATCC GCGCGCTGCA GCAGCTGCTG   960
GACGAGCATG ACGCGGTGAG CGCCGCCTTC CAGGCAGGCG TCCTGTCGCC CACCATCTCC  1020
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GAGCAGCACA CGCGTTATAG TAACTCCCAT CACCTCTAAC ACGCACAGCT GAAAGTTCTT  1560
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Seq ID NO: 198 Protein sequence:
Protein Accession #: NP_004307

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MESSAKMESG GAGQQPQPQP QQPFLPPAAC FFATAAAAAA AAAAAAAQSA QQQQQQQQQQ   60
QQQQAPQLRP AADGQPSGGG HKSAPKQVKR QRSSSPELMR CKRRLNFSGF GYSLPQQQPA  120
AVARRNERER NRVKLVNLGF ATLREHVPNG AANKKMSKVE TLRSAVEYIR ALQQLLDEHD  180
AVSAAFQAGV LSPTISPNYS NDLNSMAGSP VSSYSSDEGS YDPLSPEEQE LLDFTNWF
```

Seq ID NO: 199 DNA sequence
Nucleic Acid Accession #: NM_007015
Coding sequence: 1-1005

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGACAGAGA ACTCCGACAA AGTTCCCATT GCCCTGGTGG GACCTGATGA CGTGGAATTC    60
TGCAGCCCCC CGGCGTACGC TACGCTGACG GTGAAGCCCT CCAGCCCCGC GCGGCTGCTC   120
AAGGTGGGAG CCGTGGTCCT CATTTCGGGA GCTGTGCTGC TGCTCTTTGG GGCCATCGGG   180
GCCTTCTACT TCTGGAAGGG GAGCGACAGT CACATTTACA ATGTCCATTA CACCATGAGT   240
ATCAATGGGA AACTACAAGA TGGGTCAATG GAAATAGACG CTGGGAACAA CTTGGAGACC   300
TTTAAAATGG GAAGTGGAGC TGAAGAAGCA ATTGCAGTTA ATGATTTCCA GAATGGCATC   360
ACAGGAATTC GTTTTGCTGG AGGAGAGAAG TGCTACATTA AAGCGCAAGT GAAGGCTCGT   420
ATTCCTGAGG TGGGCGCCGT GACCAAACAG AGCATCTCCT CCAAACTGGA AGGCAAGATC   480
ATGCCAGTCA AATATGAAGA AAATTCTCTT ATCTGGGTGG CTGTAGATCA GCCTGTGAAG   540
GACAACAGCT TCTTGAGTTC TAAGGTGTTA GAACTCTGCG GTGACCTTCC TATTTTCTGG   600
CTTAAACCAA CCTATCCAAA AGAAATCCAG AGGGAAAGAA GAGAAGTGGT AAGAAAAATT   660
GTTCCAACTA CCACAAAAAG ACCACACAGT GGACCACGGA GCAACCCAGG CGCTGGAAGA   720
CTGAATAATG AAACCAGACC CAGTGTTCAA GAGGACTCAC AAGCCTTCAA TCCTGATAAT   780
```

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CCTTATCATC AGCAGGAAGG GGAAAGCATG ACATTCGACC CTAGACTGGA TCACGAAGGA   840
ATCTGTTGTA TAGAATGTAG GCGGAGCTAC ACCCACTGCC AGAAGATCTG TGAACCCCTG   900
GGGGGCTATT ACCCATGGCC TTATAATTAT CAAGGCTGCC GTTCGGCCTG CAGAGTCATC   960
ATGCCATGTA GCTGGTGGGT GGCCCGTATC TTGGGCATGG TGTGAAATCA CTTCATATAT  1020
CACGTGCTGT AAAATAAGAA CTAGCTGAAG AGACAACCAA AGAAGCATTA AGGCAGGTTG  1080
ATGCTGATGG GACCATAAAA TATTTTTACA CGCAGCCTGA GCGGTTATTC TTGACACTCT  1140
TAACAGAATT TTTTTAATCG TTTTCCAGAA CTTTAGTATA TGCAAATGCA CTGAAAGGGT  1200
AGTTCAAGTC TAAAATGCCA TAACCCCGTT ATTTGTTATT TTTTATTTGC ATTGATTTGC  1260
CATAAGTCTT CCCTTGCTTG CATCTTCCAA AGCTATTTCG AAATAAACAC GAAAATTTAC  1320
AGTTTGCC
```

Seq ID NO: 200 Protein sequence:
Protein Accession #: NP_008946

```
1          11         21         31         41         51
|          |          |          |          |          |
MTENSDKVPI ALVGPDDVEF CSPPAYATLT VKPSSPARLL KVGAVVLISG AVLLLFGAIG    60
AFYFWKGSDS HIYNVHYTMS INGKLQDGSM EIDAGNNLET FKMGSGAEEA IAVNDFQNGI   120
TGIRFAGGEK CYIKAQVKAR IPEVGAVTKQ SISSKLEGKI MPVKYEENSL IWVAVDQPVK   180
DNSFLSSKVL ELCGDLPIFW LKPTYPKEIQ RERREVVRKI VPTTTKRPHS GPRSNPGAGR   240
LNNETRPSVQ EDSQAFNPDN PYHQQEGESM TFDPRLDHEG ICCIECRRSY THCQKICEPL   300
GGYYPWPYNY QGCRSACRVI MPCSWWVARI LGMV
```

Seq ID NO: 201 DNA sequence
Nucleic Acid Accession #: NM_000728.2
Coding sequence: 112..495

```
1          11         21         31         41         51
|          |          |          |          |          |
GTAATAAGAG CGGGGTCTCC GCGGGGAAGG CGCCCACAGC AGGTGTGGTG TTCATCCCGG    60
GTCGACCGGC CGCTCGCGCT GCCCTGAAAC TCTAGTCGCC AGAGAGGCGG CATGGGTTTC   120
CGGAAGTTCT CCCCCTTCCT GGCTCTCAGT ATCTTGGTCC TGTACCAGGC GGGCAGCCTC   180
CAGGCGGCGC CATTCAGGTC TGCCCTGGAG AGCAGCCCAG ACCCGGCCAC ACTCAGTAAA   240
GAGGACGCGC GCCTCCTGCT GGCTGCACTG GTGCAGGACT ATGTGCAGAT GAAGGCCAGT   300
GAGCTGAAGC AGGAGCAGGA GACACAGGGC TCCAGCTCCG CTGCCCAGAA GAGAGCCTGC   360
AACACTGCCA CCTGTGTGAC TCATCGGCTG GCAGGCTTGC TGAGCAGATC AGGGGGCATG   420
GTGAAGAGCA ACTTCGTGCC CACCAATGTG GGTTCCAAAG CCTTTGGCAG GCGCCGCAGG   480
GACCTTCAAG CCTGAGCAGA TGAATGACTC CAGGAAGAAG GTGTGTCCTA AATCCAATGA   540
CATATCCTTA TAAGAGATTC ACTCAGAAGA CACATGTGGA GAAGGTGACA TGACAGAGGC   600
AAGGAGGCAC AAGCCAAGGA AGTCTGTGTC TACCAGAAGC CAGAATCACA GAACAGTCTC   660
TGGAAGAAGA GCAGCCCTGC TGACACCTAG AGTTTGGACT TCCAGCTTCC AGAACTGTGA   720
GAGAATAATT TCTGTTGTTT TAAGCCACAA AGTTTGTGGT AATTTGTTAT GACAGCCCTA   780
GGAAACTAAT ACAATACATT TTCATTTATT TTGGGTAAAT GCCTTGGAGT GGGATTGCTG   840
GGTTATTTGG AAAGTGTGTA TTTAACTCTG TAAGAAACTG CCAAACTATT TTCTGAAGTG   900
ACTGTACCAC TTCGCCTTCT TGCCAGCCAC ATATGAGAGC TCTAGTATTT CCACAAATAG   960
GTATGTAGCA GTATCTCATT GCTGTTTTAA TTTGTATTTC CCCAATGACT AATGACGTTG  1020
AGCATCTATT TTACCATATG TTTATCACCT TTATTGAAGG GTCTGTTTAA ATCTTCTGCT  1080
AAATTTTTGT TGGCTTGCTT GCTTTATTAG TGTTGAGTTT TTAGAGCTCT TTATATGTTG  1140
TGGATGCAAG ATTGTTTTCA GATATATAGT TTGGAAACTT CCTTCCCCTG AATCTGCGGA  1200
TTGCTTTTTC ATTTTCTTAG CAGTGTCTCT CACAGAGAAA AAGTTGTAAT TTGAATAAGA  1260
TCCAATTCAT CTTTTTTTTT CTTTTATGTA TTGTGCTTTT AGTTCATGTC TAAGAACTCT  1320
TTGCCTAACT AAGGTCCCAA GGTCACAATA ACCTTATTCT ATACTTTCTT GTAAAAGTTT  1380
TATAGTTTTA TATTTTATAT GTAGATTAGT GATCTATTTT GAGTTAATTT TTGTATAAGG  1440
TGAGAGGTGT AGGTTGAAAT TCATACCTGT GAATATAGAT ACCCAATTGT TTCAGTGCCA  1500
TTTGTTAAAA AGACTGTTAT TTCACCATTT AATTGCCCCT GCACCTTTGT CAAAAAGCAA  1560
CTGATCATAT TTGTGTGGGT ATATTTCTGG GTTCTCAATT CTGTCTCATT GATTGATTTG  1620
ACCATTCTTT TGCCAATGTC ATACTGCCTT GATTAGTGTA GTGTTAAAGT GAATCTCAAA  1680
ACCAGATAAT GTGGGTCTAC CAACATTGTT CATTCTTGTT CAAAAAGATT TTAGCTACAT  1740
CTAAAATATT TTCTACATCT TTTATACATT TTAGAATCAG TGTGTTACTA TCTACAAAAT  1800
TTCTGATGAG ATTTTTAATG GGATTGTGTT AAATCAGTGG GTTAATTTTG GGAGAATTAG  1860
CATATTAATA ATATTAAGTC GTTCAATTCA TGAACACAAT ACATGTTTTC ACTTATTTAG  1920
GTTTTCTCTG TTTTTTTTTT TTTAACAGTG TTCTCAGTTT TCAACAGAAA TATTCTACAC  1980
ATATCTTGTT AGATTTTTAA CTATTTTATT TTTTGGTGCT AATGTAAATG GTACTTAAAC  2040
ATTTTTGTTT TTAATTGTTC ATTGCTAGTA GATAGAAATA CAATATTTAA AATATTAGGA  2100
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
```

Seq ID NO: 202 Protein sequence:
Protein Accession #: NP_000719.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MGFRKFSPFL ALSILVLYQA GSLQAAPFRS ALESSPDPAT LSKEDARLLL AALVQDYVQM    60
KASELKQEQE TQGSSSAAQK RACNTATCVT HRLAGLLSRS GGMVKSNFVP TNVGSKAFGR   120
RRRDLQA
```

Seq ID NO: 203 DNA sequence
Nucleic Acid Accession #: NM_001741
Coding sequence: 71..496

```
1          11         21         31         41         51
|          |          |          |          |          |
CTCTGGCTGG ACGCCGCCGC CGCCGCTGCC ACCGCCTCTG ATCCAAGCCA CCTCCCGCCA    60
GAGAGGTGTC ATGGGCTTCC AAAAGTTCTC CCCCTTCCTG GCTCTCAGCA TCTTGGTCCT   120
GTTGCAGGCA GGCAGCCTCC ATGCAGCACC ATTCAGGTCT GCCCTGGAGA GCAGCCCAGC   180
AGACCCGGCC ACGCTCAGTG AGGACGAAGC GCGCCTCCTG CTGGCTGCAC TGGTGCAGGA   240
CTATGTGCAG ATGAAGGCCA GTGAGCTGGA GCAGGAGCAA GAGAGAGAGG GCTCCAGCCT   300
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GGACAGCCCC AGATCTAAGC GGTGCGGTAA TCTGAGTACT TGCATGCTGG GCACATACAC    360
GCAGGACTTC AACAAGTTTC ACACGTTCCC CCAAACTGCA ATTGGGGTTG GAGCACCTGG    420
AAAGAAAAGG GATATGTCCA GCGACTTGGA GAGAGACCAT CGCCCTCATG TTAGCATGCC    480
CCAGAATGCC AACTAAACTC CTCCCTTTCC TTCCTAATTT CCCTTCTTGC ATCCTTCCTA    540
TAACTTGATG CATGTGGTTT GGTTCCTCTC TGGTGGCTCT TTGGGCTGGT ATTGGTGGCT    600
TTCCTTGTGG CAGAGGATGT CTCAAACTTC AGATGGGAGG AAAGAGAGCA GGACTCACAG    660
GTTGGAAGAG AATCACCTGG GAAAATACCA GAAAATGAGG GCCGCTTTGA GTCCCCCAGA    720
GATGTCATCA GAGCTCCTCT GTCCTGCTTC TGAATGTGCT GATCATTTGA GGAATAAAAT    780
TATTTTTCCC C
```

Seq ID NO: 204 Protein sequence:
Protein Accession #: NP_001732

```
1          11         21         31         41         51
|          |          |          |          |          |
MGFQKFSPFL ALSILVLLQA GSLHAAPFRS ALESSPADPA TLSEDEARLL LAALVQDYVQ     60
MKASELEQEQ EREGSSLDSP RSKRCGNLST CMLGTYTQDF NKFHTFPQTA IGVGAPGKKR    120
DMSSDLERDH RPHVSMPQNA N
```

Seq ID NO: 205 DNA sequence
Nucleic Acid Accession #: NM_005361
Coding sequence: 1-945

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGCCTCTTG AGCAGAGGAG TCAGCACTGC AAGCCTGAAG AAGGCCTTGA GGCCCGAGGA     60
GAGGCCCTGG GCCTGGTGGG TGCGCAGGCT CCTGCTACTG AGGAGCAGCA GACCGCTTCT    120
TCCTCTTCTA CTCTAGTGGA AGTTACCCTG GGGGAGGTGC CTGCTGCCGA CTCACCGAGT    180
CCTCCCCACA GTCCTCAGGG AGCCTCCAGC TTCTCGACTA CCATCAACTA CACTCTTTGG    240
AGACAATCCG ATGAGGGCTC CAGCAACCAA GAAGAGGAGG GGCCAAGAAT GTTTCCCGAC    300
CTGGAGTCCG AGTTCCAAGC AGCAATCAGT AGGAAGATGG TTGAGTTGGT TCATTTTCTG    360
CTCCTCAAGT ATCGAGCCAG GGAGCCGGTC ACAAAGGCAG AAATGCTGGA GAGTGTCCTC    420
AGAAATTGCC AGGACTTCTT TCCCGTGATC TTCAGCAAAG CCTCCGAGTA CTTGCAGCTG    480
GTCTTTGGCA TCGAGGTGGT GGAAGTGGTC CCCATCAGCC ACTTGTACAT CCTTGTCACC    540
TGCCTGGGCC TCTCCTACGA TGGCCTGCTG GGCGACAATC AGGTCATGCC CAAGACAGGC    600
CTCCTGATAA TCGTCCTGGC CATAATCGCA ATAGAGGGCG ACTGTGCCCC TGAGGAGAAA    660
ATCTGGGAGG AGCTGAGTAT GTTGGAGGTG TTTGAGGGGA GGGAGGACAG TGTCTTCGCA    720
CATCCCAGGA AGCTGCTCAT GCAAGATCTG GTGCAGGAAA ACTACCTGGA GTACCGGCAG    780
GTGCCCGGCA GTGATCCTGC ATGCTACGAG TTCCTGTGGG GTCCAAGGGC CCTCATTGAA    840
ACCAGCTATG TGAAAGTCCT GCACCATACA CTAAAGATCG GTGGAGAACC TCACATTTCC    900
TACCCACCCC TGCATGAACG GGCTTTGAGA GAGGGAGAAG AGTGA
```

Seq ID NO: 206 Protein sequence:
Protein Accession #: NP_005352

```
1          11         21         31         41         51
|          |          |          |          |          |
MPLEQRSQHC KPEEGLEARG EALGLVGAQA PATEEQQTAS SSSTLVEVTL GEVPAADSPS     60
PPHSPQGASS FSTTINYTLW RQSDEGSSNQ EEEGPRMFPD LESEFQAAIS RKMVELVHFL    120
LLKYRAREPV TKAEMLESVL RNCQDFFPVI FSKASEYLQL VFGIEVVEVV PISHLYILVT    180
CLGLSYDGLL GDNQVMPKTG LLIIVLAIIA IEGDCAPEEK IWEELSMLEV FEGREDSVFA    240
HPRKLLMQDL VQENYLEYRQ VPGSDPACYE FLWGPRALIE TSYVKVLHHT LKIGGEPHIS    300
YPPLHERALR EGEE
```

Seq ID NO: 207 DNA sequence
Nucleic Acid Accession #: NM_021115
Coding sequence: 743-2893

```
1          11         21         31         41         51
|          |          |          |          |          |
AAAGGAAGGG AGGGAGGGAG AAAGGAGAAG TTGGTTTAGA GGCCAGCCGG ACGAGCTTTG     60
GGCACCGCCC TTAGGAGGGC CACCCTCAGA GTCTGACAGC AGGTGAAGGT CCTAAATCTC    120
CCCAAACTAA CTGGTGTCTT TTCTCCTCTT CCAAGATGCT CTTCCCGAGG GAGATGCTAG    180
CCCTTTGGGT CCTTACCTCC TGCCCTCAGG AGCCCCGGAG AGAGGCAGTC CTGGCAAAGA    240
GCACCCTGAA GAGAGAGTGG TAACAGCGCC CCCCAGTTCC TCACAGTCGG CGGAAGTGCT    300
GGGCGAGCTG GTGCTGGATG GGACCGCACC CTCTGCACAT CACGACATCC CAGCCCTGTC    360
ACCGCTGCTT CCAGAGGAGG CCCGCCCCAA GCACGCCTTG CCCCCCAAGA AGAAACTGCC    420
TTCGCTCAAG CAGGTGAACT CTGCCAGGAA GCAGCTGAGG CCCAAGGCCA CCTCCGCAGC    480
CACTGTCCAA AGGGCAGGGT CCCAGCCAGC GTCCCAGGGC CTAGATCTCC TCTCCTCCTC    540
CACGGAGAAG CCTGGCCCAC CGGGGGACCC GGACCCCATC GTGGCCTCCG AGGAGGCATC    600
AGAAGTGCCC CTTTGGCTGG ACCGAAAGGA GAGTGCGGTC CCTACAACAC CCGCACCCCT    660
GCAAATCTCC CCCTTCACTT CGCAGCCCTA TGTGGCCCAC ACACTCCCCC AGAGGCCAGA    720
ACCCGGGGAG CCTGGGCCTG ACATGGCCCA GGAGGCCCCC CAGGAGGACA CCAGCCCCAT    780
GGCCCTGATG GACAAAGGTG AGAATGAGCT GACTGGGTCA GCCTCAGAGG AGAGCCAGGA    840
GACCACTACC TCCACCATTA TCACCACCAC GGTCATCACC ACCGAGCAGG CACCAGCTCT    900
CTGCAGTGTG AGCTTCTCCA ATCCTGAGGG GTACATTGAC TCCAGCGACT ACCCACTGCT    960
GCCCCTCAAC AACTTTCTGG AGTGCACATA CAACGTGACA GTCTACACTG GCTATGGGGT   1020
GGAGCTCCAG GTGAAGAGTG TGAACCTGTC CGATGGGGAA CTGCTCTCCA TCCGCGGGGT   1080
GGACGGCCCT ACCCTGACCG TCCTGGCCAA CCAGACACTC CTGGTGGAGG GGCAGGTAAT   1140
CCGAAGCCCC ACCAACACCA TCTCCGTCTA CTTCCGGACC TTCCAGGACG ACGGCCTTGG   1200
GACCTTCCAG CTTCACTACC AGGCCTTCAT GCTGAGCTGC AACTTTCCCC GCCGGCCTGA   1260
CTCTGGGGAT GTCACGGTGA TGGACCTGCA CTCAGGTGGG GTGGCCCACT TTCACTGCCA   1320
CCTGGGCTAT GAGCTCCAGG GCGCTAAGAT GCTGACATGC ATCAATGCCT CCAAGCCGCA   1380
CTGGAGCAGC CAGGAGCCCA TCTGCTCAGC TCCTTGTGGA GGGGCAGTGC ACAATGCCAC   1440
CATCGGCCGC GTCCTCTCCC CAAGTTACCC TGAAAACACA AATGGGAGCC AATTCTGCAT   1500
CTGGACGATT GAAGCTCCAG AGGGCCAGAA GCTGCACCTG CACTTTGAGA GGCTGTTGCT   1560
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GCATGACAAG GACAGGATGA CGGTTCACAG CGGGCAGACC AACAAGTCAG CTCTTCTCTA  1620
CGACTCCCTT CAAACCGAGA GTGTCCCTTT TGAGGGCCTG CTGAGCGAAG GCAACACCAT  1680
CCGCATCGAG TTCACGTCCG ACCAGGCCCG GGCGGCCTCC ACCTTCAACA TCCGATTTGA  1740
AGCGTTTGAG AAAGGCCACT GCTATGAGCC CTACATCCAG AATGGGAACT TCACTACATC  1800
CGACCCGACC TATAACATTG GGACTATAGT GGAGTTCACC TGCGACCCCG GCCACTCCCT  1860
GGAGCAGGGC CCGGCCATCA TCGAATGCAT CAATGTGCGG GACCCATACT GGAATGACAC  1920
AGAGCCCCTG TGCAGAGCCA TGTGTGGTGG GGAGCTCTCT GCTGTGGCTG GGGTGGTATT  1980
GTCCCCAAAC TGGCCCGAGC CCTACGTGGA AGGTGAAGAT TGTATCTGGA AGATCCACGT  2040
GGGAGAAGAG AAACGGATCT TCTTAGATAT CCAGTTCCTG AATCTGAGCA ACAGTGACAT  2100
CTTGACCATC TACGATGGCG ACGAGGTCAT GCCCCACATC TTGGGGCAGT ACCTTGGGAA  2160
CAGTGGCCCC CAGAAACTGT ACTCCTCCAC GCCAGACTTA ACCATCCAGT TCCATTCGGA  2220
CCCTGCTGGC CTCATCTTTG GAAAGGGCCA GGGATTTATC ATGAACTACA TAGAGGTATC  2280
AAGGAATGAC TCCTGCTCGG ATTTACCCGA GATCCAGAAT GGCTGGAAAA CCACTTCTCA  2340
CACGGAGTTG GTGCGGGGAG CCAGAATCAC CTACCAGTGT GACCCCGGCT ATGACATCGT  2400
GGGGAGTGAC ACCCTCACCT GCCAGTGGGA CCTCAGCTGG AGCAGCGACC CCCCATTTTG  2460
TGAGAAAATT ATGTACTGCA CCGACCCCGG AGAGGTGGAT CACTCGACCC GCTTAATTTC  2520
GGATCCTGTG CTGCTGGTGG GGACCACCAT CCAATACACC TGCAACCCCG GTTTTGTGCT  2580
TGAAGGGAGT TCTCTTCTGA CCTGCTACAG CCGTGAAACA GGGACTCCCA TCTGGACGTC  2640
TCGCCTGCCC CACTGCGTTT CAGAAGCGGC AGCAGAGACG TCGCTGGAAG GGGGGAACAT  2700
GGCCCTGGCT ATCTTCATCC CGGTCCTCAT CATCTCCTTA CTGCTGGGAG GAGCCTACAT  2760
TTACATCACA AGATGTCGCT ACTATTCCAA CCTCCGCCTG CCTCTGATGT ACTCCCACCC  2820
CTACAGCCAG ATCACCGTGG AAACCGAGTT TGACAACCCC ATTTACGAGA CAGGGGGAAC  2880
CCAAAAGGTT TAGGGTTTCA TTTAAAAAGA GGTACCCTTT AAAAAGGGGC TTGTGAACTC  2940
AACCCCAATT TCCCCGAGAC ATTTATCCAA AGGCCCTGGG GGCCTTGATT TAAACCCCCA  3000
AAAGGCGGCT GTTTTTTGGT TAAACTTTTT AACAAAGGGT TACGGGTTTT TTCCCCGGAT  3060
TTTATAAATT TTAAAAGTG
```

Seq ID NO: 208 Protein sequence:
Protein Accession #: NP_066938

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1          11         21         31         41         51
|          |          |          |          |          |
MAQEAPQEDT SPMALMDKGE NELTGSASEE SQETTTSTII TTTVITTEQA PALCSVSFSN    60
PEGYIDSSDY PLLPLNNFLE CTYNVTVYTG YGVELQVKSV NLSDGELLSI RGVDGPTLTV   120
LANQTLLVEG QVIRSPTNTI SVYFRTFQDD GLGTFQLHYQ AFMLSCNFPR RPDSGDVTVM   180
DLHSGGVAHF HCHLGYELQG AKMLTCINAS KPHWSSQEPI CSAPCGGAVH NATIGRVLSP   240
SYPENTNGSQ FCIWTIEAPE GQKLHLHFER LLLHDKDRMT VHSGQTNKSA LLYDSLQTES   300
VPFEGLLSEG NTIRIEFTSD QARAASTFNI RFEAFEKGHC YEPYIQNGNF TTSDPTYNIG   360
TIVEFTCDPG HSLEQGPAII ECINVRDPYW NDTEPLCRAM CGGELSAVAG VVLSPNWPEP   420
YVEGEDCIWK IHVGEEKRIF LDIQFLNLSN SDILTIYDGD EVMPHILGQY LGNSGPQKLY   480
SSTPDLTIQF HSDPAGLIFG KGQGFIMNYI EVSRNDSCSD LPEIQNGWKT TSHTELVRGA   540
RITYQCDPGY DIVGSDTLTC QWDLSWSSDP PFCEKIMYCT DPGEVDHSTR LISDPVLLVG   600
TTIQYTCNPG FVLEGSSLLT CYSRETGTPI WTSRLPHCVS EAAAETSLEG GNMALAIFIP   660
VLIISLLLGG AYIYITRCRY YSNLRLPLMY SHPYSQITVE TEFDNPIYET GGTQKV
```

Seq ID NO: 209 DNA sequence
Nucleic Acid Accession #: NM_001327.1
Coding sequence: 89-631

```
1          11         21         31         41         51
|          |          |          |          |          |
AGCAGGGGGC GCTGTGTGTA CCGAGAATAC GAGAATACCT CGTGGGCCCT GACCTTCTCT    60
CTGAGAGCCG GGCAGAGGCT CCGGAGCCAT GCAGGCCGAA GGCCGGGGCA CAGGGGGTTC   120
GACGGGCGAT GCTGATGGCC CAGGAGGCCC TGGCATTCCT GATGGCCCAG GGGGCAATGC   180
TGGCGGCCCA GGAGAGGCGG GTGCCACGGG CGGCAGAGGT CCCCGGGGCG CAGGGGCAGC   240
AAGGGCCTCG GGGCCGGGAG GAGGCGCCCC GCGGGGTCCG CATGGCGGCG CGGCTTCAGG   300
GCTGAATGGA TGCTGCAGAT GCGGGGCCAG GGGGCCGGAG AGCCGCCTGC TTGAGTTCTA   360
CCTCGCCATG CCTTTCGCGA CACCCATGGA AGCAGAGCTG GCCCGCAGGA GCCTGGCCCA   420
GGATGCCCCA CCGCTTCCCG TGCCAGGGGT GCTTCTGAAG GAGTTCACTG TGTCCGGCAA   480
CATACTGACT ATCCGACTGA CTGCTGCAGA CCACCGCCAA CTGCAGCTCT CCATCAGCTC   540
CTGTCTCCAG CAGCTTTCCC TGTTGATGTG GATCACGCAG TGCTTTCTGC CCGTGTTTTT   600
GGCTCAGCCT CCCTCAGGGC AGAGGCGCTA AGCCCAGCCT GGCGCCCCTT CCTAGGTCAT   660
GCCTCCTCCC CTAGGGAATG GTCCCAGCAC GAGTGGCCAG TTCATTGTGG GGGCCTGATT   720
GTTTGTCGCT GGAGGAGGAC GGCTTACATG TTTGTTTCTG TAGAAAATAA AACTGAGCTA
```

Seq ID NO: 210 Protein sequence:
Protein Accession #: NP_001318.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MQAEGRGTGG STGDADGPGG PGIPDGPGGN AGGPGEAGAT GGRGPRGAGA ARASGPGGGA    60
PRGPHGGAAS GLNGCCRCGA RGPESRLLEF YLAMPFATPM EAELARRSLA QDAPPLPVPG   120
VLLKEFTVSG NILTIRLTAA DHRQLQLSIS SCLQQLSLLM WITQCFLPVF LAQPPSGQRR
```

Seq ID NO: 211 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 52-459

```
1          11         21         31         41         51
|          |          |          |          |          |
CCTCGTGGGC CCTGACCTTC TCTCTGAGAG CCGGGCAGAG GCTCCGGAGC CATGCAGGCC    60
GAAGGCCAGG GCACAGGGGG TTCGACGGGC GATGCTGATG GCCCAGGAGG CCCTGGCATT   120
CCTGATGGCC CAGGGGGCAA TGCTGGCGGC CCAGGAGAGG CGGGTGCCAC GGGCGGCAGA   180
GGTCCCCGGG GCGCAGGGGC AGCAAGGGCC TCGGGGCCGA GAGGAGGCGC CCCGCGGGGT   240
CCGCATGGCG GTGCCGCTTC TGCGCAGGAT GGAAGGTGCC CCTGCGGGGC CAGGAGGCCG   300
```

GACAGCCGCC TGCTTCAGTT CCGACTGACT GCTGCAGACC ACCGCCAACT GCAGCTCTCC 360
ATCAGCTCCT GTCTCCAGCA GCTTTCCCTG TTGATGTGGA TCACGCAGTG CTTTCTGCCC 420
GTGTTTTTGG CTCAGGCTCC CTCAGGGCAG AGGCGCTAAG CCCAGCCTGG CGCCCCTTCC 480
TAGGTCATGC CTCCTCCCCT AGGGAATGGT CCCAGCACGA GTGGCCAGTT CATTGTGGGG 540
GCCTGATTGT TTGTCGCTGG AGGAGGACGG CTTACATGTT TGTTTCTGTA GAAAATAAAG 600
CTGAGCTA

Seq ID NO: 212 Protein sequence:
Protein Accession #: Eos sequence

1 11 21 31 41 51
| | | | | |
MQAEGQGTGG STGDADGPGG PGIFDGPGGN AGGPGEAGAT GGRGPRGAGA ARASGPRGGA 60
PRGPHGGAAS AQDGRCPCGA RRPDSRLLQF RLTAADHRQL QLSISSCLQQ LSLLMWITQC 120
FLPVFLAQAP SGQRR

Seq ID NO: 213 DNA sequence
Nucleic Acid Accession #: NM_000555
Coding sequence: 416..1498

1 11 21 31 41 51
| | | | | |
CTTATTTTTT ATGAATGTCG GATAGCTGCA CCAGCTTGGT GGGGAAAGGG TTTGATGAAT 60
AGCACAAAGA CACTGGCTGT TCCCTGGAGG CTGTCCCTTT AAAGGAGAAT CTTAGTTTAT 120
TCTGGGGGGA GGGGATGCAC ACATTAGAGT AGGAAAGAGG GCTTGGAATA AAATGAAAAC 180
ACTCCCCCTT CATAGTCATT GTACTGAAAT GCAAAGACTG CTTCCTAAGC TGGAGATGCT 240
AACCTTGGGT AGCTCCTTCT GTTCTCTTCA AGGGGAATTT TGTCAGGCTA TGGATTCATT 300
TACAACTGTT AGTCATGTGG GCATGTGTGA GGAAACAGAT GCCAGTTTTA ATGTATTTAG 360
CCCGAAGTTC CAATTTGATA GGAGCCACTG TCAGTCTCTG AGGTTCCACC AAAATATGGA 420
ACTTGATTTT GGACACTTTG ACGAAAGAGA TAAGACATCC AGGAACATGC GAGGCTCCCG 480
GATGAATGGG TTGCCTAGCC CCACTCACAG CGCCCACTGT AGCTTCTACC GAACCAGAAC 540
CTTGCAGGCA CTGAGTAATG AGAAGAAAGC CAAGAAGGTA CGTTTCTACC GCAATGGGGA 600
CCGCTACTTC AAGGGGATTG TGTACGCTGT GTCCTCTGAC CGTTTTCGCA GCTTTGACGC 660
CTTGCTGGCT GACCTGACGC GATCTCTGTC TGACAACATC AACCTGCCTC AGGGAGTGCG 720
TTACATTTAC ACCATTGATG GATCCAGGAA GATCGGAAGC ATGGATGAAC TGGAGGAAGG 780
GGAAAGCTAT GTCTGTTCCT CAGACAACTT CTTTAAAAAG GTGGAGTACA CCAAGAATGT 840
CAATCCCAAC TGGTCTGTCA ACGTAAAAAC ATCTGCCAAT ATGAAAGCCC CCCAGTCCTT 900
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Seq ID NO: 214 Protein sequence:
Protein Accession #: NP_000546

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LVTIIRSGVK PRKAVRVLLN KKTAHSFEQV LTDITEAIKL ETGVVKKLYT LDGKQVTCLH   240
DFFGDDDVFI ACGPEKFRYA QDDFSLDENE CRVMKGNPSA TAGPKASPTP QKTSAKSPGP   300
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Seq ID NO: 215 DNA sequence
Nucleic Acid Accession #: NM_130467
Coding sequence: 312..644

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TCCTGTGGCA CAGTCCGTGG CTTTGAGGGA AAAGGGCCTC GCGGTGGTCC TCCGCCTTCC   240
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TTAAGATAGA GGATGCACCT GGAGATGGTC CTGATGTCAG GGAGGGGACT CTGCCCACTT   600
TTGATCCCAC TAAAGTGCTG GAAGCAGGTG AAGGGCAACT ATAGGTTTAA ACCAAGACAA   660
ATGAAGACTG AAACCAAGAA TATTGTTCTT ATGCTGGAAA TTTGACTGCT AACATTCTCT   720
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Seq ID NO: 216 Protein sequence:
Protein Accession #: NP_569734

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MSEHVTRSQS SERGNDQESS QPVGPVIVQQ PTEEKRQEEE PPTDNQGIAP SGEIKNEGAP    60
AVQGTDVEAF QQELALLKIE DAPGDGPDVR EGTLPTFDPT KVLEAGEGQL
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Seq ID NO: 217 DNA sequence
Nucleic Acid Accession #: NM_001476.1
Coding sequence: 82..435

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GATGAAGTGG AACCAGCAAC ACCTGAAGAA GGGGAACCAG CAACTCAACG TCAGGATCCT   240
GCAGCTGCTC AGGAGGGAGA GGATGAGGGA GCATCTGCAG GTCAAGGGCC GAAGCCTGAA   300
GCTGATAGCC AGGAACAGGG TCACCCACAG ACTGGGTGTG AGTGTGAAGA TGGTCCTGAT   360
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CAATCACAGT GTTAAAAGAA GACACGTTGA AATGATGCAG GCTGCTCCTA TGTTGGAAAT   480
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Seq ID NO: 218 Protein sequence:
Protein Accession #: NP_001467.1

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DEGASAGQGP KPEADSQEQG HPQTGCECED GPDGQEVDPP NPEEVKTPEE GEKQSQC
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Seq ID NO: 219 DNA sequence
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Coding sequence: 90-3671

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GCTTCTCGCT CCTCCTGCCC GCAGCCCGGG CCACCTCCAG GAGGGAAGTC TGTGATTGCA   180
ATGGGAAGTC CAGGCAGTGT ATCTTTGATC GGGAACTTCA CAGACAAACT GGTAATGGAT   240
TCCGCTGCCT CAACTGCAAT GACAACACTG ATGGCATTCA CTGCGAGAAG TGCAAGAATG   300
GCTTTTACCG GCACAGAGAA AGGGACCGCT GTTTGCCCTG CAATTGTAAC TCCAAAGGTT   360
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TGGATGCAGT ACAGATGGTG ATTACAGAAG CCCAGAAGGT TGATACCAGA GCCAAGAACG  3360
CTGGGGTTAC AATCCAAGAC ACACTCAACA CATTAGACGG CCTCCTGCAT CTGATGGACC  3420
AGCCTCTCAG TGTAGATGAA GAGGGGCTGG TCTTACTGGA GCAGAAGCTT TCCCGAGCCA  3480
AGACCCAGAT CAACAGCCAA CTGCGGCCCA TGATGTCAGA GCTGGAAGAG AGGGCACGTC  3540
AGCAGAGGGG CCACCTCCAT TTGCTGGAGA CAAGCATAGA TGGGATTCTG GCTGATGTGA  3600
AGAACTTGGA GAACATTAGG GACAACCTGC CCCCAGGCTG CTACAATACC CAGGCTCTTG  3660
AGCAACAGTG AAGCTGCCAT AAATATTTCT CAACTGAGGT TCTTGGGATA CAGATCTCAG  3720
GGCTCGGGAG CCATGTCATG TGAGTGGGTG GGATGGGGAC ATTTGAACAT GTTTAATGGG  3780
TATGCTCAGG TCAACTGACC TGACCCCATT CCTGATCCCA TGGCCAGGTG GTTGTCTTAT  3840
TGCACCATAC TCCTTGCTTC CTGATGCTGG GCAATGAGGC AGATAGCACT GGGTGTGAGA  3900
ATGATCAAGG ATCTGGACCC CAAAGAATAG ACTGGATGGA AAGACAAACT GCACAGGCAG  3960
ATGTTTGCCT CATAATAGTC GTAAGTGGAG TCCTGGAATT TGGACAAGTG CTGTTGGGAT  4020
ATAGTCAACT TATTCTTTGA GTAATGTGAC TAAAGGAAAA AACTTTGACT TTGCCCAGGC  4080
ATGAAATTCT TCCTAATGTC AGAACAGAGT GCAACCCAGT CACACTGTGG CCAGTAAAAT  4140
ACTATTGCCT CATATTGTCC TCTGCAAGCT TCTTGCTGAT CAGAGTTCCT CCTACTTACA  4200
ACCCAGGGTG TGAACATGTT CTCCATTTTC AAGCTGGAAG AAGTGAGCAG TGTTGGAGTG  4260
AGGACCTGTA AGGCAGGCCC ATTCAGAGCT ATGGTGCTTG CTGGTGCCTG CCACCTTCAA  4320
GTTCTGGACC TGGGCATGAC ATCCTTTCTT TTAATGATGC CATGGCAACT TAGAGATTGC  4380
ATTTTTATTA AAGCATTTCC TACCAGCAAA GCAAATGTTG GGAAAGTATT TACTTTTTCG  4440
GTTTCAAAGT GATAGAAAAG TGTGGCTTGG GCATTGAAAG AGGTAAAATT CTCTAGATTT  4500
ATTAGTCCTA ATTCAATCCT ACTTTTCGAA CACCAAAAAT GATGCGCATC AATGTATTTT  4560
ATCTTATTTT CTCAATCTCC TCTCTCTTTC CTCCACCCAT AATAAGAGAA TGTTCCTACT  4620
CACACTTCAG CTGGGTCACA TCCATCCCTC CATTCATCCT TCCATCCATC TTTCCATCCA  4680
TTACCTCCAT CCATCCTTCC AACATATATT TATTGAGTAC CTACTGTGTG CCAGGGGCTG  4740
GTGGGACAGT GGTGACATAG TCTCTGCCCT CATAGAGTTG ATTGTCTAGT GAGGAAGACA  4800
AGCATTTTTA AAAAATAAAT TTAAACTTAC AAACTTTGTT TGTCACAAGT GGTGTTTATT  4860
GCAATAACCG CTTGGTTTGC AACCTCTTTG CTCAACAGAA CATATGTTGC AAGACCCTCC  4920
CATGGGGGCA CTTGAGTTTT GGCAAGGCTG ACAGAGCTCT GGGTTGTGCA CATTTCTTTG  4980
CATTCCAGCT GTCACTCTGT GCCTTTCTAC AACTGATTGC AACAGACTGT TGAGTTATGA  5040
TAACACCAGT GGGAATTGCT GGAGGAACCA GAGGCACTTC CACCTTGGCT GGGAAGACTA  5100
TGGTGCTGCC TTGCTTCTGT ATTTCCTTGG ATTTTCCTGA AAGTGTTTTT AAATAAAGAA  5160
CAATTGTTAG ATGCC
```

Seq ID NO: 220 Protein sequence:
Protein Accession #:NP_005553

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1         11        21        31        41        51
|         |         |         |         |         |
```

```
MPALWLGCCL CFSLLLPAAR ATSRREVCDC NGKSRQCIFD RELHRQTGNG FRCLNCNDNT    60
DGIHCEKCKN GFYRHRERDR CLPCNCNSKG SLSARCDNSG RCSCKPGVTG ARCDRCLPGF   120
HMLTDAGCTQ DQRLLDSKCD CDPAGIAGPC DAGRCVCKPA VTGERCDRCR SGYYNLDGGN   180
PEGCTQCFCY GHSASCRSSA EYSVHKITST FHQDVDGWKA VQRNGSPAKL QWSQRHQDVF   240
SSAQRLDPVY FVAPAKFLGN QQVSYGQSLS FDYRVDRGGR HPSAHDVILE GAGLRITAPL   300
MPLGKTLPCG LTKTYTFRLN EHPSNNWSPQ LSYFEYRRLL RNLTALRIRA TYGEYSTGYI   360
DNVTLISARP VSGAPAPWVE QCICPVGYKG QFCQDCASGY KRDSARLGPF GTCIPCNCQG   420
GGACDPDTGD CYSGDENPDI ECADCPIGFY NDPHDPRSCK PCPCHNGPSC SVMPETEEVV   480
CNNCPPGVTG ARCELCADGY FGDPFGEHGP VRPCQPCQCN NNVDPSASGN CDRLTGRCLK   540
CIHNTAGIYC DQCKAGYFGD PLAPNPADKC RACNCNPMGS EPVGCRSDGT CVCKPGFGGP   600
NCEHGAFSCP ACYNQVKIQM DQFMQQLQRM EALISKAQGG DGVVPDTELE GRMQQAEQAL   660
QDILRDAQIS EGASRSLGLQ LAKVRSQENS YQSRLDDLKM TVERVRALGS QYQNRVRDTH   720
RLITQMQLSL AESEASLGNT NIPASDHYVG PNGFKSLAQE ATRLAESHVE SASNMEQLTR   780
ETEDYSKQAL SLVRKALHEG VGSGSGSPDG AVVQGLVEKL EKTKSLAQQL TREATQAEIE   840
ADRSYQHSLR LLDSVSRLQG VSDQSFQVEE AKRIKQKADS LSTLVTRHMD EFKRTQKNLG   900
NWKEEAQQLL QNGKSGREKS DQLLSRANLA KSRAQEALSM GNATFYEVES ILKNLREFDL   960
QVDNRKAEAE EAMKRLSYIS QKVSDASDKT QQAERALGSA AADAQRAKNG AGEALEISSE  1020
IEQEIGSLNL EANVTADGAL AMEKGLASLK SEMREVEGEL ERKELEFDTN MDAVQMVITE  1080
AQKVDTRAKN AGVTIQDTLN TLDGLLHLMD QPLSVDEEGL VLLEQKLSRA KTQINSQLRP  1140
MMSELEERAR QQRGHLHLLE TSIDGILADV KNLENIRDNL PPGCYNTQAL EQQ
```

Seq ID NO: 221 DNA sequence
Nucleic Acid Accession #: NM_016529
Coding sequence: 13-1854

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1          11         21         31         41         51
|          |          |          |          |          |
GTCAAGAAAA GAATGTCTGT AATTGTTCGA ACTCCTTCAG GACGACTTCG GCTTTACTGT    60
AAAGGGGCTG ATAATGTGAT TTTTGAGAGA CTTTCAAAAG ACTCAAAATA TATGGAGGAA   120
ACATTATGCC ATCTGGAATA CTTTGCCACG GAAGGCTTGC GGACTCTCTG TGTGGCTTAT   180
GCTGATCTCT CTGAGAATGA GTATGAGGAG TGGCTGAAAG TCTATCAGGA AGCCAGCACC   240
ATATTGAAGG ACAGAGCTCA ACGGTTGGAA GAGTGTTACG AGATCATTGA GAAGAATTTG   300
CTGCTACTTG GAGCCACAGC CATAGAAGAT CGCCTTCAAG CAGGAGTTCC AGAAACCATC   360
GCAACACTGT TGAAGGCAGA AATTAAAATA TGGGTGTTGA CAGGAGACAA ACAAGAAACT   420
GCGATTAATA TAGGGTATTC CTGCCGATTG GTATCGCAGA ATATGGCCCT TATCCTATTG   480
AAGGAGGACT CTTTGGATGC CACAAGGGCA GCCATTACTC AGCACTGCAC TGACCTTGGG   540
AATTTGCTGG GCAAGGAAAA TGACGTGGCC CTCATCATCG ATGGCCACAC CCTGAAGTAC   600
GCGCTCTCCT TCGAAGTCCG GAGGAGTTTC CTGGATTTGG CACTCTCGTG CAAAGCGGTC   660
ATATGCTGCA GAGTGTCTCC TCTGCAGAAG TCTGAGATAG TGGATGTGGT GAAGAAGCGG   720
GTGAAGGCCA TCACCCTCGC CATCGGAGAC GGCGCCAACG ATGTCGGGAT GATCCAGACA   780
GCCCACGTGG GTGTGGGAAT CAGTGGGAAT GAAGGCATGC AGGCCACCAA CAACTCGGAT   840
TACGCCATCG CACAGTTTTC CTACTTAGAG AAGCTTCTGT TGGTTCATGG AGCCTGGAGC   900
TACAACCGGG TGACCAAGTG CATCTTGTAC TGCTTCTATA AGAACGTGGT CCTGTATATT   960
ATTGAGCTTT GGTTCGCCTT TGTTAATGGA TTTTCTGGGC AGATTTTATT TGAACGTTGG  1020
TGCATCGGCC TGTACAATGT GATTTTCACC GCTTTGCCGC CCTTCACTCT GGGAATCTTT  1080
GAGAGGTCTT GCACTCAGGA GAGCATGCTC AGGTTTCCCC AGCTCTACAA AATCACCCAG  1140
AATGGCGAAG GCTTCAACAC AAAGGTTTTC TGGGGTCACT GCATCAACGC CTTGGTCCAC  1200
TCCCTCATCC TCTTCTGGTT TCCCATGAAA GCTCTGGAGC ATGATACTGT GTTTGACAGT  1260
GGTCATGCTA CCGACTATTT ATTTGTTGGA AATATTGTTT ACACATATGT TGTTGTTACT  1320
GTTTGTCTGA AAGCTGGTTT GGAGACCACA GCTTGGACTA AATTCAGTCA TCTGGCTGTC  1380
TGGGGAAGCA TGCTGACCTG GCTGGTGTTT TTTGGCATCT ACTCGACCAT CTGGCCCACC  1440
ATTCCCATTG CTCCAGATAT GAGAGGACAG GCAACTATGG TCCTGAGCTC CGCACACTTC  1500
TGGTTGGGAT TATTTCTGGT TCCTACTGCC TGTTTGATTG AAGATGTGGC ATGGAGAGCA  1560
GCCAAGCACA CCTGCAAAAA GACATTGCTG GAGGAGGTGC AGGAGCTGGA AACCAAGTCT  1620
CGAGTCCTGG GAAAAGCGGT GCTGCGGGAT AGCAATGGAA AGAGGCTGAA CGAGCGCGAC  1680
CGCCTGATCA AGAGGCTGGG CCGGAAGACG CCCCCGACGC TGTTCCGGGG CAGCTCCCTG  1740
CAGCAGGGCG TCCCGCATGG GTATGCTTTT TCTCAAGAAG AACACGGAGC TGTTAGTCAG  1800
GAAGAAGTCA TCCGTGCTTA TGACACCACC AAAAAGAAAT CCAGGAAGAA ATAAGACATG  1860
AATTTTCCTG ACTGATCTTA GGAAAGAGAT TCAGTTTGTT GCACCCAGTG TTAACACATC  1920
TTTGTCAGAG AAGACTGGCG TCCAAGGCCA AAACACCAGG AAACACATTT CTGTGGCCTT  1980
AGTTAAGCAG TTTGTTAGTT ACATATTCCC TCGCAAACCT GGAGTGCAGA CCACAGGGGA  2040
AGCTATCTTT GCCCTCCCAA CTCGTCTGCA GTGCTTAGCC TAACTTTTGT TTATGTCGTT  2100
ATGAAGCATT CAACTGTGCT CTGTGAGGTC TCAAATTAAA AACATTATGT TTCACCAATA  2160
AGAAAAAAAA AAAAAAA
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Seq ID NO: 222 Protein sequence:
Protein Accession #: NP_057613

```
1          11         21         31         41         51
|          |          |          |          |          |
MSVIVRTPSG RLRLYCKGAD NVIFERLSKD SKYMEETLCH LEYFATEGLR TLCVAYADLS    60
ENEYEEWLKV YQEASTILKD RAQRLEECYE IIEKNLLLLG ATAIEDRLQA GVPETIATLL   120
KAEIKIWVLT GDKQETAINI GYSCRLVSQN MALILLKEDS LDATRAAITQ HCTDLGNLLG   180
KENDVALIID GHTLKYALSF EVRRSFLDLA LSCKAVICCR VSPLQKSEIV DVVKKRVKAI   240
TLAIGDGAND VGMIQTAHVG VGISGNEGMQ ATNNSDYAIA QFSYLEKLLL VHGAWSYNRV   300
TKCILYCFYK NVVLYIIELW FAFVNGFSGQ ILFERWCIGL YNVIFTALPP FTLGIFERSC   360
TQESMLRFPQ LYKITQNGEG FNTKVFWGHC INALVHSLIL FWFPMKALEH DTVFDSGHAT   420
DYLFVGNIVY TYVVVTVCLK AGLETTAWTK FSHLAVWGSM LTWLVFFGIY STIWPTIPIA   480
PDMRGQATMV LSSAHFWLGL FLVPTACLIE DVAWRAAKHT CKKTLLEEVQ ELETKSRVLG   540
KAVLRDSNGK RLNERDRLIK RLGRKTPPTL FRGSSLQQGV PHGYAFSQEE HGAVSQEEVI   600
RAYDTTKKKS RKK
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Seq ID NO: 223 DNA sequence
Nucleic Acid Accession #: BC017001
Coding sequence: 1-394

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1          11         21         31         41         51
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|          |          |          |          |          |
AACGCTGGGC AGGGCCGGCG CGGGTCGGGG GGCGCCCGAG GGGCCCGGGC CGAGCGGCGG    60
CGCGCAGGGC GGCAGCATCC ACTCGGGCCG CATCGCCGCG GTGCACAACG TGCCGCTGAG   120
CGTGCTCATC CGGCCGCTGC CGTCCGTGTT GGACCCCGCC AAGGTGCAGA GCCTCGTGGA   180
CACGATCCGG GAGGACCCAG ACAGCGTGCC CCCCATCGAT GTCCTCTGGA TCAAAGGGGC   240
CCAGGGAGGT GACTACTTCT ACTCCTTTGG GGGCTGCCAC CGCTACGCGG CCTACCAGCA   300
ACTGCAGCGA GAGACCATCC CCGCCAAGCT TGTCCAGTCC ACTCTCTCAG ACCTAAGGGT   360
GTACCTGGGA GCATCCACAC CAGACTTGCA GTAGCAGCCT CCTTGGCACC TGCTGCCACC   420
TTCAAGAGCC CAGAAGACAC ACCTGGCCTC CAGCAGGCTG GGCCATGCAG AAGGGATAGC   480
AGGGGTGCAT TCTCTTTGCA CCTGGCGAGA GGGTCTGACT CTGGGCACCC CTCTCACCGG   540
CTACAAGGCC TTGGACTCAC TGTACAGTGT GGGAGCCCCA GTTCCCACCT CTGTGACAAT   600
AGGATCATGG CCTTACCCTT GAAGCATTAC CGAGAAGGAG AACAGAGATG GGCTTGAAGA   660
GCCACGTGCT GCCGGCTCCA AATTCCCAAG GACAAGGATC CCTCTGCATT TTTGTCTATG   720
TAACCTCTTA TATGGACTAC ATTCAGCTGC AAGGAAAGGA AAACCTTGAT TGCAGTGGTT   780
TAAACAAACA GAAGATTGTT TTTCCACATA GCATGGATTC TGGAGATGGG TGGCTAATGG   840
TATTGGTTCA ACAACTCCAC GGAGGTAGGG GTCACGTCTT GGATCCTTTT GCCTTAATCT   900
CAGTGCTCGT TACTTCATGG TCCCAAGATG GCTGCTGTAT CCCCAAGAAT CATGTCTGCG   960
TTCAAGGAAG GAGGGGTGGA GGAAGAGGAA GGGCCAAACT AGCTGGACCC GTCACCTTCT  1020
ATCAGAAAGT AAAACCTCGT CAGAAGTCTG TTTCCTGCTC TCTCCCTCTG CATATCTTCA  1080
CTTAGATGCC CTTGGCCCGA GCCAGCTACC ATTGCACCTC TAGCTGCAAA CAAAGCTAAG  1140
ACAGCAGGGA ACAGAATTGT CATGGCTGAA TAGACCAATC GTGTTCCATC TACTGAGACT  1200
GGCACACTGC CTCCTGCAAT AAAACTGGGA TCCCATTACC AAGAGAGAAA TGCAGAATTG  1260
TGTACCAGTT AGCTTTTGCT GTGTAACAAA CCATCCCCAA ACTTGGCAGC TAGAAACAAA  1320
CCCTGTATTT TCCCACAATC CTATGGGTTG GCAATTTGGG CTGGGCTCAA CAGGGCAGTT  1380
CTGCTGCTCA CACCTGGGAT CCCTCATGGA GCTAAGGTCA GCTGTTACCT CAGCTGGGCC  1440
TGGATGGTCT AGGATAGCCT TACTCACTTG CCTGGCAGGT GACAGGCTGT TGGCTGGAAT  1500
TGCTTGGTTC TCCTCCATGT GGCCTCTCCA GCAGGCTAGC TCAGGCTTAT TCACATGATG  1560
GCTTCAGGAT TCCAAAGAGA GTGAGAGTAG AAGCTGAAAG ACTTCTTGAG TTCTTGGCCT  1620
GGAACTGGGA CTAGGACAGT GTCACTTCTG CTAAGTTCTT TTGGTCAGAG CAAATCACAA  1680
GGCTTTACCC AGATTCAAGG GATGAGAAAC AGACTACATG TCTTGATGAG GGGAACCACA  1740
AAGAGCTTGT GGCCATTTTT CACCTATCAC AAATAATTTT GGATGGGTAT TTATTTGGAT  1800
AAAGGTATTT CCCTCTTCCC CCTTTCTCTC TGTCTCATGG GGCCTCACTC TGCCAAGTTG  1860
GAAGGCACTA AGACATTGTC CTGGCCCTCA GGGTCTAGGG GAAGAGGTGT TGGGGCAGGA  1920
AGTGAGTCTC TCCATGGGCT GGACCCACTG TAGTAGGAGT GCCTCCTTGT CTGCACTGCT  1980
GGTATGGGGT TAGGCCAGGT AGGACATTCC AGAGGGGCTT CTGAAAACCA AGAGTCCCTG  2040
GGGAAAGGGA ACAGAGTAAG GCAGGCCTTG TTCTCACTGC CCTCTAAGGG AACTTGGTCA  2100
CTCGGCACTT TTAAGCCTCA GTTTCTCCAG TTCAATAATA AGGACAAGAG CTTTTCCCAT  2160
GCATTCTCTT TCCCCGGGAA AGTTGACTGA GGTGACCAGT AATAGAATTG AAAAGGGAGA  2220
GTGTCTTCAG TGCAATGTGG CATCCTGGAT TGGGTCTTGG AACAAAAACA GGACATTAGT  2280
GGGAAAATTG GAAATCTGAA AAAAGTCTGA ATTTTAGTTA ATATACCAAT TTCAGTCTCT  2340
TGGTTTTGAC AGATGTACCA TGGTGATGTA AGATGTTGAC CTTGGGGTAG GCTGGGTGAA  2400
GGGTATACAG GAACTCTTTG TACTATCTCT GCAACTTCTC TGTAAATCTA GTATCATTCC  2460
AAAATAAAAG TTTATTTAAT TTAAAAAAAA AAAAAAAAAA AA
```

Seq ID NO: 224 Protein sequence:
Protein Accession #: AAH17001.1

```
1          11         21         31         41         51
|          |          |          |          |          |
TLGRAGAGRG APEGPGPSGG AQGGSIHSGR IAAVHNVPLS VLIRPLPSVL DPAKVQSLVD    60
TIREDPDSVP PIDVLWIKGA QGGDYFYSFG GCHRYAAYQQ LQRETIPAKL VQSTLSDLRV   120
YLGASTPDLQ
```

Seq ID NO: 225 DNA sequence
Nucleic Acid Accession #: NM_021048
Coding sequence: 1..1110

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGCCTCGAG CTCCAAAGCG TCAGCGCTGC ATGCCTGAAG AAGATCTTCA ATCCCAAAGT    60
GAGACACAGG GCCTCGAGGG TGCACAGGCT CCCCTGGCTG TGGAGGAGGA TGCTTCATCA   120
TCCACTTCCA CCAGCTCCTC TTTTCCATCC TCTTTTCCCT CCTCCTCCTC TTCCTCCTCC   180
TCCTCCTGCT ATCCTCTAAT ACCAAGCACC CCAGAGGAGG TTTCTGCTGA TGATGAGACA   240
CCAAATCCTC CCCAGAGTGC TCAGATAGCC TGCTCCTCCC CCTCGGTCGT TGCTTCCCTT   300
CCATTAGATC AATCTGATGA GGGCTCCAGC AGCCAAAAGG AGGAGAGTCC AAGCACCCTA   360
CAGGTCCTGC CAGACAGTGA GTCTTTACCC AGAAGTGAGA TAGATGAAAA GGTGACTGAT   420
TTGGTGCAGT TTCTGCTCTT CAAGTATCAA ATGAAGGAGC CGATCACAAA GGCAGAAATA   480
CTGGAGAGTG TCATAAAAAA TTATGAAGAC CACTTCCCTT TGTTGTTTAG TGAAGCCTCC   540
GAGTGCATGC TGCTGGTCTT TGGCATTGAT GTAAAGGAAG TGGATCCCAC TGGCCACTCC   600
TTTGTCCTTG TCACCTCCCT GGGCCTCACC TATGATGGGA TGCTGAGTGA TGTCCAGAGC   660
ATGCCCAAGA CTGGCATTCT CATACTTATC CTAAGCATAA TCTTCATAGA GGGCTACTGC   720
ACCCCTGAGG AGGTCATCTG GGAAGCACTG AATATGATGG GGCTGTATGA TGGGATGGAG   780
CACCTCATTT ATGGGGAGCC CAGGAAGCTG CTCACCCAAG ATTGGGTGCA GGAAAACTAC   840
CTGGAGTACC GGCAGGTGCC TGGCAGTGAT CCTGCACGGT ATGAGTTTCT GTGGGGTCCA   900
AGGGCTCATG CTGAAATTAG GAAGATGAGT CTCCTGAAAT TTTTGGCCAA GGTAAATGGG   960
AGTGATCCAA GATCCTTCCC ACTGTGGTAT GAGGAGGCTT TGAAAGATGA GGAAGAGAGA  1020
GCCCAGGACA GAATTGCCAC CACAGATGAT ACTACTGCCA TGGCCAGTGC AAGTTCTAGC  1080
GCTACAGGTA GCTTCTCCTA CCCTGAATAA
```

Seq ID NO: 226 Protein sequence:
Protein Accession #: NP_066386

```
1          11         21         31         41         51
|          |          |          |          |          |
MPRAPKRQRC MPEEDLQSQS ETQGLEGAQA PLAVEEDASS STSTSSSFPS SFPSSSSSS    60
```

```
SSCYPLIPST PEEVSADDET PNPPQSAQIA CSSPSVVASL PLDQSDEGSS SQKEESPSTL   120
QVLPDSESLP RSEIDEKVTD LVQFLLFKYQ MKEPITKAEI LESVIKNYED HFPLLFSEAS   180
ECMLLVFGID VKEVDPTGHS FVLVTSLGLT YDGMLSDVQS MPKTGILILI LSIIFIEGYC   240
TPEEVIWEAL NMMGLYDGME HLIYGEPRKL LTQDWVQENY LEYRQVPGSD PARYEFLWGP   300
RAHAEIRKMS LLKFLAKVNG SDPRSFPLWY EEALKDEEER AQDRIATTDD TTAMASASSS   360
ATGSFSYPE
```

Seq ID NO: 227 DNA sequence
Nucleic Acid Accession #: NM_005025.1
Coding sequence: 82-1314

```
1          11         21         31         41         51
|          |          |          |          |          |
GCGGAGCACA GTCCGCCGAG CACAAGCTCC AGCATCCCGT CAGGGGTTGC AGGTGTGTGG     60
GAGGCTTGAA ACTGTTACAA TATGGCTTTC CTTGGACTCT TCTCTTTGCT GGTTCTGCAA    120
AGTATGGCTA CAGGGGCCAC TTTCCCTGAG GAAGCCATTG CTGACTTGTC AGTGAATATG    180
TATAATCGTC TTAGAGCCAC TGGTGAAGAT GAAAATATTC TCTTCTCTCC ATTGAGTATT    240
GCTCTTGCAA TGGGAATGAT GGAACTTGGG GCCCAAGGAT CTACCCAGAA AGAAATCCGC    300
CACTCAATGG GATATGACAG CCTAAAAAAT GGTGAAGAAT TTTCTTTCTT GAAGGAGTTT    360
TCAAACATGG TAACTGCTAA AGAGAGCCAA TATGTGATGA AAATTGCCAA TTCCTTGTTT    420
GTGCAAAATG GATTTCATGT CAATGAGGAG TTTTTGCAAA TGATGAAAAA ATATTTTAAT    480
GCAGCAGTAA ATCATGTGGA CTTCAGTCAA AATGTAGCCG TGGCCAACTA CATCAATAAG    540
TGGGTGGAGA ATAACACAAA CAATCTGGTG AAAGATTTGG TATCCCCAAG GGATTTTGAT    600
GCTGCCACTT ATCTGGCCCT CATTAATGCT GTCTATTTCA AGGGGAACTG GAAGTCGCAG    660
TTTAGGCCTG AAAATACTAG AACCTTTTCT TTCACTAAAG ATGATGAAAG TGAAGTCCAA    720
ATTCCAATGA TGTATCAGCA AGGAGAATTT TATTATGGGG AATTTAGTGA TGGCTCCAAT    780
GAAGCTGGTG GTATCTACCA AGTCCTAGAA ATACCATATG AAGGAGATGA AATAAGCATG    840
ATGCTGGTGC TGTCCAGACA GGAAGTTCCT CTTGCTACTC TGGAGCCATT AGTCAAAGCA    900
CAGCTGGTTG AAGAATGGGC AAACTCTGTG AAGAAGCAAA AAGTAGAAGT ATACCTGCCC    960
AGGTTCACAG TGGAACAGGA AATTGATTTA AAAGATGTTT TGAAGGCTCT TGGAATAACT   1020
GAAATTTTCA TCAAAGATGC AAATTTGACA GGCCTCTCTG ATAATAAGGA GATTTTTCTT   1080
TCCAAAGCAA TTCACAAGTC CTTCCTAGAG GTTAATGAAG AAGGCTCAGA AGCTGCTGCT   1140
GTCTCAGGAA TGATTGCAAT TAGTAGGATG GCTGTGCTGT ATCCTCAAGT TATTGTCGAC   1200
CATCCATTTT TCTTTCTTAT CAGAAACAGG AGAACTGGTA CAATTCTATT CATGGGACGA   1260
GTCATGCATC CTGAAACAAT GAACACAAGT GGACATGATT TCGAAGAACT TTAAGTTACT   1320
TTATTTGAAT AACAAGGAAA ACAGTAACTA AGCACATTAT GTTTGCAACT GGTATATATT   1380
TAGGATTTGT GTTTTACAGT ATATCTTAAG ATAATATTTA AAATAGTTCC AGATAAAAAC   1440
AATATATGTA AATTATAAGT AACTTGTCAA GGAATGTTAT CAGTATTAAG CTAATGGTCC   1500
TGTTATGTCA TTGTGTTTGT GTGCTGTTGT TTAAAATAAA AGTACCTATT GAACATGTG
```

Seq ID NO: 228 Protein sequence:
Protein Accession #: NP_005016.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MAFLGLFSLL VLQSMATGAT FPEEAIADLS VNMYNRLRAT GEDENILFSP LSIALAMGMM    60
ELGAQGSTQK EIRHSMGYDS LKNGEEFSFL KEFSNMVTAK ESQYVMKIAN SLFVQNGFHV   120
NEEFLQMMKK YFNAAVNHVD FSQNVAVANY INKWVENNTN NLVKDLVSPR DFDAATYLAL   180
INAVYFKGNW KSQFRPENTR TFSFTKDDES EVQIPMMYQQ GEFYYGEFSD GSNEAGGIYQ   240
VLEIPYEGDE ISMMLVLSRQ EVPLATLEPL VKAQLVEEWA NSVKKQKVEV YLPRFTVEQE   300
IDLKDVLKAL GITEIFIKDA NLTGLSDNKE IFLSKAIHKS FLEVNEEGSE AAAVSGMIAI   360
SRMAVLYPQV IVDHPFFFLI RNRRTGTILF MGRVMHPETM NTSGHDFEEL
```

Seq ID NO: 229 DNA sequence
Nucleic Acid Accession #: NM_003695
Coding sequence: 12-398

```
1          11         21         31         41         51
|          |          |          |          |          |
CGACATCAGA GATGAGGACA GCATTGCTGC TCCTTGCAGC CCTGGCTGTG GCTACAGGGC    60
CAGCCCTTAC CCTGCGCTGC CACGTGTGCA CCAGCTCCAG CAACTGCAAG CATTCTGTGG   120
TCTGCCCGGC CAGCTCTCGC TTCTGCAAGA CCACGAACAC AGTGGAGCCT CTGAGGGGGA   180
ATCTGGTGAA GAAGGACTGT GCGGAGTCGT GCACACCCAG CTACACCCTG CAAGGCCAGG   240
TCAGCAGCGG CACCAGCTCC ACCCAGTGCT GCCAGGAGGA CCTGTGCAAT GAGAAGCTGC   300
ACAACGCTGC ACCCACCCGC ACCGCCCTCG CCCACAGTGC CCTCAGCCTG GGGCTGGCCC   360
TGAGCCTCCT GGCCGTCATC TTAGCCCCCA GCCTGTGACC TTCCCCCCAG GGAAGGCCCC   420
TCATGCCTTT CCTTCCCTTT CTCTGGGGAT TCCACACCTC TCTTCCCCAG CCGGCAACGG   480
GGGTGCCAGG AGCCCCAGGC TGAGGGCTTC CCCGAAAGTC TGGGACCAGG TCCAGGTGGG   540
CATGGAATGC TGATGACTTG GAGCAGGCCC CACAGACCCC ACAGAGGATG AAGCCACCCC   600
ACAGAGGATG CAGCCCCCAG CTGCATGGAA GGTGGAGGAC AGAAGCCCTG TGGATCCCCG   660
GATTTCACAC TCCTTCTGTT TTGTTGCCGT TTATTTTGTA CTCAAATCTC TACATGGAGA   720
TAAATGATTT AAACC
```

Seq ID NO: 230 Protein sequence:
Protein Accession #: NP_003686

```
1          11         21         31         41         51
|          |          |          |          |          |
MRTALLLLAA LAVATGPALT LRCHVCTSSS NCKHSVVCPA SSRFCKTTNT VEPLRGNLVK    60
KDCAESCTPS YTLQGQVSSG TSSTQCCQED LCNEKLHNAA PTRTALAHSA LSLGLALSLL   120
AVILAPSL
```

Seq ID NO: 231 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 126-752

```
1          11         21         31         41         51
|          |          |          |          |          |
CCGGGCAGGT GGCTCATGCT CGGGAGCGTG GTTGAGCGGC TGGCGCGGTT GTCCTGGAGC   60
AGGGGCGCAG GAATTCTGAT GTGAAACTAA CAGTCTGTGA GCCCTGGAAC CTCCACTCAG  120
AGAAGATGAA GGATATCGAC ATAGGAAAAG AGTATATCAT CCCCAGTCCT GGGTATAGAA  180
GTGTGAGGGA GAGAACCAGC ACTTCTGGGA CGCACAGAGA CCGTGAAGAT TCCAAGTTCA  240
GGAGAACTCG ACCGTTGGAA TGCCAAGATG CCTTGGAAAC AGCAGCCCGA GCCGAGGGCC  300
TCTCTCTTGA TGCCTCCATG CATTCTCAGC TCAGAATCCT GGATGAGGAG CATCCCAAGG  360
GAAAGTACCA TCATGGCTTG AGTGCTCTGA AGCCCATCCG GACTACTTCC AAACACCAGC  420
ACCCAGTGGA CAATGCTGGG CTTTTTTCCT GTATGACTTT TTCGTGGCTT TCTTCTCTGG  480
CCCGTGTGGC CCACAAGAAG GGGGAGCTCT CAATGGAAGA CGTGTGGTCT CTGTCCAAGC  540
ACGAGTCTTC TGACGTGAAC TGCAGAAGAC TAGAGAGACT GTGGCAAGAA GAGCTGAATG  600
AAGTTGGGCC AGACGCTGCT TCCCTGCGAA GGGTTGTGTG GATCTTCTGC CGCACCAGGC  660
TCATCCTGTC CATCGTGTGC CTGATGATCA CGCAGCTGGC TGGCTTCAGT GGACCAAATT  720
TTCAGGATGG CTGTATTCTG CGGTCAGAAT GAGAGAGTCA AGCTGGGCAG AATCTCTCGC  780
CAAGAGTTCA GCCTTCCTTT GGAGACTGCT CCATCAGTGC CGAGGTGTGT GGGAACAGGC  840
TTCACTGCAC CGCCATCTTA CTGAGTTGCT TCACGTGAGG AAAAGGGGGC TTTGGCCCTG  900
TGACTCAGTT CCACATTTTG GATTGCATAC TGGAAAAGAA GCCAATCTTC TTGCTAGTAA  960
ACCAGCAACC CGGCTGTATA CAGTGGTGAC CCAAGCAATG GATATAAACC TAAAAATCTG 1020
AGGGAGGGGA GAGGTGGAAT ACAGTAGTTC TTGGAATCTG AAGTCTCCTA TTTGATCAGG 1080
TTATTTCCTG GGACTTGGCA AAAATCTGAT TGGTGGGGAT CTCCTAGGAC CTAGTGGACA 1140
TCTGGTATTA ATTTAATCTC AGGAAAAACA AGAAATTAAC CCAGAGAGAG TCTGGGTTTT 1200
GGAATTCAGC GTAGCTACCT CCAGACCGTG GTGTCTGGCC TCCATTTTTG TCTGTCATTC 1260
AGCTCTGACT TACAGCTGCA GTCACCTTTG CTATAAGGCA CCTGGGTAGA AGGGTGGATG 1320
GGCTTCACAT CAATTTTTTT CTTCCTTTAG GGTGGGGGAT TGGTTTGGCT TTCTTTTGTT 1380
GTGGTTTTTT GTTTTATTTT TGTCAAGATT GATTTTTAGA TGCAAGGACT TGAAAAGACC 1440
CAGAAGGATG CCACCAGTTT TTCCTTGAGG CCTAGGATTT TTTATTCTGT CCCGAGCAGA 1500
GGTAATTCCT CACAACTTAG TGCACCAGTA GCACCAGCCA TTTTGAGCAG AGTACCTCTT 1560
TGGGGAGCTT TTCGTTTTGT TTTGTTTTTA ATTCTCTTTC CTTAGCAGCA AGGTCTTTTT 1620
TCCTAGAGAA TCTACTCCGT TGCAGAATCA TTGCAACCTC AGGAGCCCTC ACTGATTGAG 1680
TGCTGTCAGC CTGATATACT ACTTTGGACT CTGGAAACAG ATATGGGTTC TATTCTCTAT 1740
TTCTACTGTG TGTCGTTAAA CAACCGTCGG AGACCAGATG ACCTGTTAGA TGGCTAGTCC 1800
TGTATAACTC GACTCTGTAT GTTTCAATGT ATGTTACTGC AATGCTTCAC CTGCTGTACA 1860
GTGTTTGTGA GATGCTCTTT GAAGATGGTA CTTTTATATT T
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Seq ID NO: 232 Protein sequence:
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MKDIDIGKEY IIPSPGYRSV RERTSTSGTH RDREDSKFRR TRPLECQDAL ETAARAEGLS   60
LDASMHSQLR ILDEEHPKGK YHHGLSALKP IRTTSKHQHP VDNAGLFSCM TFSWLSSLAR  120
VAHKKGELSM EDVWSLSKHE SSDVNCRRLE RLWQEELNEV GPDAASLRRV VWIFCRTRLI  180
LSIVCLMITQ LAGFSGPNFQ DGCILRSE
```

Seq ID NO: 233 DNA sequence
Nucleic Acid Accession #: CAT cluster

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1          11         21         31         41         51
|          |          |          |          |          |
TTTTAATGGT GCTCATATAT ACTGTATTTT TTGTTGTTTA GTTTTACTTA TTGAGAGTGT   60
CACAACATGA ATCACATAAT CATGATTTTT TTTTTTTACT TTTACTCCCC AAATTATTCA  120
TGTTTCTTAG ATCGTAGTCA TTGAGAAGTC CCAATAACTC TAAACTTTTG AGTTATAACG  180
TAGTAAACTT CTCTTTCATC TTTGTGTTAG CTCTGTAGTC TTAACCTGGA TTTTAATTTT  240
TTTGTTTCCA AAGTCACAAT TGAATTATTC TTAGATACCT TAAGCCACTG AATTCAGTTC  300
TGTTTGACTG AAAGCAAAAC AACGTGACAG TTTATTTTCA AACACTAACT TCTTGATATT  360
TTGTTATGGT ATATCTTTTT ATTAAATATT TATTTTGACT AAGCTTTCAT AAAATATTTG  420
AAGCTATTTT AATCATCAAG TATGGAAAAC AAATTACTAT TGCATTTTCC TATATATGCA  480
TATATTATGG ATTAACCAGA ATTGTATCAT TTTTGGCCTA ATGTCTGGAT ATAAAAGATA  540
ATTAGCCTAC TATAGTATTA ATAAATTTTT CAGTTGGTTT GGGCAAATTT AAACCTGAAA  600
AATAGGTTAA AAAGTAGTTA CAAATTAAAC TTACTAATTT ATACCTGATT TTTTTTCTTG  660
AATTAAAGTA CATTTTAAAT GAGCTTTATA ATACCTTAAA AAGTTGGTTC TAATTTAAAA  720
TATGAAAGCT CTGGCTATCA TCCTGGGATA GTAATTTCTA ATTATATAGT ATTTCAAAAC  780
TATATATTTT TTAGTTCCTT TGAGATAACT AATTTCTAAT TATATATGTT TCAAAAACCA  840
TATCCTGTAT TTTTTTTAAG AATTGTTTTA TAAATAGGTC ATAAGATACA AGGTCTGCAT  900
TAGAAGACCC ACTCTTACTA GGTTCCCTAA GGATCTGCCA TAGATTTTTT TTTTTTTTTT  960
TTTTTTTTAG GTAGTTTAAA GCAAGCACTG ATACCAGTGG GAGTTGGTCT TGATCTAGGA 1020
GATTCTGTTA AGCATCCAAA AACAATGCCT AATTTCAGTT CTTAGGTTAT GGCTTGTGAC 1080
TCCAGATAAA AGATGGAGAA TACCTCATGT ACTGTGACTT GAAAATGAAT TCTTAAAATT 1140
CTTAGGCTCT CTCCATGTAT CTTTCTTAAG GAAAAGTTTC TGAGTGTGAT CTCTCTTTTG 1200
CCATAGTATC AAGTGGAGGG TAGTTCAGAA AAGTTAATAG GAAATCTTTT GTGACAGCAG 1260
ACTATAATAG AAGTTTGAGT AATATTTTAA TAAATTTATA TAATTCAAAT GATAAAAATG 1320
TATCAATGTT ATCCAATGAT TTTTATTAAA AAATTACCTT ATTATTAGAA CTGTGCCTAT 1380
TACATAAAAA GTGCTCATGT ATTTGAATTT TAAATAATTT ATTTAAATCA AGACCACCAT 1440
AAGTCATTAA TAATTTAATA ATTGTTTTAA ATCAGTGGTT TTCAACCCTC ACTTCATATT 1500
AGAATCATCT GAGGACTTTT AATATGGAAT CCACCTCATA ACAATTAAGT CTAAATTTCT 1560
GGAAGATGGA GCCATGCTTG TTTTTCCAAA AGCTCTTTGA GTGATTCTAA TTTGTAGTCA 1620
GAGTTGAAGA CCACTGCTCT AAATTAGTGC AGGAAAATGC TTTTATTTCT CCCATGTTAA 1680
CTTTTAAAAC TAGTAATGTA CCCAGTTAAG TTTTGATGGT TTAAATTCCA CTAAAGAACA 1740
TATTCTTCTA ATAACTAGCA TTTATTACAT GAAATTTAAG AGTTTAAGTT CCATCAAACT 1800
AGCCCTTGTG TAAGATTATT ATTTCTTCTC TATAACTTCA AAATAGATAT TTCATTCAAA 1860
CTGTTCAGGT GAGAAAACAT AATGGATTTT TTTTTTTTTC CTCTGGAGCT GCCTGTTCAG 1920
TGAGATGGAG GAGGTGGGCA CATTTAAGGT CAGTTCACTA ACCTATGGTT CAGAGTTCTG 1980
ATCATATGGA AGTTTGGAAA AGAGAGCTTA TCACAGGTTT GTATGCTGGT GAATGGATAG 2040
TTTTAATTCT CACTGTCTCA AAAGAGAATC AGCTCTCCAG CAGTTCTAGA AAAGCTTTGA 2100
CAATCCCCAA GGGGCAGTGT TACCTTACTC CTTCACTGCT TCTTAGAAGG TAGAATTAAG 2160
TTTCTGGAAT TGCACCTACA TGTTTTCTTA TTAACATTCA GAATTGGGAA TATTAATTTT 2220
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TCCAGTGAGT AGTTTTCTGA AATTGGTAAC TTGGAGAGTA AAATAACGTA TTTTGCTTTT  2280
CAATTTTGTG TTTGTTTACT TTTATGTAAA AATTTGATAT GTGAATTACA CAGTTCTAAT  2340
AAAACCTCAT GCCTTTTCAT TACATCTAAT TTGAACTCTC AACTTCAGTG CCAGAAGTGC  2400
TTTAAAGATG CTTTAATGAA AAGTATTAAG AAAATATATA GATTTGTATG TCAGTTTATA  2460
CTTCAGAAAT CCATATATTT GTCATATTTA TTTTTTTAGA AACCTCCTAA TTGGATAACT  2520
AGATGGTATT TAAAATGAAT GCCCAAAAAT ATCTTGTACC TTTGTCCAAA AGTTTATCTG  2580
TTGGAAGCCG CCAGCCATTC ATGTAGAGAG TTTATAAGAA AATAATTTAA AATTGTATGC  2640
ATTTTATATT ACTATGGTAT CTGTGTACCA TATTTCTAAG TATTCATTAT TAAATTGGTA  2700
CTTCTTAAAA CCATAACCTG GCTTGCCTTT TAGTGTTAAA CACAAAATCC AACATTGTAT  2760
ATAGAGATTC TTCTTTTATG AAGAAGAGCT GACGTAATTT ATTACCAGTG CATCTGCACA  2820
AAGACATTAA CATAAGTCTC TGAGCAGTGA TACATTTTCA AACATGAAGA GTGACAACCA  2880
CCACATTAAA CAACCACGGC AACACTCAGA CTTGGCACTT TCCTACGAAT CCATCCTATA  2940
TGTGCCTGGT ATCGCCTCTG GCATAACTTA CACGAATCGT CCTCCCTACT TGTCTACGCT  3000
CCTTCATCAA GCACTTGCCA ACACATTCAC CTCTAACTTG TACAACCTTA CCAACTCACC  3060
ACAACATCTG CAACTCTACC CTATCAACTG CCAACCTAAA GACCCCCAAC ACAACACAAC  3120
CCCCAAACAC AAAACCACTA AATCATAACC ACCACACACG CCACACACCA CACACCCACC  3180
CACACAACCA ACACACCACG ACCAAACACC CCACCACAAA CAAGCTAACA ACCACAAACA  3240
GACAACACAT CACATACACT CACTACCCCC CCATACTCCC ACCCACCA
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Seq ID NO: 234 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 27-281

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1          11         21         31         41         51
|          |          |          |          |          |
AGCAGGAGGA GAGCTGGCGG GAAGACATGC ACCCCTTGAA GACCCAGAGA GAGGCCGTCT    60
GTCTACCGCG TAGCAGTTAC ATCAGACTGA GACACTTCCT GTTTACAGGA GACTATAAAA   120
TTCCTGCCCC GTGCTCATTT GGGGCTGACG CCATTTTAGG CCTCAGCCCA TCTGCACCCA   180
GGCGCTCACT GAAACAGTGT GTTGCTCCAC ACCGCCTTGT TTTGCTTGTT GGCGCGCTCT   240
CAGGGTTCCG ACCAATCCAA GAGCCTTGCA GAAAGCATTA ACGTGCTTTT CTCTTTGGCA   300
GAGTTTTTCT TTGCTCTGAT CTTGGAGACA TCCCTCTGCC TAGTGGAAAC ATAAGGAATA   360
CAGAAAGAAT GCAAGGAGAT AGACCAACGT GAGATTCTCC TTCATGCACT CAAGAGAAAG   420
ATGTTGCAGG AAGAGCTAGT CTTTCAGGCT GGGCTGGTGA CCTGAGAAAG AATGTCCAGC   480
TTTTCTTCTC CACTTGGCAT ATCAAGAGCC AGGCGTGGAA GACTAAAACA GGAAATGTTT   540
ATAAAAACTG TTCAGCGGTT CGCCAACAAG AAGTGGTAAA GTAGCAAAAA TGGGGATGGA   600
GATGCCAGGA GGAAAGATGC CAGGGGTAAA GTGGGAAAAT GGGAACCTGA AGCCAGGAGG   660
TCAAGCCAAG CCAACAGGTG TTCTGTTTTT CATCACAGAA CTAATAAGTG GTGCTGAGGA   720
CTCAAACCCG GGGAAGCCCA CTCTAGAACC CATGCTGGTC ATCCATATCC CCAAGGCCCT   780
GGTCAGAACA CAGCTAAGCA GATGGCTTGG GTCATCAGGA CGTCCATTAC ATCCAAAGGA   840
AGACAGCCTG TGACGTTTCA AAAGCAAAAG TCCCCTACCA GCCAGTGAAG CTACCTGATT   900
TCTCAGTATC TTACGCCCAG TGACACGATC TACCCTCAAA ACTTAAAAAA AAAAGGGAAA   960
CATAAACACA TAACAGCAGC AGCAATAATT AAAGATGAGA TGAGAACAAT TAAGAAAAAA  1020
GGAAAGGTCT CCTGTGACTG TTTTATTTTT AGGGAAACAG AGAGGAAGAA GAATGATTTT  1080
TCTTTTGATG ACTCTATATC CAACTCTGAG GTTTGATTAA AGAAATGACC TTGAACCACA  1140
GCAAAGAAAA ATAAAAGACA ATTTCCAGTA AGTATGCCAG TTCGAATTAA TGATTTACTT  1200
TTTATTTTTA AACTGAATTC AGCAGAGATT TACATGCATT ACGATGATTA ACATCTGAAA  1260
TTTGACCTTG AAATAATCTT TACATTGTAA ATTCTTAATG ATCAAAACAA GGTTCTCAGT  1320
GATTAAAACA TATTAGTAAT TAATTATTAA AGGAGAATAA TTGCAAATAC AACATTCCTA  1380
AAATCTCAAG GCTTTTAAAG CATTTGTACA AATGACTGGA CATTTTTTAA ATTTGAAAAA  1440
AAAAAAAAGC CCTCCATCTG ATTCTCATTT TCATTGTCAG TGCAACAACA AAAAAGGTAT  1500
GCACTTCTCT TCTCATTTTC CACTGTCTCG CAAGCTAGAA ATTCTCACGA CTACCTTTGA  1560
TCCCATCAAA GCCAAAGAAA GAAAAGAAAA TTGTTCTGTA CAGATATATG ACATTAAAAA  1620
ATAATCCC
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Seq ID NO: 235 Protein sequence:
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MHPLKTQREA VCLPRSSYIR LRHFLFTGDY KIPAPCSFGA DAILGLSPSA PRRSLKQCVA    60
PHRLVLLVGA LSGFRPIQEP CRKH
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Seq ID NO: 236 DNA sequence
Nucleic Acid Accession #: NM_002075
Coding sequence: 406..1428

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1          11         21         31         41         51
|          |          |          |          |          |
CCACAATAGG GGCAGACCTG TCCATCCTTC TCTGTGGGTC CCCTGTACCT TTCTCCCCCA    60
ACAGGATCAG ACCCAGAGGC AGCTGGTTGG GGTTTGTCGA GAAGAAGGAT TATCCAGATC   120
AGTCCTTTCT AATCTCAGCT CCTGCCTGTA CCCTCCCATA CTCACCAAAC CCTCTTCCCC   180
ACCACCCTGA GCTGAGGAGC ACAGTTTGAG GCCCCCCCAA CCCCCCGCCG GTCGGGGCCA   240
GGCCAGGCCA GGCCAGCTCC TCTGGCAGCA GAGCCTGGGC AGGTGACGGG CGGGCGCGGG   300
CGTCGCAGCT GAGGGAGTAA GGAGGCTCCC AGGAACCGGA GCTGGAAACC CGGCCGAGGT   360
CCAGCCAGAG CCCAAGAGCC AGAGTGACCC CTCGACCTGT CAGCCATGGG GGAGATGGAG   420
CAACTGCGTC AGGAAGCGGA GCAGCTCAAG AAGCAGATTG CAGATGCCAG GAAAGCCTGT   480
GCTGACGTTA CTCTGGCAGA GCTGGTGTCT GGCCTAGAGG TGGTGGGACG AGTCCAGATG   540
CGGACGCGGC GGACGTTAAG GGGACACCTG GCCAAGATTT ACGCCATGCA CTGGGCCACT   600
GATTCTAAGC TGCTGGTAAG TGCCTCGCAA GATGGGAAGC TGATCGTGTG GGACAGCTAC   660
ACCACCAACA AGGTGCACGC CATCCCACTG CGCTCCTCCT GGGTCATGAC CTGTGCCTAT   720
GCCCCATCAG GGAACTTTGT GGCATGTGGG GGGCTGGACA ACATGTGTTC CATCTACAAC   780
CTCAAATCCC GTGAGGGCAA TGTCAAGGTC AGCCGGGAGC TTTCTGCTCA CACAGGTTAT   840
CTCTCCTGCT GCCGCTTCCT GGATGACAAC AATATTGTGA CCAGCTCGGG GGACACCACG   900
TGTGCCTTGT GGGACATTGA GACTGGGCAG CAGAAGACTG TATTTGTGGG ACACACGGGT   960
GACTGCATGA GCCTGGCTGT GTCTCCTGAC TTCAATCTCT TCATTTCGGG GGCCTGTGAT  1020
GCCAGTGCCA AGCTCTGGGA TGTGCGAGAG GGGACCTGCC GTCAGACTTT CACTGGCCAC  1080
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GAGTCGGACA TCAACGCCAT CTGTTTCTTC CCCAATGGAG AGGCCATCTG CACGGGCTCG 1140
GATGACGCTT CCTGCCGCTT GTTTGACCTG CGGGCAGACC AGGAGCTGAT CTGCTTCTCC 1200
CACGAGAGCA TCATCTGCGG CATCACGTCC GTGGCCTTCT CCCTCAGTGG CCGCCTACTA 1260
TTCGCTGGCT ACGACGACTT CAACTGCAAT GTCTGGGACT CCATGAAGTC TGAGCGTGTG 1320
GGCATCCTCT CTGGCCACGA TAACAGGGTG AGCTGCCTGG GAGTCACAGC TGACGGGATG 1380
GCTGTGGCCA CAGGTTCCTG GGACAGCTTC CTCAAAATCT GGAACTGAGG AGGCTGGAGA 1440
AAGGGAAGTG GAAGGCAGTG AACACACTCA GCAGCCCCCT GCCCGACCCC ATCTCATTCA 1500
GGTGTTCTCT TCTATATTCC GGGTGCCATT CCCACTAAGC TTTCTCCTTT GAGGGCAGTG 1560
GGGAGCATGG GACTGTGCCT TTGGGAGGCA GCATCAGGGA CACAGGGGCA AAGAACTGCC 1620
CCATCTCCTC CCATGGCCTT CCCTCCCCAC AGTCCTCACA GCCTCTCCCT TAATGAGCAA 1680
GGACAACCTG CCCCTCCCCA GCCCTTTGCA GGCCCAGCAG ACTTGAGTCT GAGGCCCCAG 1740
GCCCTAGGAT TCCTCCCCCA GAGCCACTAC CTTTGTCCAG GCCTGGGTGG TATAGGGCGT 1800
TTGGCCCTGT GACTATGGCT CTGGCACCAC TAGGGTCCTG GCCCTCTTCT TATTCATGCT 1860
TTCTCCTTTT TCTACCTTTT TTTCTCTCCT AAGACACCTG CAATAAAGTG TAGCACCCTG 1920
GT

Seq ID NO: 237 Protein sequence:
Protein Accession #: NP_002066

1 11 21 31 41 51

MGEMEQLRQE AEQLKKQIAD ARKACADVTL AELVSGLEVV GRVQMRTRRT LRGHLAKIYA 60
MHWATDSKLL VSASQDGKLI VWDSYTTNKV HAIPLRSSWV MTCAYAPSGN FVACGGLDNM 120
CSIYNLKSRE GNVKVSRELS AHTGYLSCCR FLDDNNIVTS SGDTTCALWD IETGQQKTVF 180
VGHTGDCMSL AVSPDFNLFI SGACDASAKL WDVREGTCRQ TFTGHESDIN AICFFPNGEA 240
ICTGSDDASC RLFDLRADQE LICFSHESII CGITSVAFSL SGRLLFAGYD DFNCNVWDSM 300
KSERVGILSG HDNRVSCLGV TADGMAVATG SWDSFLKIWN

Seq ID NO: 238 DNA sequence
Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51

TCCCAATGTG TNGAACCTAC CATAAATTCT TTTCTTACNG GACAATCTTA TNCTAANCAA 60
TACCATTTGC TTTTAAGGCA GATAATCCTC CAAGTTTTCT AATGATATCT GAAACTATTA 120
ACTGATTCTG TGAATTATGA AATCTGAAAA GGAATTGGAA GTTGCTAAAA ATCTATCATT 180
TGCATTGACC AGTGTGAAGC ACAGTGGAAT GAGAATGCGT GCCCTGACAC CAAAGAAAAA 240
TAAGTGACTG GAAAGCTGAA GAATCACCGG CTTCAGTGAC ATGGAACCCA GTGATTTGAT 300
TTTTGACGAG TATCGGGTGA CTTTGAGGTG GTCAAGAAAC CACACTTTAA GAACAATGTC 360
CAAAAAGGGG AAAAAAAAGA GCAACCAAAG AAAAAAAATC CATAAAATTG CACAGAAGAA 420
AAGAAAGAAA AATAAAATAC ACAATATGGA CGATGGAGAA AAACAGTTAC ATTTCTTTAT 480
GGATCAAGAA GTTTGTGTAC ACATAATCTC ATTTTGAGAT ATATAACTAT TTTTGTCTTT 540
CAGAAGTGAA TCAAAATATT TCAAAATGCT GTCTTATGAA ACTACAATAT TCTCACAGAT 600
TAGAAAAGTT TTTCTGTAAA AGTCAGATAG TAAATATTTT AGGTTTTGCA GTGTCTTTTG 660
CAACTACTCA ACTTTCCTAC TGTAGCACAA GAGTAGCTGT GGTACTGTGC AAATAAATTG 720
CTTGTGTTCC AATAAAGCTT CATTTACAAA AACATGCCAT GGGCCATATT TGGCCTGTAC 780
ACTGTTGTTT GCCAAGTCCT AATATAGTTG CTTAGCAAGT ATTGTGAGCT ATTTGAGGAA 840
GACATGAAAG TTCATTGGGT TGCTAAAAAG TATGTAGAAA TTCAAAGGAA AATTAAAATT 900
TAGGCTAAGT TATAATACAC TGTTTTAACA ATTGTAAAAT GTAAGAGAAA TTTACAAATA 960
AAAATCCCAA ATAAAA

Seq ID NO: 239 DNA sequence
Nucleic Acid Accession #: NM_001786.1
Coding sequence: 130-1023

1 11 21 31 41 51

GGGGGGGGGG GGCACTTGGC TTCAAAGCTG GCTCTTGGAA ATTGAGCGGA GAGCGACGCG 60
GTTGTTGTAG CTGCCGCTGC GGCCGCCGCG GAATAATAAG CCGGGATCTA CCATACCCAT 120
TGACTAACTA TGGAAGATTA TACCAAAATA GAGAAAATTG GAGAAGGTAC CTATGGAGTT 180
GTGTATAAGG GTAGACACAA AACTACAGGT CAAGTGGTAG CCATGAAAAA AATCAGACTA 240
GAAAGTGAAG AGGAAGGGGT TCCTAGTACT GCAATTCGGG AAATTTCTCT ATTAAAGGAA 300
CTTCGTCATC CAAATATAGT CAGTCTTCAG GATGTGCTTA TGCAGGATTC CAGGTTATAT 360
CTCATCTTTG AGTTTCTTTC CATGGATCTG AAGAAATACT TGGATTCTAT CCCTCCTGGT 420
CAGTACATGG ATTCTTCACT TGTTAAGAGT TATTTATACC AAATCCTACA GGGGATTGTG 480
TTTTGTCACT CTAGAAGAGT TCTTCACAGA GACTTAAAAC CTCAAAATCT CTTGATTGAT 540
GACAAAGGAA CAATTAAACT GGCTGATTTT GGCCTTGCCA GAGCTTTTGG AATACCTATC 600
AGAGTATATA CACATGAGGT AGTAACACTC TGGTACAGAT CTCCAGAAGT ATTGCTGGGG 660
TCAGCTCGTT ACTCAACTCC AGTTGACATT TGGAGTATAG GCACCATATT TGCTGAACTA 720
GCAACTAAGA AACCACTTTT CCATGGGGAT TCAGAAATTG ATCAACTCTT CAGGATTTTC 780
AGAGCTTTGG GCACTCCCAA TAATGAAGTG TGGCCAGAAG TGGAATCTTT ACAGGACTAT 840
AAGAATACAT TTCCCAAATG GAAACCAGGA AGCCTAGCAT CCCATGTCAA AAACTTGGAT 900
GAAAATGGCT TGGATTTGCT CTCGAAAATG TTAATCTATG ATCCAGCCAA ACGAATTTCT 960
GGCAAAATGG CACTGAATCA TCCATATTTT AATGATTTGG ACAATCAGAT TAAGAAGATG 1020
TAGCTTTCTG ACAAAAAGTT TCCATATGTT ATGTCAACAG ATAGTTGTGT TTTTATTGTT 1080
AACTCTTGTC TATTTTTGTC TTATATATAT TTCTTTGTTA TCAAACTTCA GCTGTACTTC 1140
GTCTTCTAAT TTCAAAAATA TAACTTAAAA ATGTAAATAT TCTATATGAA TTTAAATATA 1200
ATTCTGTAAA TGTGAAAAAA AAAAAAAAAA AAAAA

Seq ID NO: 240 Protein sequence:
Protein Accession #: NP_001777.1

1 11 21 31 41 51

MEDYTKIEKI GEGTYGVVYK GRHKTTGQVV AMKKIRLESE EEGVPSTAIR EISLLKELRH 60
PNIVSLQDVL MQDSRLYLIF EFLSMDLKKY LDSIPPGQYM DSSLVKSYLY QILQGIVFCH 120

```
SRRVLHRDLK PQNLLIDDKG TIKLADFGLA RAFGIPIRVY THEVVTLWYR SPEVLLGSAR  180
YSTPVDIWSI GTIFAELATK KPLFHGDSEI DQLFRIFRAL GTPNNEVWPE VESLQDYKNT  240
FPKWKPGSLA SHVKNLDENG LDLLSKMLIY DPAKRISGKM ALNHPYFNDL DNQIKKM
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Seq ID NO: 241 DNA sequence
Nucleic Acid Accession #: NM_033379.1
Coding sequence: 132-854

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1          11         21         31         41         51
|          |          |          |          |          |
CGCCCGCGCG CGGGCTCAAC TTTGTAGAGC GAGGGGCCAA CTTGGCAGAG CGCGCGGCCA   60
GCTTTGCAGA GAGCGCCCTC CAGGGACTAT GCGTGCGGGG ACACGGGATC TACCCATACC  120
ATTGACTAAC TATGGAAGAT TATACCAAAA TAGAGAAAAT TGGAGAAGGT ACCTATGGAG  180
TTGTGTATAA GGGTAGACAC AAAACTACAG GTCAAGTGGT AGCCATGAAA AAAATCAGAC  240
TAGAAAGTGA AGAGGAAGGG GTTCCTAGTA CTGCAATTCG GGAAATTTCT CTATTAAAGG  300
AACTTCGTCA TCCAAATATA GTCAGTCTTC AGGATGTGCT TATGCAGGAT TCCAGGTTAT  360
ATCTCATCTT TGAGTTTCTT TCCATGGATC TGAAGAAATA CTTGGATTCT ATCCCTCCTG  420
GTCAGTACAT GGATTCTTCA CTTGTTAAGG TAGTAACACT CTGGTACAGA TCTCCAGAAG  480
TATTGCTGGG GTCAGCTCGT TACTCAACTC CAGTTGACAT TTGGAGTATA GGCACCATAT  540
TTGCTGAACT AGCAACTAAG AAACCACTTT TCCATGGGGA TTCAGAAATT GATCAACTCT  600
TCAGGATTTT CAGAGCTTTG GGCACTCCCA ATAATGAAGT GTGGCCAGAA GTGGAATCTT  660
TACAGGACTA TAAGAATACA TTTCCCAAAT GGAAACCAGG AAGCCTAGCA TCCCATGTCA  720
AAAACTTGGA TGAAAATGGC TTGGATTTGC TCTCGAAAAT GTTAATCTAT GATCCAGCCA  780
AACGAATTTC TGGCAAAATG GCACTGAATC ATCCATATTT TAATGATTTG GACAATCAGA  840
TTAAGAAGAT GTAGCTTTCT GACAAAAAGT TTCCATATGT TATGTCAACA GATAGTTGTG  900
TTTTTATTGT TAACTCTTGT CTATTTTTGT CTTATATATA TTTCTTTGTT ATCAAACTTC  960
AGCTGTACTT CGTCTTCTAA TTTCAAAAAT ATAACTTAAA AATGTAAATA TTCTATATGA 1020
ATTTAAATAT AATTCTGTAA ATGTGAAAAA AAAAAAAAAA AAAAAA
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Seq ID NO: 242 Protein sequence:
Protein Accession #: NP_203698.1

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1          11         21         31         41         51
|          |          |          |          |          |
MEDYTKIEKI GEGTYGVVYK GRHKTTGQVV AMKKIRLESE EEGVPSTAIR EISLLKELRH   60
PNIVSLQDVL MQDSRLYLIF EFLSMDLKKY LDSIPPGQYM DSSLVKVVTL WYRSPEVLLG  120
SARYSTPVDI WSIGTIFAEL ATKKPLFHGD SEIDQLFRIF RALGTPNNEV WPEVESLQDY  180
KNTFPKWKPG SLASHVKNLD ENGLDLLSKM LIYDPAKRIS GKMALNHPYF NDLDNQIKKM
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Seq ID NO: 243 DNA sequence
Nucleic Acid Accession #: AF101051.1
Coding sequence: 221-856

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1          11         21         31         41         51
|          |          |          |          |          |
GAGCAACCTC AGCTTCTAGT ATCCAGACTC CAGCGCCGCC CCGGGCGCGG ACCCCAACCC   60
CGACCCAGAG CTTCTCCAGC GGCGGCGCAG CGAGCAGGGC TCCCCGCCTT AACTTCCTCC  120
GCGGGGCCCA GCCACCTTCG GGAGTCCGGG TTGCCCACCT GCAAACTCTC CGCCTTCTGC  180
ACCTGCCACC CCTGAGCCAG CGCGGGCGCC CGAGCGAGTC ATGGCCAACG CGGGGCTGCA  240
GCTGTTGGGC TTCATTCTCG CCTTCCTGGG ATGGATCGGC GCCATCGTCA GCACTGCCCT  300
GCCCCAGTGG AGGATTTACT CCTATGCCGG CGACAACATC GTGACCGCCC AGGCCATGTA  360
CGAGGGGCTG TGGATGTCCT GCGTGTCGCA GAGCACCGGG CAGATCCAGT GCAAAGTCTT  420
TGACTCCTTG CTGAATCTGA GCAGCACATT GCAAGCAACC CGTGCCTTGA TGGTGGTTGG  480
CATCCTCCTG GGAGTGATAG CAATCTTTGT GGCCACCGTT GGCATGAAGT GTATGAAGTG  540
CTTGGAAGAC GATGAGGTGC AGAAGATGAG GATGGCTGTC ATTGGGGGTG CGATATTTCT  600
TCTTGCAGGT CTGGCTATTT TAGTTGCCAC AGCATGGTAT GGCAATAGAA TCGTTCAAGA  660
ATTCTATGAC CCTATGACCC CAGTCAATGC CAGGTACGAA TTTGGTCAGG CTCTCTTCAC  720
TGGCTGGGCT GCTGCTTCTC TCTGCCTTCT GGGAGGTGCC CTACTTTGCT GTTCCTGTCC  780
CCGAAAAACA ACCTCTTACC CAACACCAAG GCCCTATCCA AAACCTGCAC CTTCCAGCGG  840
GAAAGACTAC GTGTGACACA GAGGCAAAAG GAGAAAATCA TGTTGAAACA AACCGAAAAT  900
GGACATTGAG ATACTATCAT TAACATTAGG ACCTTAGAAT TTTGGGTATT GTAATCTGAA  960
GTATGGTATT ACAAAACAAA CAAACAAACA AAAAACCCAT GTGTTAAAAT ACTCAGTGCT 1020
AAACATGGCT TAATCTTATT TTATCTTCTT TCCTCAATAT AGGAGGGAAG ATTTTACCAT 1080
TTGTATTACT GCTTCCCATT GAGTAATCAT ACTCAAATGG GGGAAGGGGT GCTCCTTAAA 1140
TATATATAGA TATGTATATA TACATGTTTT TCTATTAAAA ATAGACAGTA AAATACTATT 1200
CTCATTATGT TGATACTAGC ATACTTAAAA TATCTCTAAA ATAGGTAAAT GTATTTAATT 1260
CCATATTGAT GAAGATGTTT ATTGGTATAT TTTCTTTTTC GTCCTTATAT ACATATGTAA 1320
CAGTCAAATA TCATTTACTC TTCTTCATTA GCTTTGGGTG CCTTTGCCAC AAGACCTAGC 1380
CTAATTTACC AAGGATGAAT TCTTTCAATT CTTCATGCGT GCCCTTTTCA TATACTTATT 1440
TTATTTTTTA CCATAATCTT ATAGCACTTG CATCGTTATT AAGCCCTTAT TTGTTTTGTG 1500
TTTCATTGGT CTCTATCTCC TGAATCTAAC ACATTTCATA GCCTACATTT TAGTTTCTAA 1560
AGCCAAGAAG AATTTATTAC AAATCAGAAC TTTGGAGGCA AATCTTTCTG CATGACCAAA 1620
GTGATAAATT CCTGTTGACC TTCCCACACA ATCCCTGTAC TCTGACCCAT AGCACTCTTG 1680
TTTGCTTTGA AAATATTTGT CCAATTGAGT AGCTGCATGC TGTTCCCCCA GGTGTTGTAA 1740
CACAACTTTA TTGATTGAAT TTTTAAGCTA CTTATTCATA GTTTTATATC CCCCTAAACT 1800
ACCTTTTTGT TCCCCATTCC TTAATTGTAT TGTTTTCCCA AGTGTAATTA TCATGCGTTT 1860
TATATCTTCC TAATAAGGTG TGGTCTGTTT GTCTGAACAA AGTGCTAGAC TTTCTGGAGT 1920
GATAATCTGG TGACAAATAT TCTCTCTGTA GCTGTAAGCA AGTCACTTAA TCTTTCTACC 1980
TCTTTTTTCT ATCTGCCAAA TTGAGATAAT GATACTTAAC CAGTTAGAAG AGGTAGTGTG 2040
AATATTAATT AGTTTATATT ACTCTCATTC TTTGAACATG AACTATGCCT ATGTAGTGTC 2100
TTTATTTGCT CAGCTGGCTG AGACACTGAA GAAGTCACTG AACAAAACCT ACACACGTAC 2160
CTTCATGTGA TTCACTGCCT TCCTCTCTCT ACCAGTCTAT TTCCACTGAA CAAAACCTAC 2220
ACACATACCT TCATGTGGTT CAGTGCCTTC CTCTCTCTAC CAGTCTATTT CCACTGAACA 2280
AAACCTACGC ACATACCTTC ATGTGGCTCA GTGCCTTCCT CTCTCTACCA GTCTATTTCC 2340
ATTCTTTCAG CTGTGTCTGA CATGTTTGTG CTCTGTTCCA TTTTAACAAC TGCTCTTACT 2400
TTTCCAGTCT GTACAGAATG CTATTTCACT TGAGCAAGAT GATGTATGGA AAGGGTGTTG 2460
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GCACTGGTGT CTGGAGACCT GGATTTGAGT CTTGGTGCTA TCAATCACCG TCTGTGTTTG 2520
AGCAAGGCAT TTGGCTGCTG TAAGCTTATT GCTTCATCTG TAAGCGGTGG TTTGTAATTC 2580
CTGATCTTCC CACCTCACAG TGATGTTGTG GGGATCCAGT GAGATAGAAT ACATGTAAGT 2640
GTGGTTTTGT AATTTGAAAA GTGCTATACT AAGGGAAAGA ATTGAGGAAT TAACTGCATA 2700
CGTTTTGGTG TTGCTTTTCA AATGTTTGAA AATAAAAAAA TGTTAAGAAA TGGGTTTCTT 2760
GCCTTAACCA GTCTCTCAAG TGATGAGACA GTGAAGTAAA ATTGAGTGCA CTAAACGAAT 2820
AAGATTCTGA GGAAGTCTTA TCTTCTGCAG TGAGTATGGC CCAATGCTTT CTGTGGCTAA 2880
ACAGATGTAA TGGGAAGAAA TAAAAGCCTA CGTGTTGGTA AATCCAACAG CAAGGGAGAT 2940
TTTTGAATCA TAATAACTCA TAAGGTGCTA TCTGTTCAGT GATGCCCTCA GAGCTCTTGC 3000
TGTTAGCTGG CAGCTGACGC TGCTAGGATA GTTAGTTTGG AAATGGTACT TCATAATAAA 3060
CTACACAAGG AAAGTCAGCC ACCGTGTCTT ATGAGGAATT GGACCTAATA AATTTTAGTG 3120
TGCCTTCCAA ACCTGAGAAT ATATGCTTTT GGAAGTTAAA ATTTAAATGG CTTTTGCCAC 3180
ATACATAGAT CTTCATGATG TGTGAGTGTA ATTCCATGTG GATATCAGTT ACCAAACATT 3240
ACAAAAAAAT TTTATGGCCC AAAATGACCA ACGAAATTGT TACAATAGAA TTTATCCAAT 3300
TTTGATCTTT TTATATTCTT CTACCACACC TGGAAACAGA CCAATAGACA TTTTGGGGTT 3360
TTATAATGGG AATTTGTATA AAGCATTACT CTTTTTCAAT AAATTGTTTT TTAATTTAAA 3420
AAAAGGAAAA AAAAAAAAAA AAA
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Seq ID NO: 244 Protein sequence:
Protein Accession #: AAD16433.1

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1          11         21         31         41         51
|          |          |          |          |          |
MANAGLQLLG FILAFLGWIG AIVSTALPQW RIYSYAGDNI VTAQAMYEGL WMSCVSQSTG 60
QIQCKVFDSL LNLSSTLQAT RALMVVGILL GVIAIFVATV GMKCMKCLED DEVQKMRMAV 120
IGGAIFLLAG LAILVATAWY GNRIVQEFYD PMTPVNARYE FGQALFTGWA AASLCLLGGA 180
LLCCSCPRKT TSYPTPRPYP KPAPSSGKDY V
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Seq ID NO: 245 DNA sequence
Nucleic Acid Accession #: CAT cluster

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1          11         21         31         41         51
|          |          |          |          |          |
TTTTTTTTTT TTTTTTTTTT TTTTTCAAGG AGAGCACAAG GAACTTTATT AATGACTTTC 60
TTAATGGTTA AATGCTGTTT ACCAAGTGAC CCAGAGGCAG CGTGGTTTAG TGGTTTCAAC 120
AGCATGGTCC CGAGAGTCTG ACAAACCTCA GTTCAAATCC TTCTTTTGTC TTCACTTAGT 180
TTTTCTTCCT GAGATTTAGT TTCTTCATCG TTAACAATGA GGATATTAAT ATGTTTCACA 240
CAGTTGTTAT GAAGAATGCA TATATTAGAA TGCCTGTAGT CTCAGCTACT CAGGAGGCTA 300
AGGTGGGGAG GTCGCTCAAG CCCAGGAATT CAAAGCTGCA ATGCATTATG ATTACAGCTG 360
TTAATAGCCA CTGCACTTCA GCCTGGGCAA TGTAGTAAGA TCCCATCTCT GGCTCGGAGG 420
GTCCTACGCC CACGGAGTCT CGCTGATTGC TAGCACAGCA GTCTGAGATC AAACTGCA
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Seq ID NO: 246 DNA sequence
Nucleic Acid Accession #: XM_058553.2
Coding sequence: 897-1400

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AATTTTCAGA AGTTTCGTAT GGGGATGGTT TTATATAAAT TCAGGTTTTT CCCACAATAA 60
TAAATGTATT TAGTCTCAGT GCTCAATAGA AGAGATTTCT AATAGAAAAG GATTCAAACT 120
GTGAAACCAT TTCTCTTTTA ATGTTTCACA TTCCTGTTAC AGATTTGTTC TCTTGTGACT 180
CTGTTATCCA TAATATGGAC AGTTCTTGAG TCCTAACATT GAGAGGTTTT CCCTTAGTGC 240
ATAGAGGGAA TGAGTATTAA TTGGAGAAGC TTAAAGTATT GCCACTTTAG CACTGAAGAT 300
TGGGATGAGA GGAGGTGAAA CCTCACTAGA AAAAGGGACA ATGTTAGTGT GGCCCTTCCT 360
GATCATGTTT AAGAAAAGTC ATGAAAATGG TGAACTAGTG TTTCCAAGCA TATTGGAAGG 420
GTTGAGTGTA TACTGTCTGT CAAAGACTTC CAGCATTTCC AGGTCCTAGA GAGGAACAAG 480
ACTGGTAACC TGCCTATCTG TATTTTTAAG AACCCAGGAG GAAAGCTTTA TAATAGAACA 540
TTATTTCTGT GTTTATGTAT AAGGGGTTTT TTGTTTTTTT AAAGACAGGA TCTCACTCCA 600
TTGTCCAGGC CAAGTGCAAT GGCACGAACC TCATAGCTCC TGGACTTAAG TGATCTGCCT 660
GCCTTTGCCT CCTGAGTAGC TGGGACTACA GGCATGAGCC CCCATGCCTG GCTAAGTTTG 720
TTTTTTTGTT TGTTTGTTTG TTTGTTTTTG GGGGGGGTTG TTTTGTTTTT TGTAGAGACG 780
TAGTCTTGCT TTGTTGCCAG GCTAGTCTCA AACTCCTGGC TTCAAGTGAT CCTCCTGCCT 840
CAGCCTCCCA GAGTGCTAGG ATTACAGCAC TTGGATTCAG CTTCTTCATT TCCAACATGG 900
AAGAAACTTA CACCGACTCC CTGGACCCTG AGAAGCTATT GCAATGCCCC TATGACAAAA 960
ACCATCAAAT CAGGGCTTGC AGGTTTCCTT ATCATCTTAT CAAGTGCAGA AAGAATCATC 1020
CTGATGTTGC AAGCAAATTG GCTACTTGTC CCTTCAATGC TCGCCACCAG GTTCCTCGAG 1080
CTGAAATTAG TCATCATATC TCAAGCTGTG ATGACAGAAG TTGTATTGAG CAAGATGTTG 1140
TCAACCAAAC CAGGAGCCTT AGACAAGAGA CTCTGGCTGA GAGCACTTGG CAGTGCCCTC 1200
CTTGCGATGA AGACTGGGAT AAAGATTTGT GGGAGCAGAC CAGCACCCCA TTTGTCTGGG 1260
GCACAACTCA CTACTCTGAC AACAACAGCC CTGCGAGCAA CATAGTTACA GAACATAAGA 1320
ATAACCTGGC TTCAGGCATG CGAGTTCCCA AATCTCTGCC GTATGTTCTG CCATGGAAAA 1380
ACAATGGAAA TGCACAGTAA CTGAATACCT ATCTCATCAA ATGCCAGACC CTAGAAGACT 1440
GTTGCTTCTT CTTCTACCAG TGGGTTCTCA TTTTCCTCCT AATCTAATTA TAGAATGGTA 1500
AACTCCCTGT GACTTTCCAA ACTGACAAGC ACACTTTTTT CCTCCCCCCT TGAATCCTCA 1560
TTTAATGCAA GAACCCTCAT ACTCAGAAGC TTCCAAATAA ACCTTTGATA CAGATTG
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Seq ID NO: 247 Protein sequence:
Protein Accession #: XP_058553.1

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1          11         21         31         41         51
|          |          |          |          |          |
MEETYTDSLD PEKLLQCPYD KNHQIRACRF PYHLIKCRKN HPDVASKLAT CPFNARHQVP 60
RAEISHHISS CDDRSCIEQD VVNQTRSLRQ ETLAESTWQC PPCDEDWDKD LWEQTSTPFV 120
WGTTHYSDNN SPASNIVTEH KNNLASGMRV PKSLPYVLPW KNNGNAQ
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Seq ID NO: 248 DNA sequence
Nucleic Acid Accession #: NM_003392
Coding sequence: 758..1855

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AACTGATTAT GAAACATACG ATGTTAATTC GGAGCTGCAT TTCCCAGCTG GGCACTCTCG   120
CGCGCTGGTC CCCGGGGCCT CGCCCCCCAC CCCCTGCCCT TCCCTCCCGC GTCCTGCCCC   180
CATCCTCCAC CCCCCGCGCT GGCCACCCCG CCTCCTTGGC AGCCTCTGGC GGCAGCGCGC   240
TCCACTCGCC TCCCGTGCTC CTCTCGCCCA TGGAATTAAT TCTGGCTCCA CTTGTTGCTC   300
GGCCCAGGTT GGGGAGAGGA CGGAGGGTGG CCGCAGCGGG TTCCTGAGTG AATTACCCAG   360
GAGGGACTGA GCACAGCACC AACTAGAGAG GGGTCAGGGG GTGCGGGACT CGAGCGAGCA   420
GGAAGGAGGC AGCGCCTGGC ACCAGGGCTT TGACTCAACA GAATTGAGAC ACGTTTGTAA   480
TCGCTGGCGT GCCCCGCGCA CAGGATCCCA GCGAAAATCA GATTTCCTGG TGAGGTTGCG   540
TGGGTGGATT AATTTGGAAA AAGAAACTGC CTATATCTTG CCATCAAAAA ACTCACGGAG   600
GAGAAGCGCA GTCAATCAAC AGTAAACTTA AGAGACCCCC GATGCTCCCC TGGTTTAACT   660
TGTATGCTTG AAAATTATCT GAGAGGGAAT AAACATCTTT TCCTTCTTCC CTCTCCAGAA   720
GTCCATTGGA ATATTAAGCC CAGGAGTTGC TTTGGGGATG GCTGGAAGTG CAATGTCTTC   780
CAAGTTCTTC CTAGTGGCTT TGGCCATATT TTTCTCCTTC GCCCAGGTTG TAATTGAAGC   840
CAATTCTTGG TGGTCGCTAG GTATGAATAA CCCTGTTCAG ATGTCAGAAG TATATATTAT   900
AGGAGCACAG CCTCTCTGCA GCCAACTGGC AGGACTTTCT CAAGGACAGA AGAAACTGTG   960
CCACTTGTAT CAGGACCACA TGCAGTACAT CGGAGAAGGC GCGAAGACAG GCATCAAAGA  1020
ATGCCAGTAT CAATTCCGAC ATCGACGGTG GAACTGCAGC ACTGTGGATA ACACCTCTGT  1080
TTTTGGCAGG GTGATGCAGA TAGGCAGCCG CGAGACGGCC TTCACATACG CCGTGAGCGC  1140
AGCAGGGGTG GTGAACGCCA TGAGCCGGGC GTGCCGCGAG GGCGAGCTGT CCACCTGCGG  1200
CTGCAGCCGC GCCGCGCGCC CCAAGGACCT GCCGCGGGAC TGGCTCTGGG GCGGCTGCGG  1260
CGACAACATC GACTATGGCT ACCGCTTTGC CAAGGAGTTC GTGGACGCCC GCGAGCGGGA  1320
GCGCATCCAC GCCAAGGGCT CCTACGAGAG TGCTCGCATC CTCATGAACC TGCACAACAA  1380
CGAGGCCGGC CGCAGGACGG TGTACAACCT GGCTGATGTG GCCTGCAAGT GCCATGGGGT  1440
GTCCGGCTCA TGTAGCCTGA AGACATGCTG GCTGCAGCTG GCAGACTTCC GCAAGGTGGG  1500
TGATGCCCTG AAGGAGAAGT ACGACAGCGC GGCGGCCATG CGGCTCAACA GCCGGGGCAA  1560
GTTGGTACAG GTCAACAGCC GCTTCAACTC GCCCACCACA CAAGACCTGG TCTACATCGA  1620
CCCCAGCCCT GACTACTGCG TGCGCAATGA GAGCACCGGC TCGCTGGGCA CGCAGGGCCG  1680
CCTGTGCAAC AAGACGTCGG AGGGCATGGA TGGCTGCGAG CTCATGTGCT GCGGCCGTGG  1740
GTACGACCAG TTCAAGACCG TGCAGACGGA GCGCTGCCAC TGCAAGTTCC ACTGGTGCTG  1800
CTACGTCAAG TGCAAGAAGT GCACGGAGAT CGTGGACCAG TTTGTGTGCA AGTAGTGGGT  1860
GCCACCCAGC ACTCAGCCCC GCTCCCAGGA CCCGCTTATT TATAGAAAGT ACAGTGATTC  1920
TGGTTTTTGG TTTTTAGAAA TATTTTTTAT TTTTCCCCAA GAATTGCAAC CGGAACCATT  1980
TTTTTTCCTG TTACCATCTA AGAACTCTGT GGTTTATTAT TAATATTATA ATTATTATTT  2040
GGCAATAATG GGGGTGGGAA CCACGAAAAA TATTTATTTT GTGGATCTTT GAAAAGGTAA  2100
TACAAGACTT CTTTTGGATA GTATAGAATG AAGGGGGAAA TAACACATAC CCTAACTTAG  2160
CTGTGTGGGA CATGGTACAC ATCCAGAAGG TAAAGAAATA CATTTTCTTT TTCTCAAATA  2220
TGCCATCATA TGGGATGGGT AGGTTCCAGT TGAAAGAGGG TGGTAGAAAT CTATTCACAA  2280
TTCAGCTTCT ATGACCAAAA TGAGTTGTAA ATTCTCTGGT GCAAGATAAA AGGTCTTGGG  2340
AAAACAAAAC AAAACAAAAC AAACCTCCCT TCCCCAGCAG GGCTGCTAGC TTGCTTTCTG  2400
CATTTTCAAA ATGATAATTT ACAATGGAAG GACAAGAATG TCATATTCTC AAGGAAAAAA  2460
GGTATATCAC ATGTCTCATT CTCCTCAAAT ATTCCATTTG CAGACAGACC GTCATATTCT  2520
AATAGCTCAT GAAATTTGGG CAGCAGGGAG GAAAGTCCCC AGAAATTAAA AAATTTAAAA  2580
CTCTTATGTC AAGATGTTGA TTTGAAGCTG TTATAAGAAT TGGGATTCCA GATTTGTAAA  2640
AAGACCCCCA ATGATTCTGG ACACTAGATT TTTTGTTTGG GGAGGTTGGC TTGAACATAA  2700
ATGAAATATC CTGTATTTTC TTAGGGATAC TTGGTTAGTA AATTATAATA GTAGAAATAA  2760
TACATGAATC CCATTCACAG GTTTCTCAGC CCAAGCAACA AGGTAATTGC GTGCCATTCA  2820
GCACTGCACC AGAGCAGACA ACCTATTTGA GGAAAAACAG TGAAATCCAC CTTCCTCTTC  2880
ACACTGAGCC CTCTCTGATT CCTCCGTGTT GTGATGTGAT GCTGGCCACG TTTCCAAACG  2940
GCAGCTCCAC TGGGTCCCCT TTGGTTGTAG GACAGGAAAT GAAACATTAG GAGCTCTGCT  3000
TGGAAAACAG TTCACTACTT AGGGATTTTT GTTTCCTAAA ACTTTTATTT TGAGGAGCAG  3060
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TATCACTGTT ATGATCCTGT GTTTAGATTA TCCACTCATG CTTCTCCTAT TGTACTGCAG  3180
GTGTACCTTA AAACTGTTCC CAGTGTACTT GAACAGTTGC ATTTATAAGG GGGGAAATGT  3240
GGTTTAATGG TGCCTGATAT CTCAAAGTCT TTTGTACATA ACATATATAT ATATATACAT  3300
ATATATAAAT ATAAATATAA ATATATCTCA TTGCAGCCAG TGATTTAGAT TTACAGCTTA  3360
CTCTGGGGTT ATCTCTCTGT CTAGAGCATT GTTGTCCTTC ACTGCAGTCC AGTTGGGATT  3420
ATTCCAAAAG TTTTTTGAGT CTTGAGCTTG GGCTGTGGCC CCGCTGTGAT CATACCCTGA  3480
GCACGACGAA GCAACCTCGT TTCTGAGGAA GAAGCTTGAG TTCTGACTCA CTGAAATGCG  3540
TGTTGGGTTG AAGATATCTT TTTTTCTTTT CTGCCTCACC CCTTTGTCTC CAACCTCCAT  3600
TTCTGTTCAC TTTGTGGAGA GGGCATTACT TGTTCGTTAT AGACATGGAC GTTAAGAGAT  3660
ATTCAAAACT CAGAAGCATC AGCAATGTTT CTCTTTTCTT AGTTCATTCT GCAGAATGGA  3720
AACCCATGCC TATTAGAAAT GACAGTACTT ATTAATTGAG TCCCTAAGGA ATATTCAGCC  3780
CACTACATAG ATAGCTTTTT TTTTTTTTTT TTTTTTTTAA TAAGGACACC TCTTTCCAAA  3840
CAGGCCATCA AATATGTTCT TATCTCAGAC TTACGTTGTT TTAAAAGTTT GGAAAGATAC  3900
ACATCTTTTC ATACCCCCCC TTAGGAGGTT GGGCTTTCAT ATCACCTCAG CCAACTGTGG  3960
CTCTTAATTT ATTGCATAAT GATATCCACA TCAGCCAACT GTGGCTCTTT AATTTATTGC  4020
ATAATGATAT TCACATCCCC TCAGTTGCAG TGAATTGTGA GCAAAAGATC TTGAAAGCAA  4080
AAAGCACTAA TTAGTTTAAA ATGTCACTTT TTTGGTTTTT ATTATACAAA AACCATGAAG  4140
TACTTTTTTT ATTTGCTAAA TCAGATTGTT CCTTTTTAGT GACTCATGTT TATGAAGAGA  4200
GTTGAGTTTA ACAATCCTAG CTTTTAAAAG AAACTATTTA ATGTAAAATA TTCTACATGT  4260
CATTCAGATA TTATGTATAT CTTCTAGCCT TTATTCTGTA CTTTTAATGT ACATATTTCT  4320
GTCTTGCGTG ATTTGTATAT TTCACTGGTT TAAAAAACAA ACATCGAAAG GCTTATTCCA  4380
AATGGAAGAT AGAATATAAA ATAAAACGTT ACTTGTAAAA AAAAAAAA
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Seq ID NO: 249 Protein sequence:
Protein Accession #: NP_003383

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1          11         21         31         41         51
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MAGSAMSSKF FLVALAIFFS FAQVVIEANS WWSLGMNNPV QMSEVYIIGA QPLCSQLAGL    60
SQGQKKLCHL YQDHMQYIGE GAKTGIKECQ YQFRHRRWNC STVDNTSVFG RVMQIGSRET   120
APTYAVSAAG VVNAMSRACR EGELSTCGCS RAARPKDLPR DWLWGGCGDN IDYGYRFAKE   180
FVDARERERI HAKGSYESAR ILMNLHNNEA GRRTVYNLAD VACKCHGVSG SCSLKTCWLQ   240
LADFRKVGDA LKEKYDSAAA MRLNSRGKLV QVNSRFNSPT TQDLVYIDPS PDYCVRNEST   300
GSLGTQGRLC NKTSEGMDGC ELMCCGRGYD QFKTVQTERC HCKFHWCCYV KCKKCTEIVD   360
QFVCK
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Seq ID NO: 250 DNA sequence
Nucleic Acid Accession #: NM_014058
Coding sequence: 56..1324

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TCGGCCAGAT GTGGTGAGGG CTAGGAAAAG AGTTTGTTGG GAACCCTGGG TTATCGGCCT   120
CGTCATCTTC ATATCCCTGA TTGTCCTGGC AGTGTGCATT GGACTCACTG TTCATTATGT   180
GAGATATAAT CAAAAGAAGA CCTACAATTA CTATAGCACA TTGTCATTTA CAACTGACAA   240
ACTATATGCT GAGTTTGGCA GAGAGGCTTC TAACAATTTT ACAGAAATGA GCCAGAGACT   300
TGAATCAATG GTGAAAAATG CATTTTATAA ATCTCCATTA AGGGAAGAAT TTGTCAAGTC   360
TCAGGTTATC AAGTTCAGTC AACAGAAGCA TGGAGTGTTG GCTCATATGC TGTTGATTTG   420
TAGATTTCAC TCTACTGAGG ATCCTGAAAC TGTAGATAAA ATTGTTCAAC TTGTTTTACA   480
TGAAAAGCTG CAAGATGCTG TAGGACCCCC TAAAGTAGAT CCTCACTCAG TTAAAATTAA   540
AAAAATCAAC AAGACAGAAA CAGACAGCTA TCTAAACCAT TGCTGCGGAA CACGAAGAAG   600
TAAAACTCTA GGTCAGAGTC TCAGGATCGT TGGTGGGACA GAAGTAGAAG AGGGTGAATG   660
GCCCTGGCAG GCTAGCCTGC AGTGGGATGG GAGTCATCGC TGTGGAGCAA CCTTAATTAA   720
TGCCACATGG CTTGTGAGTG CTGCTCACTG TTTTACAACA TATAAGAACC CTGCCAGATG   780
GACTGCTTCC TTTGGAGTAA CAATAAAACC TTCGAAAATG AAACGGGGTC TCCGGAGAAT   840
AATTGTCCAT GAAAAATACA AACACCCATC ACATGACTAT GATATTTCTC TTGCAGAGCT   900
TTCTAGCCCT GTTCCCTACA CAAATGCAGT ACATAGAGTT TGTCTCCCTG ATGCATCCTA   960
TGAGTTTCAA CCAGGTGATG TGATGTTTGT GACAGGATTT GGAGCACTGA AAAATGATGG  1020
TTACAGTCAA AATCATCTTC GACAAGCACA GGTGACTCTC ATAGACGCTA CAACTTGCAA  1080
TGAACCTCAA GCTTACAATG ACGCCATAAC TCCTAGAATG TTATGTGCTG GCTCCTTAGA  1140
AGGAAAAACA GATGCATGCC AGGGTGACTC TGGAGGACCA CTGGTTAGTT CAGATGCTAG  1200
AGATATCTGG TACCTTGCTG GAATAGTGAG CTGGGGAGAT GAATGTGCGA AACCCAACAA  1260
GCCTGGTGTT TATACTAGAG TTACGGCCTT GCGGGACTGG ATTACTTCAA AAACTGGTAT  1320
CTAAGAGAGA AAAGCCTCAT GGAACAGATA ACATTTTTTT TTGTTTTTTG GGTGTGGAGG  1380
CCATTTTTAG AGATACAGAA TTGGAGAAGA CTTGCAAAAC AGCTAGATTT GACTGATCTC  1440
AATAAACTGT TTGCTTGATG CAAAAAAAAA A
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Seq ID NO: 251 Protein sequence:
Protein Accession #: NP_054777

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DKLYAEFGRE ASNNFTEMSQ RLESMVKNAF YKSPLREEFV KSQVIKFSQQ KHGVLAHMLL   120
ICRFHSTEDP ETVDKIVQLV LHEKLQDAVG PPKVDPHSVK IKKINKTETD SYLNHCCGTR   180
RSKTLGQSLR IVGGTEVEEG EWPWQASLQW DGSHRCGATL INATWLVSAA HCFTTYKNPA   240
RWTASFGVTI KPSKMKRGLR RIIVHEKYKH PSHDYDISLA ELSSPVPYTN AVHRVCLPDA   300
SYEFQPGDVM FVTGFGALKN DGYSQNHLRQ AQVTLIDATT CNEPQAYNDA ITPRMLCAGS   360
LEGKTDACQG DSGGPLVSSD ARDIWYLAGI VSWGDECAKP NKPGVYTRVT ALRDWITSKT   420
GI
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Seq ID NO: 252 DNA sequence
Nucleic Acid Accession #: NM_003504.2
Coding sequence: 71-1771

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CGCCGTGGCT ATGTTCGTGT CCGATTTCCG CAAAGAGTTC TACGAGGTGG TCCAGAGCCA   120
GAGGGTCCTT CTCTTCGTGG CCTCGGACGT GGATGCTCTG TGTGCGTGCA AGATCCTTCA   180
GGCCTTGTTC CAGTGTGACC ACGTGCAATA TACGCTGGTT CCAGTTTCTG GGTGGCAAGA   240
ACTTGAAACT GCATTTCTTG AGCATAAAGA ACAGTTTCAT TATTTTATTC TCATAAACTG   300
TGGAGCTAAT GTAGACCTAT TGGATATTCT TCAACCTGAT GAAGACACTA TATTCTTTGT   360
GTGTGACACC CATAGGCCAG TCAATGTCGT CAATGTATAC AACGATACCC AGATCAAATT   420
ACTCATTAAA CAAGATGATG ACCTTGAAGT TCCCGCCTAT GAAGACATCT TCAGGGATGA   480
AGAGGAGGAT GAAGAGCATT CAGGAAATGA CAGTGATGGG TCAGAGCCTT CTGAGAAGCG   540
CACACGGTTA GAAGAGGAGA TAGTGGAGCA AACCATGCGG AGGAGGCAGC GGCGAGAGTG   600
GGAGGCCCGG AGAAGAGACA TCCTCTTTGA CTACGAGCAG TATGAATATC ATGGGACATC   660
GTCAGCCATG GTGATGTTTG AGCTGGCTTG GATGCTGTCC AAGGACCTGA ATGACATGCT   720
GTGGTGGGCC ATCGTTGGAC TAACAGACCA GTGGGTGCAA GACAAGATCA CTCAAATGAA   780
ATACGTGACT GATGTTGGTG TCCTGCAGCG CCACGTTTCC CGCCACAACC ACCGGAACGA   840
GGATGAGGAG AACACACTCT CCGTGGACTG CACACGGATC TCCTTTGAGT ATGACCTCCG   900
CCTGGTGCTC TACCAGCACT GGTCCCTCCA TGACAGCCTG TGCAACACCA GCTATACCGC   960
AGCCAGGTTC AAGCTGTGGT CTGTGCATGG ACAGAAGCGG CTCCAGGAGT TCCTTGCAGA  1020
CATGGGTCTT CCCCTGAAGC AGGTGAAGCA GAAGTTCCAG GCCATGGACA TCTCCTTGAA  1080
GGAGAATTTG CGGGAAATGA TTGAAGAGTC TGCAAATAAA TTTGGGATGA AGGACATGCG  1140
CGTGCAGACT TTCAGCATTC ATTTTGGGTT CAAGCACAAG TTTCTGGCCA GCGACGTGGT  1200
CTTTGCCACC ATGTCTTTGA TGGAGAGCCC CGAGAAGGAT GGCTCAGGGA CAGATCACTT  1260
CATCCAGGCT CTGGACAGCC TCTCCAGGAG TAACCTGGAC AAGCTGTACC ATGGCCTGGA  1320
ACTCGCCAAG AAGCAGCTGC GAGCCACCCA GCAGACCATT GCCAGCTGCC TTTGCACCAA  1380
CCTCGTCATC TCCCAGGGGC CTTTCCTGTA CTGCTCTCTC ATGGAGGGCA CTCCAGATGT  1440
CATGCTGTTC TCTAGGCCGG CATCCCTAAG CCTGCTCAGC AAACACCTGC TCAAGTCCTT  1500
TGTGTGTTCG ACAAAGAACC GGCGCTGCAA ACTGCTGCCC CTGGTGATGG CTGCCCCCCT  1560
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GAGCATGGAG CATGGCACAG TGACCGTGGT GGGCATCCCC CCAGAGACCG ACAGCTCGGA  1620
CAGGAAGAAC TTTTTTGGGA GGGCGTTTGA GAAGGCAGCG GAAAGCACCA GCTCCCGGAT  1680
GCTGCACAAC CATTTTGACC TCTCAGTAAT TGAGCTGAAA GCTGAGGATC GGAGCAAGTT  1740
TCTGGACGCA CTTATTTCCC TCCTGTCCTA GGAATTTGAT TCTTCCAGAA TGACCTTCTT  1800
ATTTATGTAA CTGGCTTTCA TTTAGATTGT AAGTTATGGA CATGATTTGA GATGTAGAAG  1860
CCATTTTTTA TTAAATAAAA TGCTTATTTT AGGCTCCGTC CCCAAAAAAA AAAAAAAAAA  1920
AAAAAAAAAA AA
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Seq ID NO: 253 Protein sequence:
Protein Accession #: NP_003495.1

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1          11         21         31         41         51
|          |          |          |          |          |
MFVSDFRKEF YEVVQSQRVL LFVASDVDAL CACKILQALF QCDHVQYTLV PVSGWQELET   60
AFLEHKEQFH YFILINCGAN VDLLDILQPD EDTIFFVCDT HRPVNVVNVY NDTQIKLLIK  120
QDDDLEVPAY EDIFRDEEED EEHSGNDSDG SEPSEKRTRL EEEIVEQTMR RRQRREWEAR  180
RRDILFDYEQ YEYHGTSSAM VMFELAWMLS KDLNDMLWWA IVGLTDQWVQ DKITQMKYVT  240
DVGVLQRHVS RHNHRNEDEE NTLSVDCTRI SFEYDLRLVL YQHWSLHDSL CNTSYTAARF  300
KLWSVHGQKR LQEFLADMGL PLKQVKQKFQ AMDISLKENL REMIEESANK FGMKDMRVQT  360
FSIHFGFKHK FLASDVVFAT MSLMESPEKD GSGTDHFIQA LDSLSRSNLD KLYHGLELAK  420
KQLRATQQTI ASCLCTNLVI SQGPFLYCSL MEGTPDVMLF SRPASLSLLS KHLLKSFVCS  480
TKNRRCKLLP LVMAAPLSME HGTVTVVGIP PETDSSDRKN FFGRAFEKAA ESTSSRMLHN  540
HFDLSVIELK AEDRSKFLDA LISLLS
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Seq ID NO: 254 DNA sequence
Nucleic Acid Accession #: NM_022337
Coding sequence: 48..683

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1          11         21         31         41         51
|          |          |          |          |          |
GGCTGCGCTT CCCTGGTCAG GCACGGCACG TCTGGCCGGC CGCCAGGATG CAGGCCCCGC    60
ACAAGGAGCA CCTGTACAAG TTGCTGGTGA TTGGCGACCT GGGCGTGGGG AAGACCAGTA   120
TCATCAAGCG CTACGTGCAC CAGAACTTCT CCTCGCACTA CCGGGCCACA ATCGGCGTGG   180
ACTTCGCGCT CAAGGTGCTC CACTGGGACC CGGAGACTGT GGTGCGCCTG CAGCTCTGGG   240
ATATCGCAGG TCAAGAAAGA TTTGGAAACA TGACGAGGGT CTATTACCGA GAAGCTATGG   300
GTGCATTTAT TGTCTTCGAT GTCACCAGGC CAGCCACATT TGAAGCAGTG GCAAAGTGGA   360
AAAATGATTT GGACTCCAAG TTAAGTCTCC CTAATGGCAA ACCGGTTTCA GTGGTTTTGT   420
TGGCCAACAA ATGTGACCAG GGGAAGGATG TGCTCATGAA CAATGGCCTC AAGATGGACC   480
AGTTCTGCAA GGAGCACGGT TTCGTAGGAT GGTTTGAAAC ATCAGCAAAG GAAAATATAA   540
ACATTGATGA AGCCTCCAGA TGCCTGGTGA AACACATACT TGCAAATGAG TGTGACCTAA   600
TGGAGTCTAT TGAGCCGGAC GTCGTGAAGC CCCATCTCAC ATCAACCAAG GTTGCCAGCT   660
GCTCTGGCTG TGCCAAATCC TAGTAGGCAC CTTTGCTGGT GTCTGGTAGG AATGACCTCA   720
TTGTTCCACA AATTGTGCCT CTATTTTTAC CATTTTGGGT AAACGTCAGG ATAGATATAC   780
CACATGTGGC AAGCCAAAGA TCTATGCCTC TGTTTTTTCA ATGAGAGAGA AATAGCAAAT   840
GTTCTTTCTA TGCTTTCCTC ACCATCATCA CAGTGTTTAC AAACTTTTGA AAATATTTAG   900
TCTGTTACAA ACTTCTGTCA TGTAGCTGAC CAAAATCCTG CAGGGCCACA GTCGGCACTG   960
TTATTTGCTT CTTTTAATCA GCAAAGGCCT CAAGTCTTAA AATAAAAGGG GAGAAGAACA  1020
AACTAGCTGT CAAGTCAAGG ACTGGCTTTC ACCTTGCCCT GGTGTCTTTT TCCAGATTTC  1080
AATATATTCT CTGATGGCCT GACAGGCCTA TTAAGTAGAT GTGATATTTT CTTCCAAGAT  1140
GACCTCCATT CTCGGCAGAC CTAAGAGTTG CCTCTGAGTT AGCTCTTTGG AATCGTGAAC  1200
ACAGGTGTGC TATATTGTCC TTGTCCTAAC TGTCACTTGC CATGGCCTGA ATGTTGGCTT  1260
AACTGAATAT TGTATGAAAA GACATGCCTC CATATGTGCC TTTCTGTTAG CTCTCTTTGA  1320
CTCAAGCTGT GGGGCTCCTC TATACATGCT ATACATGTAA TATATATTAT ATATATTTTT  1380
GCAAGTGAAC AATAAAACAT TAAAAGATAA AA
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Seq ID NO: 255 Protein sequence:
Protein Accession #: NP_071732

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1          11         21         31         41         51
|          |          |          |          |          |
MQAPHKEHLY KLLVIGDLGV GKTSIIKRYV HQNFSSHYRA TIGVDFALKV LHWDPETVVR   60
LQLWDIAGQE RFGNMTRVYY REAMGAFIVF DVTRPATFEA VAKWKNDLDS KLSLPNGKPV  120
SVVLLANKCD QGKDVLMNNG LKMDQFCKEH GFVGWFETSA KENINIDEAS RCLVKHILAN  180
ECDLMESIEP DVVKPHLTST KVASCSGCAK S
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Seq ID NO: 256 DNA sequence
Nucleic Acid Accession #: NM_016321
Coding sequence: 25..1464

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1          11         21         31         41         51
|          |          |          |          |          |
GGAACCGCCC GCTGCCAGCC CGGCCAGGCA CCCCTGCAGC ATGGCCTGGA ACACCAACCT   60
CCGCTGGCGG CTGCCGCTCA CCTGCCTGCT CCTGCAGGTG ATTATGGTGA TTCTCTTCGG  120
GGTGTTCGTG CGCTACGACT TCGAGGCCGA CGCCCACTGG TGGTCAGAGA GGACGCACAA  180
GAACTTGAGC GACATGGAGA ACGAATTCTA CTATCGCTAC CCAAGCTTCC AGGACGTGCA  240
CGTGATGGTC TTCGTGGGCT TCGGCTTCCT CATGACTTTC CTGCAGCGCT ACGGCTTCAG  300
CGCCGTGGGC TTCAACTTCC TGTTGGCAGC CTTCGGCATC CAGTGGGCGC TGCTCATGCA  360
GGGCTGGTTC CACTTCTTAC AAGACCGCTA CATCGTCGTG GGCGTGGAGA ACCTCATCAA  420
CGCTGACTTC TGCGTGGCCT CTGTCTGCGT GGCCTTTGGG GCAGTTCTGG GTAAAGTCAG  480
CCCCATTCAG CTGCTCATCA TGACTTTCTT CCAAGTGACC CTCTTCGCTG TGAATGAGTT  540
CATTCTCCTT AACCTGCTAA AGGTGAAGGA TGCAGGAGGC TCCATGACCA TCCACACATT  600
TGGCGCCTAC TTTGGGCTCA CAGTGACCCG GATCCTCTAC CGACGCAACC TAGAGCAGAG  660
CAAGGAGAGA CAGAATTCTG TGTACCAGTC GGACCTCTTT GCCATGATTG GCACCCTCTT  720
CCTGTGGATG TACTGGCCCA GCTTCAACTC AGCCATATCC TACCATGGGG ACAGCCAGCA  780
CCGAGCCGCC ATCAACACCT ACTGCTCCTT GGCAGCCTGC GTGCTTACCT CGGTGGCAAT  840
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ATCCAGTGCC CTGCACAAGA AGGGCAAGCT GGACATGGTG CACATCCAGA ATGCCACGCT   900
CGCAGGAGGG GTGGCCGTGG GTACCGCTGC TGAGATGATG CTCATGCCTT ACGGTGCCCT   960
CATCATCGGC TTCGTCTGCG GCATCATCTC CACCCTGGGT TTTGTATACC TGACCCCATT  1020
CCTGGAGTCC CGGCTGCACA TCCAGGACAC ATGTGGCATT AACAATCTGC ATGGCATTCC  1080
TGGCATCATA GGCGGCATCG TGGGTGCTGT GACAGCGGCC TCCGCCAGCC TTGAAGTCTA  1140
TGGAAAAGAA GGGCTTGTCC ATTCCTTTGA CTTTCAAGGT TTCAACGGGG ACTGGACCGC  1200
AAGAACACAG GGAAAGTTCC AGATTTATGG TCTCTTGGTG ACCCTGGCCA TGGCCCTGAT  1260
GGGTGGCATC ATTGTGGGGC TCATTTTGAG ATTACCATTC TGGGGACAAC CTTCAGATGA  1320
GAACTGCTTT GAGGATGCGG TCTACTGGGA GATGCCTGAA GGGAACAGCA CTGTCTACAT  1380
CCCTGAGGAC CCCACCTTCA AGCCCTCAGG ACCCTCAGTA CCCTCAGTAC CCATGGTGTC  1440
CCCACTACCC ATGGCTTCCT CGGTACCCTT GGTACCCTAG GCTCCCAGGG CAGGTGAGGA  1500
GCAGGCTCCA CAGACTSTCC TGGGGCCCAG AGGAGCTGGT GCTGACCTAG CTAGGGATGC  1560
AAGAGTGAGC AAGCAGCACC CCCACCTGCT GGCTTGGCCT CAAGGTGCCT CCACCCCTGC  1620
CCTCCCCTTC ATCCCAGGGG GTCTGMCTGA GAATGGAGAA GGAGAAGCTA CAAAGTGGGC  1680
ATCCAAGCCG GGTTCTGGCT GCAGAAGTTC TGCCTCTGCC TGGGGTCTTG GCCACATTGG  1740
AGAAAAACAG GCTCAAAGTG GGGCTGGGAC CTGGTGGGTG AACCTGAGCT CTCCCAGGAG  1800
ACAACTTAGC TGCCAGTCAC CACCTATGAG GCTCTTCTAC CCCGTGCCTG CACCTCGGCC  1860
AGCATCTCCT ATGCTCCCTG GGTCCCCCAG ACCTCTCTGT GTTGTGTGCG TGGCAGCCTC  1920
CAGGAATAAA CATTCTTGTT GTCCTTTGTA AAAAAAAAAA AAAAAAA
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Seq ID NO: 257 Protein sequence:
Protein Accession #: NP_057405

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1          11         21         31         41         51
|          |          |          |          |          |
MAWNTNLRWR LPLTCLLLQV IMVILFGVFV RYDFEADAHW WSERTHKNLS DMENEFYYRY    60
PSFQDVHVMV FVGFGFLMTF LQRYGFSAVG FNFLLAAFGI QWALLMQGWF HFLQDRYIVV   120
GVENLINADF CVASVCVAFG AVLGKVSPIQ LLIMTFFQVT LFAVNEFILL NLLKVKDAGG   180
SMTIHTFGAY FGLTVTRILY RRNLEQSKER QNSVYQSDLF AMIGTLFLWM YWPSFNSAIS   240
YHGDSQHRAA INTYCSLAAC VLTSVAISSA LHKKGKLDMV HIQNATLAGG VAVGTAAEMM   300
LMPYGALIIG FVCGIISTLG FVYLTPFLES RLHIQDTCGI NNLHGIPGII GGIVGAVTAA   360
SASLEVYGKE GLVHSFDFQG FNGDWTARTQ GKFQIYGLLV TLAMALMGGI IVGLILRLPF   420
WGQPSDENCF EDAVYWEMPE GNSTVYIPED PTFKPSGPSV PSVPMVSPLP MASSVPLVP
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Seq ID NO: 258 DNA sequence
Nucleic Acid Accession #: NM_002358.2
Coding sequence: 75..692

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1          11         21         31         41         51
|          |          |          |          |          |
GGGAAGTGCT GTTGGAGCCG CTGTGGTTGC TGTCCGCGGA GTGGAAGCGC GTGCTTTTGT    60
TTGTGTCCCT GGCCATGGCG CTGCAGCTCT CCCGGGAGCA GGGAATCACC CTGCGCGGGA   120
GCGCCGAAAT CGTGGCCGAG TTCTTCTCAT TCGGCATCAA CAGCATTTTA TATCAGCGTG   180
GCATATATCC ATCTGAAACC TTTACTCGAG TGCAGAAATA CGGACTCACC TTGCTTGTAA   240
CTACTGATCT TGAGCTCATA AAATACCTAA ATAATGTGGT GGAACAACTG AAAGATTGGT   300
TATACAAGTG TTCAGTTCAG AAACTGGTTG TAGTTATCTC AAATATTGAA AGTGGTGAGG   360
TCCTGGAAAG ATGGCAGTTT GATATTGAGT GTGACAAGAC TGCAAAAGAT GACAGTGCAC   420
CCAGAGAAAA GTCTCAGAAA GCTATCCAGG ATGAAATCCG TTCAGTGATC AGACAGATCA   480
CAGCTACGGT GACATTTCTG CCACTGTTGG AAGTTTCTTG TTCATTTGAT CTGCTGATTT   540
ATACAGACAA AGATTTGGTT GTACCTGAAA AATGGGAAGA GTCGGGACCA CAGTTTATTA   600
CCAATTCTGA GGAAGTCCGC CTTCGTTCAT TTACTACTAC AATCCACAAA GTAAATAGCA   660
TGGTGGCCTA CAAAATTCCT GTCAATGACT GAGGATGACA TGAGGAAAAT AATGTAATTG   720
TAATTTTGAA ATGTGGTTTT CCTGAAATCA GGTCATCTAT AGTTGATATG TTTTATTTCA   780
TTGGTTAATT TTTACATGGA GAAAACCAAA ATGATACTTA CTGAACTGTG TGTAATTGTT   840
CCTTTATTTT TTTGGTACCT ATTTGACTTA CCATGGAGTT AACATCATGA ATTTATTGCA   900
CATTGTTCAA AAGGAACCAG GAGGTTTTTT TGTCAACATT GTGATGTATA TTCCTTTGAA   960
GATAGTAACT GTAGATGGAA AAACTTGTGC TATAAAGCTA GATGCTTTCC TAAATCAGAT  1020
GTTTTGGTCA AGTAGTTTGA CTCAGTATAG GTAGGGAGAT ATTTAAGTAT AAAATACAAC  1080
AAAGGAAGTC TAAATATTCA GAATCTTTGT TAAGGTCCTG AAAGTAACTC ATAATCTATA  1140
AACAATGAAA TATTGCTGTA TAGCTCCTTT TGACCTTCAT TTCATGTATA GTTTTCCCTA  1200
TTGAATCAGT TTCCAATTAT TTGACTTTAA TTTATGTAAC TTGAACCTAT GAAGCAATGG  1260
ATATTTGTAC TGTTTAATGT TCTGTGATAC AGAACTCTTA AAAATGTTTT TTCATGTGTT  1320
TTATAAAATC AAGTTTTAAG TGAAAGTGAG GAAATAAAGT TAAGTTTGTT TTAAAAAAAA  1380
AAAAAAAAAA
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Seq ID NO: 259 Protein sequence:
Protein Accession #: NP_002349.1

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1          11         21         31         41         51
|          |          |          |          |          |
MALQLSREQG ITLRGSAEIV AEFFSFGINS ILYQRGIYPS ETFTRVQKYG LTLLVTTDLE    60
LIKYLNNVVE QLKDWLYKCS VQKLVVVISN IESGEVLERW QFDIECDKTA KDDSAPREKS   120
QKAIQDEIRS VIRQITATVT FLPLLEVSCS FDLLIYTDKD LVVPEKWEES GPQFITNSEE   180
VRLRSFTTTI HKVNSMVAYK IPVND
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Seq ID NO: 260 DNA sequence
Nucleic Acid Accession #: NM_001211
Coding sequence: 43..3195

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1          11         21         31         41         51
|          |          |          |          |          |
AAAGGCCTGC AGCAGGACGA GGACCTGAGC CAGGAATGCA GGATGGCGGC GGTGAAGAAG    60
GAAGGGGGTG CTCTGAGTGA AGCCATGTCC CTGGAGGGAG ATGAATGGGA ACTGAGTAAA   120
GAAAATGTAC AACCTTTAAG GCAAGGGCGG ATCATGTCCA CGCTTCAGGG AGCACTGGCA   180
CAAGAATCTG CCTGTAACAA TACTCTTCAG CAGCAGAAAC GGGCATTTGA ATATGAAATT   240
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CGATTTTACA CTGGAAATGA CCCTCTGGAT GTTTGGGATA GGTATATCAG CTGGACAGAG 300
CAGAACTATC CTCAAGGTGG GAAAGAGAGT AATATGTCAA CGTTATTAGA AAGAGCTGTA 360
GAAGCACTAC AAGGAGAAAA ACGATATTAT AGTGATCCTC GATTTCTCAA TCTCTGGCTT 420
AAATTAGGGC GTTTATGCAA TGAGCCTTTG GATATGTACA GTTACTTGCA CAACCAAGGG 480
ATTGGTGTTT CACTTGCTCA GTTCTATATC TCATGGGCAG AAGAATATGA AGCTAGAGAA 540
AACTTTAGGA AAGCAGATGC GATATTTCAG GAAGGGATTC AACAGAAGGC TGAACCACTA 600
GAAAGACTAC AGTCCCAGCA CCGACAATTC CAAGCTCGAG TGTCTCGGCA AACTCTGTTG 660
GCACTTGAGA AAGAAGAAGA GGAGGAAGTT TTTGAGTCTT CTGTACCACA ACGAAGCACA 720
CTAGCTGAAC TAAAGAGCAA AGGGAAAAAG ACAGCAAGAG CTCCAATCAT CCGTGTAGGA 780
GGTGCTCTCA AGGCTCCAAG CCAGAACAGA GGACTCCAAA ATCCATTTCC TCAACAGATG 840
CAAAATAATA GTAGAATTAC TGTTTTTGAT GAAAATGCTG ATGAGGCTTC TACAGCAGAG 900
TTGTCTAAGC CTACAGTCCA GCCATGGATA GCACCCCCCA TGCCCAGGGC CAAAGAGAAT 960
GAGCTGCAAG CAGGCCCTTG GAACACAGGC AGGTCCTTGG AACACAGGCC TCGTGGCAAT 1020
ACAGCTTCAC TGATAGCTGT ACCCGCTGTG CTTCCCAGTT TCACTCCATA TGTGGAAGAG 1080
ACTGCACAAC AGCCAGTTAT GACACCATGT AAAATTGAAC CTAGTATAAA CCACATCCTA 1140
AGCACCAGAA AGCCTGGAAA GGAAGAAGGA GATCCTCTAC AAAGGGTTCA GAGCCATCAG 1200
CAAGCGTCTG AGGAGAAGAA AGAGAAGATG ATGTATTGTA AGGAGAAGAT TTATGCAGGA 1260
GTAGGGGAAT TCTCCTTTGA AGAAATTCGG GCTGAAGTTT TCCGGAAGAA ATTAAAAGAG 1320
CAAAGGGAAG CCGAGCTATT GACCAGTGCA GAGAAGAGAG CAGAAATGCA GAAACAGATT 1380
GAAGAGATGG AGAAGAAGCT AAAAGAAATC CAAACTACTC AGCAAGAAAG AACAGGTGAT 1440
CAGCAAGAAG AGACGATGCC TACAAAGGAG ACAACTAAAC TGCAAATTGC TTCCGAGTCT 1500
CAGAAAATAC CAGGAATGAC TCTATCCAGT TCTGTTTGTC AAGTAAACTG TTGTGCCAGA 1560
GAAACTTCAC TTGCGGAGAA CATTTGGCAG GAACAACCTC ATTCTAAAGG TCCCAGTGTA 1620
CCTTTCTCCA TTTTTGATGA GTTTCTTCTT TCAGAAAAGA AGAATAAAAG TCCTCCTGCA 1680
GATCCCCCAC GAGTTTTAGC TCAACGAAGA CCCCTTGCAG TTCTCAAAAC CTCAGAAAGC 1740
ATCACCTCAA ATGAAGATGT GTCTCCAGAT GTTTGTGATG AATTTACAGG AATTGAACCC 1800
TTGAGCGAGG ATGCCATTAT CACAGGCTTC AGAAATGTAA CAATTTGTCC TAACCCAGAA 1860
GACACTTGTG ACTTTGCCAG AGCAGCTCGT TTTGTATCCA CTCCTTTTCA TGAGATAATG 1920
TCCTTGAAGG ATCTCCCTTC TGATCCTGAG AGACTGTTAC CGGAAGAAGA TCTAGATGTA 1980
AAGACCTCTG AGGACCAGCA GACAGCTTGT GGCACTATCT ACAGTCAGAC TCTCAGCATC 2040
AAGAAGCTGA GCCCAATTAT TGAAGACAGT CGTGAAGCCA CACACTCCTC TGGCTTCTCT 2100
GGTTCTTCTG CCTCGGTTGC AAGCACCTCC TCCATCAAAT GTCTTCAAAT TCCTGAGAAA 2160
CTAGAACTTA CTAATGAGAC TTCAGAAAAC CCTACTCAGT CACCATGGTG TTCACAGTAT 2220
CGCAGACAGC TACTGAAGTC CCTACCAGAG TTAAGTGCCT CTGCAGAGTT GTGTATAGAA 2280
GACAGACCAA TGCCTAAGTT GGAAATTGAG AAGGAAATTG AATTAGGTAA TGAGGATTAC 2340
TGCATTAAAC GAGAATACCT AATATGTGAA GATTACAAGT TATTCTGGGT GGCGCCAAGA 2400
AACTCTGCAG AATTAACAGT AATAAAGGTA TCTTCTCAAC CTGTCCCATG GGACTTTTAT 2460
ATCAACCTCA AGTTAAAGGA ACGTTTAAAT GAAGATTTTG ATCATTTTTG CAGCTGTTAT 2520
CAATATCAAG ATGGCTGTAT TGTTTGGCAC CAATATATAA ACTGCTTCAC CCTTCAGGAT 2580
CTTCTCCAAC ACAGTGAATA TATTACCCAT GAAATAACAG TGTTGATTAT TTATAACCTT 2640
TTGACAATAG TGGAGATGCT ACACAAAGCA GAAATAGTCC ATGGTGACTT GAGTCCAAGG 2700
TGTCTGATTC TCAGAAACAG AATCCACGAT CCCTATGATT GTAACAAGAA CAATCAAGCT 2760
TTGAAGATAG TGGACTTTTC CTACAGTGTT GACCTTAGGG TGCAGCTGGA TGTTTTTACC 2820
CTCAGCGGCT TTCGGACTGT ACAGATCCTG GAAGGACAAA AGATCCTGGC TAACTGTTCT 2880
TCTCCCTACC AGGTAGACCT GTTTGGTATA GCAGATTTAG CACATTTACT ATTGTTCAAG 2940
GAACACCTAC AGGTCTTCTG GGATGGGTCC TTCTGGAAAC TTAGCCAAAA TATTTCTGAG 3000
CTAAAAGATG GTGAATTGTG GAATAAATTC TTTGTGCGGA TTCTGAATGC CAATGATGAG 3060
GCCACAGTGT CTGTTCTTGG GGAGCTTGCA GCAGAAATGA ATGGGGTTTT TGACACTACA 3120
TTCCAAAGTC ACCTGAACAA AGCCTTATGG AAGGTAGGGA AGTTAACTAG TCCTGGGGCT 3180
TTGCTCTTTC AGTGAGCTAG GCAATCAAGT CTCACAGATT GCTGCCTCAG AGCAATGGTT 3240
GTATTGTGGA ACACTGAAAC TGTATGTGCT GTAATTTAAT TTAGGACACA TTTAGATGCA 3300
CTACCATTGC TGTTCTACTT TTTGGTACAG GTATATTTTG ACGTCACTGA TATTTTTTAT 3360
ACAGTGATAT ACTTACTCAT GGCCTTGTCT AACTTTTGTG AAGAACTATT TTATTCTAAA 3420
CAGACTCATT ACAAATGGTT ACCTTGTTAT TTAACCCATT TGTCTCTACT TTTCCCTGTA 3480
CTTTTCCCAT TTGTAATTTG TAAAATGTTC TCTTATGATC ACCATGTATT TTGTAAATAA 3540
TAAAATAGTA TCTGTTAAAA AAAAAAAAAA AAAAAAAAAA AAA

Seq ID NO: 261 Protein sequence:
Protein Accession #: NP_001202

1 11 21 31 41 51

MAAVKKEGGA LSEAMSLEGD EWELSKENVQ PLRQGRIMST LQGALAQESA CNNTLQQQKR 60
AFEYEIRFYT GNDPLDVWDR YISWTEQNYP QGGKESNMST LLERAVEALQ GEKRYYSDPR 120
FLNLWLKLGR LCNEPLDMYS YLHNQGIGVS LAQFYISWAE EYEARENFRK ADAIFQEGIQ 180
QKAEPLERLQ SQHRQFQARV SRQTLLALEK EEEEEVFESS VPQRSTLAEL KSKGKKTARA 240
PIIRVGGALK APSQNRGLQN PFPQQMQNNS RITVFDENAD EASTAELSKP TVQPWIAPPM 300
PRAKENELQA GPWNTGRSLE HRPRGNTASL IAVPAVLPSF TPYVEETAQQ PVMTPCKIEP 360
SINHILSTRK PGKEEGDPLQ RVQSHQQASE EKKEKMMYCK EKIYAGVGEF SFEEIRAEVF 420
RKKLKEQREA ELLTSAEKRA EMQKQIEEME KKLKEIQTTQ QERTGDQQEE TMPTKETTKL 480
QIASESQKIP GMTLSSSVCQ VNCCARETSL AENIWQEQPH SKGPSVPFSI FDEFLLSEKK 540
NKSPPADPPR VLAQRRPLAV LKTSESITSN EDVSPDVCDE FTGIEPLSED AIITGFRNVT 600
ICPNPEDTCD FARAARFVST PFHEIMSLKD LPSDPERLLP EEDLDVKTSE DQQTACGTIY 660
SQTLSIKKLS PIIEDSREAT HSSGFSGSSA SVASTSSIKC LQIPEKLELT NETSENPTQS 720
PWCSQYRRQL LKSLPELSAS AELCIEDRPM PKLEIEKEIE LGNEDYCIKR EYLICEDYKL 780
FWVAPRNSAE LTVIKVSSQP VPWDFYINLK LKERLNEDFD HFCSCYQYQD GCIVWHQYIN 840
CFTLQDLLQH SEYITHEITV LIIYNLLTIV EMLHKAEIVH GDLSPRCLIL RNRIHDPYDC 900
NKNNQALKIV DFSYSVDLRV QLDVFTLSGF RTVQILEGQK ILANCSSPYQ VDLFGIADLA 960
HLLLFKEHLQ VFWDGSFWKL SQNISELKDG ELWNKFFVRI LNANDEATVS VLGELAAEMN 1020
GVFDTTFQSH LNKALWKVGK LTSPGALLFQ

Seq ID NO: 262 DNA sequence
Nucleic Acid Accession #: NM_003784
Coding sequence: 365..1507

1 11 21 31 41 51

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|          |          |          |          |          |
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TAAAACTGAA TTCTCAGAAT TTTAGAACAA ATTTTTGTCT AGAAATGCTG ACTTTGGTTC   120
ATTAGGTAGT GGTAAAACAG GCTCCCTTCG AAGCTCTCCT TCATCACCTT CCTAAGTGCA   180
TGTACAGGGA AGCTCTCCTT CATCACCTTC CTAAGTGCAT GGGGGAAAAT ACCTAGGGCT   240
CAACAGTCTT GAGAAGTGTG GAAACATTTT CTTTGTGAGT GAGAACAGAT CACCTAGAGA   300
AAGGAAACCA GATTCCCATC ACTGCTTCTG GGTATCAGAT GCTAGCGCTG CACTCCATTT   360
TGCAATGGCC TCCCTTGCTG CAGCAAATGC AGAGTTTTGC TTCAACCTGT TCAGAGAGAT   420
GGATGACAAT CAAGGAAATG GAAATGTGTT CTTTTCCTCT CTGAGCCTCT TCGCTGCCCT   480
GGCCCTGGTC CGCTTGGGCG CTCAAGATGA CTCCCTCTCT CAGATTGATA AGTTGCTTCA   540
TGTTAACACT GCCTCAGGAT ATGGAAACTC TTCTAATAGT CAGTCAGGGC TCCAGTCTCA   600
ACTGAAAAGA GTTTTTTCTG ATATAAATGC ATCCCACAAG GATTATGATC TCAGCATTGT   660
GAATGGGCTT TTTGCTGAAA AAGTGTATGG CTTTCATAAG GACTACATTG AGTGTGCCGA   720
AAAATTATAC GATGCCAAAG TGGAGCGAGT TGACTTTACG AATCATTTAG AAGACACTAG   780
ACGTAATATT AATAAGTGGG TTGAAAATGA AACACATGGC AAAATCAAGA ACGTGATTGG   840
TGAAGGTGGC ATAAGCTCAT CTGCTGTAAT GGTGCTGGTG AATGCTGTGT ACTTCAAAGG   900
CAAGTGGCAA TCAGCCTTCA CCAAGAGCGA AACCATAAAT TGCCATTTCA AATCTCCCAA   960
GTGCTCTGGG AAGGCAGTCG CCATGATGCA TCAGGAACGG AAGTTCAATT TGTCTGTTAT  1020
TGAGGACCCA TCAATGAAGA TTCTTGAGCT CAGATACAAT GGTGGCATAA ACATGTACGT  1080
TCTGCTGCCT GAGAATGACC TCTCTGAAAT TGAAAACAAA CTGACCTTTC AGAATCTAAT  1140
GGAATGGACC AATCCAAGGC GAATGACCTC TAAGTATGTT GAGGTATTTT TTCCTCAGTT  1200
CAAGATAGAG AAGAATTATG AAATGAAACA ATATTTGAGA GCCCTAGGGC TGAAAGATAT  1260
CTTTGATGAA TCCAAAGCAG ATCTCTCTGG GATTGCTTCG GGGGGTCGTC TGTATATATC  1320
AAGGATGATG CACAAATCTT ACATAGAGGT CACTGAGGAG GGCACCGAGG CTACTGCTGC  1380
CACAGGAAGT AATATTGTAG AAAAGCAACT CCCTCAGTCC ACGCTGTTTA GAGCTGACCA  1440
CCCATTCCTA TTTGTTATCA GGAAGGATGA CATCATCTTA TTCAGTGGCA AAGTTTCTTG  1500
CCCTTGAAAA TCCAATTGGT TTCTGTTATA GCAGTCCCCA CAACATCAAA GRACCACCAC  1560
AAGTCAATAG ATYTGRGTTT AATTGGAAAA ATGTGGTGTT TCCTTTGAGT TTATTTCTTC  1620
CTAACATTGG TCAGCAGATG ACACTGGTGA CTTGACCCTT CCTAGACACC TGGTTGATTG  1680
TCCTGATCCC TGCTCTTAGC ATTCTACCAC CATGTGTCTC ACCCATTTCT AATTTCATTG  1740
TCTTTCTTCC CACGCTCATT TCTATCATTC TCCCCCATGA CCCGTCTGGA AATTATGGAG  1800
RGTGCTCAAC TGGTAAGGAG AACGTAGAAG TAGCCCTAGG GATCCTTTTT GAAACTCTAC  1860
AGTTATCGCA GATATTCTAG CTTCATTGTA AGCAATCTAG GAAATAAGCC CTGCTGCTTT  1920
CTAGAAATAA GTGTGAAGGA TAAATTTTCT TTGTTGACCT ATGAAGATTT TAGAGTTTAC  1980
CTTCATATGT TTGATTTTAA ATCAGTGTAT AATCTAGATG GTAAAAAATG TGAAATTGGG  2040
ATTAGGGACC TACCAAAATA TTTCATTAAT GCTTTCAATT GACAAATTTT GGCCTTTCTT  2100
TGATAAGACA ATATGTACAT GTTTTTTCAA ATATTAAAGA TCTTTTAACT GTTGGCAGTT  2160
GTTATCTACA GAATCATATT TCATATGCTG TGTAGTTTAT AAGTTTTTCC TCTATTTATC  2220
AGAATAAAGA AATACAACAT ACCTGTAAA
```

Seq ID NO: 263 Protein sequence:
Protein Accession #: NP_003775

```
1          11         21         31         41         51
|          |          |          |          |          |
MASLAAANAE FCFNLFREMD DNQGNGNVFF SSLSLFAALA LVRLGAQDDS LSQIDKLLHV    60
NTASGYGNSS NSQSGLQSQL KRVFSDINAS HKDYDLSIVN GLFAEKVYGF HKDYIECAEK   120
LYDAKVERVD FTNHLEDTRR NINKWVENET HGKIKNVIGE GGISSSAVMV LVNAVYFKGK   180
WQSAFTKSET INCHFKSPKC SGKAVAMMHQ ERKFNLSVIE DPSMKILELR YNGGINMYVL   240
LPENDLSEIE NKLTFQNLME WTNPRRMTSK YVEVFFPQFK IEKNYEMKQY LRALGLKDIF   300
DESKADLSGI ASGGRLYISR MMHKSYIEVT EEGTEATAAT GSNIVEKQLP QSTLFRADHP   360
FLFVIRKDDI ILFSGKVSCP
```

Seq ID NO: 264 DNA sequence
Nucleic Acid Accession #: AB052906
Coding sequence: 74-814

```
1          11         21         31         41         51
|          |          |          |          |          |
AAAACCTTGA GGTGATTCAT CTTCCAGGCT CTCCTTCCAT CAAGTCTCTC CTCCCTAGCG   '60
CTCTGGGTCC TTAATGGCAG CAGCCGCCGC TACCAAGATC CTTCTGTGCC TCCCGCTTCT   120
GCTCCTGCTG TCCGGCTGGT CCCGGGCTGG GCGAGCCGAC CCTCACTCTC TTTGCTATGA   180
CATCACCGTC ATCCCTAAGT TCAGACCTGG ACCACGGTGG TGTGCGGTTC AAGGCCAGGT   240
GGATGAAAAG ACTTTTCTTC ACTATGACTG TGGCAACAAG ACAGTCACAC CTGTCAGTCC   300
CCTGGGGAAG AAACTAAATG TCACAACGGC CTGGAAAGCA CAGAACCCAG TACTGAGAGA   360
GGTGGTGGAC ATACTTACAG AGCAACTGCG TGACATTCAG CTGGAGAATT ACACACCCAA   420
GGAACCCCTC ACCCTGCAGG CCAGGATGTC TTGTGAGCAG AAAGCTGAAG GACACAGCAG   480
TGGATCTTGG CAGTTCAGTT TCGATGGGCA GATCTTCCTC CTCTTTGACT CAGAGAAGAG   540
AATGTGGACA ACGGTTCATC CTGGAGCCAG AAAGATGAAA GAAAAGTGGG AGAATGACAA   600
GGTTGTGGCC ATGTCCTTCC ATTACTTCTC AATGGGAGAC TGTATAGGAT GGCTTGAGGA   660
CTTCTTGATG GGCATGGACA GCACCCTGGA GCCAAGTGCA GGAGCACCAC TCGCCATGTC   720
CTCAGGCACA ACCCAACTCA GGGCCACAGC CACCACCCTC ATCCTTTGCT GCCTCCTCAT   780
CATCCTCCCC TGCTTCATCC TCCCTGGCAT CTGAGGAGAG TCCTTTAGAG TGACAGGTTA   840
AAGCTGATAC CAAAAGGCTC CTGTGAGCAC GGTCTTGATC AAACTCGCCC TTCTGTCTGG   900
CCAGCTGCCC ACGACCTACG GTGTATGTCC AGTGGCCTCC AGCAGATCAT GATGACATCA   960
TGGACCCAAT AGCTCATTCA CTGCCTTGAT TCCTTTTGCC AACAATTTTA CCAGCAGTTA  1020
TACCTAACAT ATTATGCAAT TTTCTCTTGG TGCTACCTGA TGGAATTCCT GCACTTAAAG  1080
TTCTGGCTGA CTAAACAAGA TATATCATTT TCTTTCTTCT CTTTTTGTTT GGAAAATCAA  1140
GTACTTCTTT GAATGATGAT CTCTTTCTTG CAAATGATAT TGTCAGTAAA ATAATCACGT  1200
TAGACTTCAG ACCTCTGGGG ATTCTTTCCG TGTCCTGAAA GAGAATTTTT AAATTATTTA  1260
ATAAGAAAAA ATTTATATTA ATGATTGTTT CCTTTAGTAA TTTATTGTTC TGTACTGATA  1320
TTTAAATAAA GAGTTCTATT TCCCAAAAAA AAAAAAAAAA A
```

Seq ID NO: 265 Protein sequence:
Protein Accession #: BAB61048.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MAAAAATKIL LCLPLLLLLS GWSRAGRADP HSLCYDITVI PKFRPGPRWC AVQGQVDEKT    60
FLHYDCGNKT VTPVSPLGKK LNVTTAWKAQ NPVLREVVDI LTEQLRDIQL ENYTPKEPLT   120
LQARMSCEQK AEGHSSGSWQ FSFDGQIFLL FDSEKRMWTT VHPGARKMKE KWENDKVVAM   180
SFHYFSMGDC IGWLEDFLMG MDSTLEPSAG APLAMSSGTT QLRATATTLI LCCLLIILPC   240
FILPGI
```

Seq ID NO: 266 DNA sequence
Nucleic Acid Accession #: XM_084853.1
Coding sequence: 127-444

```
1          11         21         31         41         51
|          |          |          |          |          |
ATTGATGATA TATTTAACGA AATCAAATTT GGTGAATATG TGGACACTGG AAAGCTAATC    60
GACAAGATCA ACTTACCAGA TTTCCTAAAA GTGTACCTTA ACCACAAGCC ACCTTTTGGT   120
AACACCATGA GTGGCATCCA CAAGAGCTTT GAGGTGCTCG GTTATACCAA CTCCAAAGGG   180
AAAAAGGCCA TTCGAAGAGA GGACTTCCTG AGACTGCTCG TTACTAAAGG TGAGCATATG   240
ACGGAGGAGG AGATGTTGGA TTGCTTTGCT TCACTGTTTG GCCTGAATCC CGAGGGATGG   300
AAATCCGAGC CTGCAACCTG CTCCGTCAAA GGTTCAGAAA TTTGCCTTGA AGAAGAACTT   360
CCAGACGAAA TCACTGCAGA AATATTCGCG ACTGAAATTC TTGGCTTAAC CATTTCAGAA   420
GATTCCGGCC AGGATGGTCA GTGAAGTTAC CAGGAATGTT TAAAGCACAA AGGACTTTGG   480
GTGTGTGTGC ATGCACATGT GTGTGTTTTC CATGAGGCAC TGCTTTTTAT GCATTTCCCT   540
CCCCCCTCTC ATCTTTAGAA CATTTAGACA TTAAAGCAAG TTTCTGGTGA GCAATG
```

Seq ID NO: 267 Protein sequence:
Protein Accession #: XP_084853.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MSGIHKSFEV LGYTNSKGKK AIRREDFLRL LVTKGEHMTE EEMLDCFASL FGLNPEGWKS    60
EPATCSVKGS EICLEEELPD EITAEIFATE ILGLTISEDS GQDGQ
```

Seq ID NO: 268 DNA sequence
Nucleic Acid Accession #: NM_001898
Coding sequence: 57-482

```
1          11         21         31         41         51
|          |          |          |          |          |
GGCTCTCACC CTCCTCTCCT GCAGCTCCAG CTTTGTGCTC TGCCTCTGAG GAGACCATGG    60
CCCAGTATCT GAGTACCCTG CTGCTCCTGC TGGCCACCCT AGCTGTGGCC CTGGCCTGGA   120
GCCCCAAGGA GGAGGATAGG ATAATCCCGG GTGGCATCTA TAACGCAGAC CTCAATGATG   180
AGTGGGTACA GCGTGCCCTT CACTTCGCCA TCAGCGAGTA TAACAAGGCC ACCAAAGATG   240
ACTACTACAG ACGTCCGCTG CGGGTACTAA GAGCCAGGCA ACAGACCGTT GGGGGGGTGA   300
ATTACTTCTT CGACGTAGAG GTGGGCCGCA CCATATGTAC CAAGTCCCAG CCCAACTTGG   360
ACACCTGTGC CTTCCATGAA CAGCCAGAAC TGCAGAAGAA ACAGTTGTGC TCTTTCGAGA   420
TCTACGAAGT TCCCTGGGAG AACAGAAGGT CCCTGGTGAA ATCCAGGTGT CAAGAATCCT   480
AGGGATCTGT GCCAGGCCAT TCGCACCAGC CACCACCCAC TCCCACCCCC TGTAGTGCTC   540
CCACCCCTGG ACTGGTGGCC CCCACCCTGC GGGAGGCCTC CCCATGTGCC TGCGCCAAGA   600
GACAGACAGA GAAGGCTGCA GGAGTCCTTT GTTGCTCAGC AGGGCGCTCT GCCCTCCCTC   660
CTTCCTTCTT GCTTCTAATA GCCCTGGTAC ATGGTACACA CCCCCCCACC TCCTGCAATT   720
AAACAGTAGC ATCGCC
```

Seq ID NO: 269 Protein sequence:
Protein Accession #:NP_001889.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MAQYLSTLLL LLATLAVALA WSPKEEDRII PGGIYNADLN DEWVQRALHF AISEYNKATK    60
DDYYRRPLRV LRARQQTVGG VNYFFDVEVG RTICTKSQPN LDTCAFHEQP ELQKKQLCSF   120
EIYEVPWENR RSLVKSRCQE S
```

Seq ID NO: 270 DNA sequence
Nucleic Acid Accession #: XM_093210
Coding sequence: 13-1854

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGGCAAGCG CCGGAATCTC CTCAGCTGCC GTTTCACAAA AGAGGTACCA GGTCCGCACC    60
AAACGAGCAC ACAAGCAGCA CCAGGAGCTG CAGAAGAAGG AGGCGGCAGC GATGGACCAG   120
GGCAGAGGGA ATGGGGAGGG GGCATCCTAC CCCATATCTG AGGTGCGACT GCGGGACGTA   180
GAGCGGACTG GGCCTTTCCC GTTGGCGCGT GGCCTCAATC AGGACTTCTT GCCCACGTGC   240
GCCTTCAAAA CGGTAAGAGC TGCAACTGAA CGTGTGAGAC ATGGTGCAGA TAGGCTGAGA   300
GGCGGCGGGA GAGATGCCCA TGAACTCAAG TACCCGGACA CGCCCTCCAC TTCTACCACC   360
ACGAGTAACA CCGCCCCCAC GGGACCGCTC TCGAGGTCCC CCAAGCCAAG GACGCAAGGA   420
GGAACGCCCC GGCGCGCGGC CAGCAGCGGC GGGCACCGGC CCAATGGCCA CGGAACTCAG   480
CACTGGCAGT CGGCCCTCCT CACACCGCAG GCGTGCAGTG TGGCCGACGG AGCCTCCCGG   540
GCCGAGGACC CAGCTAGGCC GTCACCCCGG TTGCTCCCAC GGGAAGGGGC ACCAGGCAAA   600
CTGCCCAAGG CCCCGAGCCC AGGCTCCCTG GCGGAGGCCT CCGCTGGTCC CGCCCAGATC   660
ATGGCCGCCA CCAGGCTCCC GAGCCATGGC TTCCTGTCCG GGAACGGCCC GGCGTCCTGG   720
CTGTCCAGCT AG
```

Seq ID NO: 271 Protein sequence:
Protein Accession #: XP_093210

```
1          11         21         31         41         51
```

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|         |         |         |         |         |
MLRHGEQKRK RARKKWDFLP TCAFKTVRAA TERVRHGADR LRGGGRDAHE LKYPDTPSTS   60
TTTSNTAPTG PLSRSPKPRT QGGTPRRRPA AAGTRANGHG TQHWQSALLT PQACSVADGA  120
SRAEDPARPS PRLLPREGAP GKLPKAPSPG SLAEASAGLL AHVRLQNADA QRVSISQALP  180
PNSSVGRKEE RPGAGQQRRA PAPMATELST GSRPSSHRRR AVWPTEPPGP RTQLEPSPRL  240
LPREGAPGKL PKAPSPGSLA EASAGPAQIM AATRLPSRGF LSGNGPASWL SS
```

Seq ID NO: 272 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..732

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1         11        21        31        41        51
|         |         |         |         |         |
GGATACTGTG TCACTCAAAG TAATGGGAGG GAGAGAGAAC AGGGAGGGTA GGGATGCTTT   60
TGAAAAAGCT TTTTTTCCCA CTTTTAACTT GCTTTAGCGT TAAGAGTACT TACCAGCTAA  120
TAATGTGGAG GAAATTATTC TTTCTCATTG GAGATTACAG AATATATCTA TTCATCTTGA  180
ATACCCACTT GAAGCCTCTG TAGAAATGTC TCGTCCTCCG GTTGTATTTC TAAAACCTAC  240
ATGATTTTGT CTTGTTTCTG CAGTGAGAAA TTACATCCAT AGCAAAGACA AAAGTCTTTT  300
TAAATTATTT TTATTTATCT TTCATATAGT TCTTACAATT TCTAAAAAAT TAACACTCAT  360
TTAGTATCAC AATTTATGGG AGAGGGTTTT TTGTATTTTT AAGCATATGT GGCTTATATA  420
AAAATTGCAG AAGTCATAGG ACTGTCATGT ATTGCAGCTC TGAGAACCAA TGCCTGAAAC  480
TTAAGCC
```

Seq ID NO: 273 Protein sequence:
Protein Accession #: Eos sequence

```
1         11        21        31        41        51
|         |         |         |         |         |
MGGRENREGR DAFEKAFFPT FNLL
```

Seq ID NO: 274 DNA sequence
Nucleic Acid Accession #: NM_003976.2
Coding sequence: 299-961

```
1         11        21        31        41        51
|         |         |         |         |         |
CTCTGAGCTT CTCTGAGCCT TGTTTGCTCA TCTGGAAAAA GGGGATTAAA CCATTTACCT   60
CATGGAGTTG TGAAAGAATA GCTGCAAAGC ACCTAACACA TAGTAAGGTT CCCAGTGCAG  120
CTACTTCTGC TGGGTTGAGT CTAGCTGTGT AGGCCCCTTG TTCCTCACCT GGAGAAACTG  180
GGGTGGCAGG CCGGTCCCCC ACAAAAGATA ACTCATCTCT TAATTTGCAA GCTGCCTCAA  240
CAGGAGGGTG GGGGAACAGC TCAACAATGG CTGATGGGCG CTCCTGGTGT TGATAGAGAT  300
GGAACTTGGA CTTGGAGGCC TCTCCACGCT GTCCCACTGC CCCTGGCCTA GGCGGCAGCC  360
TGCCCTGTGG CCCACCCTGG CCGCTCTGGC TCTGCTGAGC AGCGTCGCAG AGGCCTCCCT  420
GGGCTCCGCG CCCCGCAGCC CTGCCCCCCG CGAAGGCCCC CCGCCTGTCC TGGCGTCCCC  480
CGCCGGCCAC CTGCCGGGGG GACGCACGGC CCGCTGGTGC AGTGGAAGAG CCCGGCGGCC  540
GCCGCCGCAG CCTTCTCGGC CCGCGCCCCC GCCGCCTGCA CCCCCATCTG CTCTTCCCCG  600
CGGGGGCCGC GCGGCGCGGG CTGGGGGCCC GGGCAGCCGC GCTCGGGCAG CGGGGGCGCG  660
GGGCTGCCGC CTGCGCTCGC AGCTGGTGCC GGTGCGCGCG CTCGGCCTGG GCCACCGCTC  720
CGACGAGCTG GTGCGTTTCC GCTTCTGCAG CGGCTCCTGC CGCCGCGCGC GCTCTCCACA  780
CGACCTCAGC CTGGCCAGCC TACTGGGCGC CGGGGCCCTG CGACCGCCCC CGGGCTCCCG  840
GCCCGTCAGC CAGCCCTGCT GCCGACCCAC GCGCTACGAA GCGGTCTCCT TCATGGACGT  900
CAACAGCACC TGGAGAACCG TGGACCGCCT CTCCGCCACC GCCTGCGGCT GCCTGGGCTG  960
AGGGCTCGCT CCAGGGCTTT GCAGACTGGA CCCTTACCGG TGGCTCTTCC TGCCTGGGAC 1020
CCTCCCGCAG AGTCCCACTA GCCAGCGGCC TCAGCCAGGG ACGAAGGCCT CAAAGCTGAG 1080
AGGCCCCTAC CGGTGGGTGA TGGATATCAT CCCCGAACAG GTGAAGGGAC AACTGACTAG 1140
CAGCCCCAGA GCCCTCACCC TGCGGATCCC AGCCTAAAAG ACACCAGAGA CCTCAGCTAT 1200
GGAGCCCTTC GGACCCACTT CTCACAGACT CTGGCACTGG CCAGGCCTCG AACCTGGGAC 1260
CCCTCCTCTG ATGAACACTA CAGTGGCTGA GGCATCAGCC CCCGCCCAGG CCCTGTAGGG 1320
ACAGCATTTG AAGGACACAT ATTGCAGTTG CTTGGTTGAA AGTGCCTGTG CTGGAACTGG 1380
CCTGTACTCA CTCATGGGAG CTGGCCCC
```

Seq ID NO: 275 Protein sequence:
Protein Accession #: NP_003967.1

```
1         11        21        31        41        51
|         |         |         |         |         |
MELGLGGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS   60
PAGHLPGGRT ARWCSGRARR PPPQPSRPAP PPPAPPSALP RGGRAARAGG PGSRARAAGA  120
RGCRLRSQLV PVRALGLGHR SDELVRFRFC SGSCRRARSP HDLSLASLLG AGALRPPPGS  180
RPVSQPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG
```

Seq ID NO: 276 DNA sequence
Nucleic Acid Accession #: NM_057091.1
Coding sequence: 783-1445

```
1         11        21        31        41        51
|         |         |         |         |         |
ACTGGCCGCT GAGAGAAGAA TCGGGTGGAG CAGAGAGCAG CTGCTGCAGG GCAGACAGCC   60
GGACCCCCAA ATCTGCACGT ACCAGCAGTC AGCCGCCCCA CGCAGGGACC GGCTTACCCC  120
TCGCTCCCCG CCCTCACTCA CTTTCTCCCG CCCTCGGCCC GGCCTCCCAG CTCTCTACTT  180
CGCGTGTCTA CAAACTCAAC TCCCGGTTTC CGTGCCTCTC CACCGCTCGA GTTCTCTACT  240
CTCCATATCC GAGGGGCCCC TCCCAGCATC TACCCCCCTC CCAACCTCGG GGGACCTAGC  300
CAAGCTAGGG GGGACTGGAT CCGACGGGTG GAGCAGCCAG GTGAGCCCCG AAAGGTGGGG  360
CGGGGCAGGG GCGCTCCCAG CCCCACCCCG GGATCTGGTG ACGCTGGGGC TGGAATTTGA  420
CACCGGACGG CTGCGGCGGC GGGCAGGAGG CTGCTGAGGG ATGGAGTTGG GCCCGGCCCC  480
CAGACAAGGC CCGGGGGCTC CGCCAGCAGC AGGTCCCTCG GGCCCCAGCC CTCGCTGCCA  540
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CCCGGGCCTG GAGCCCCACA CCCGAGGGTG CAGACTGGCT GCCAAGGCCA CACTTTTGGC    600
TAAAAGAGGC ACTGCCAGGT GTACAGTCCT GGGCATGCGC TGTTTGAGCT TCGGGGGAGA    660
GCCCAGCACT GGTCCCCGGA AAGGTGCCTA GAAGAACAAG GTGCAGGACC CCGTGCTGCC    720
TCAACAGGAG GGTGGGGGAA CAGCTCAACA ATGGCTGATG GGCGCTCCTG GTGTTGATAG    780
AGATGGAACT TGGACTTGGA GGCCTCTCCA CGCTGTCCCA CTGCCCCTGG CCTAGGCGGC    840
AGCCTGCCCT GTGGCCCACC CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCCT    900
CCCTGGGCTC CGCGCCCCGC AGCCCTGCCC CCCGCGAAGG CCCCCCGCCT GTCCTGGCGT    960
CCCCCGCCGG CCACCTGCCG GGGGGACGCA CGGCCCGCTG GTGCAGTGGA AGAGCCCGGC   1020
GGCCGCCGCC GCAGCCTTCT CGGCCCGCGC CCCCGCCGCC TGCACCCCCA TCTGCTCTTC   1080
CCCGCGGGGG CCGCGCGGCG CGGGCTGGGG GCCCGGGCAG CCGCGCTCGG GCAGCGGGGG   1140
CGCGGGGCTG CCGCCTGCGC TCGCAGCTGG TGCCGGTGCG CGCGCTCGGC CTGGGCCACC   1200
GCTCCGACGA GCTGGTGCGT TTCCGCTTCT GCAGCGGCTC CTGCCGCCGC GCGCGCTCTC   1260
CACACGACCT CAGCCTGGCC AGCCTACTGG GCGCCGGGGC CCTGCGACCG CCCCCGGGCT   1320
CCCGGCCCGT CAGCCAGCCC TGCTGCCGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG   1380
ACGTCAACAG CACCTGGAGA ACCGTGGACC GCCTCTCCGC CACCGCCTGC GGCTGCCTGG   1440
GCTGAGGGCT CGCTCCAGGG CTTTGCAGAC TGGACCCTTA CCGGTGGCTC TTCCTGCCTG   1500
GGACCCTCCC GCAGAGTCCC ACTAGCCAGC GGCCTCAGCC AGGGACGAAG GCCTCAAAGC   1560
TGAGAGGCCC CTACCGGTGG GTGATGGATA TCATCCCCGA ACAGGTGAAG GGACAACTGA   1620
CTAGCAGCCC CAGAGCCCTC ACCCTGCGGA TCCCAGCCTA AAAGACACCA GAGACCTCAG   1680
CTATGGAGCC CTTCGGACCC ACTTCTCACA GACTCTGGCA CTGGCCAGGC CTCGAACCTG   1740
GGACCCCTCC TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCCGCC CAGGCCCTGT   1800
AGGGACAGCA TTTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAAGTGCC TGTGCTGGAA   1860
CTGGCCTGTA CTCACTCATG GGAGCTGGCC CC
```

Seq ID NO: 277 Protein sequence:
Protein Accession #: NP_003967.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MELGLGGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS     60
PAGHLPGGRT ARWCSGRARR PPPQPSRPAP PPPAPPSALP RGGRAARAGG PGSRARAAGA    120
RGCRLRSQLV PVRALGLGHR SDELVRFRFC SGSCRRARSP HDLSLASLLG AGALRPPPGS    180
RPVSQPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG
```

Seq ID NO: 278 DNA sequence
Nucleic Acid Accession #: NM_057160.1
Coding sequence: 1-714

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGCCCGGCC TGATCTCAGC CCGAGGACAG CCCCTCCTTG AGGTCCTTCC TCCCCAAGCC     60
CACCTGGGTG CCCTCTTTCT CCCTGAGGCT CCACTTGGTC TCTCCGCGCA GCCTGCCCTG    120
TGGCCCACCC TGGCCGCTCT GGCTCTGCTG AGCAGCGTCG CAGAGGCCTC CCTGGGCTCC    180
GCGCCCCGCA GCCCTGCCCC CCGCGAAGGC CCCCCGCCTG TCCTGGCGTC CCCCGCCGGC    240
CACCTGCCGG GGGGACGCAC GGCCCGCTGG TGCAGTGGAA GAGCCCGGCG GCCGCCGCCG    300
CAGCCTTCTC GGCCCGCGCC CCCGCCGCCT GCACCCCCAT CTGCTCTTCC CCGCGGGGGC    360
CGCGCGGCGC GGGCTGGGGG CCCGGGCAGC CGCGCTCGGG CAGCGGGGGC GCGGGGCTGC    420
CGCCTGCGCT CGCAGCTGGT GCCGGTGCGC GCGCTCGGCC TGGGCCACCG CTCCGACGAG    480
CTGGTGCGTT TCCGCTTCTG CAGCGGCTCC TGCCGCCGCG CGCGCTCTCC ACACGACCTC    540
AGCCTGGCCA GCCTACTGGG CGCCGGGGCC CTGCGACCGC CCCCGGGCTC CCGGCCCGTC    600
AGCCAGCCCT GCTGCCGACC CACGCGCTAC GAAGCGGTCT CCTTCATGGA CGTCAACAGC    660
ACCTGGAGAA CCGTGGACCG CCTCTCCGCC ACCGCCTGCG GCTGCCTGGG CTGAGGGCTC    720
GCTCCAGGGC TTTGCAGACT GGACCCTTAC CGGTGGCTCT TCCTGCCTGG GACCCTCCCG    780
CAGAGTCCCA CTAGCCAGCG GCCTCAGCCA GGGACGAAGG CCTCAAAGCT GAGAGGCCCC    840
TACCGGTGGG TGATGGATAT CATCCCCGAA CAGGTGAAGG GACAACTGAC TAGCAGCCCC    900
AGAGCCCTCA CCCTGCGGAT CCCAGCCTAA AAGACACCAG AGACCTCAGC TATGGAGCCC    960
TTCGGACCCA CTTCTCACAG ACTCTGGCAC TGGCCAGGCC TCGAACCTGG GACCCCTCCT   1020
CTGATGAACA CTACAGTGGC TGAGGCATCA GCCCCCGCCC AGGCCCTGTA GGGACAGCAT   1080
TTGAAGGACA CATATTGCAG TTGCTTGGTT GAAAGTGCCT GTGCTGGAAC TGGCCTGTAC   1140
TCACTCATGG GAGCTGGCCC C
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Seq ID NO: 279 Protein sequence:
Protein Accession #: NP_476501.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MPGLISARGQ PLLEVLPPQA HLGALFLPEA PLGLSAQPAL WPTLAALALL SSVAEASLGS     60
APRSPAPREG PPPVLASPAG HLPGGRTARW CSGRARRPPP QPSRPAPPPP APPSALPRGG    120
RAARAGGPGS RARAAGARGC RLRSQLVPVR ALGLGHRSDE LVRFRFCSGS CRRARSPHDL    180
SLASLLGAGA LRPPPGSRPV SQPCCRPTRY EAVSFMDVNS TWRTVDRLSA TACGCLG
```

Seq ID NO: 280 DNA sequence
Nucleic Acid Accession #: NM_057090.1
Coding sequence: 29-715

```
1          11         21         31         41         51
|          |          |          |          |          |
CTGATGGGCG CTCCTGGTGT TGATAGAGAT GGAACTTGGA CTTGGAGGCC TCTCCACGCT     60
GTCCCACTGC CCCTGGCCTA GGCGGCAGGC TCCACTTGGT CTCTCCGCGC AGCCTGCCCT    120
GTGGCCCACC CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCCT CCCTGGGCTC    180
CGCGCCCCGC AGCCCTGCCC CCCGCGAAGG CCCCCCGCCT GTCCTGGCGT CCCCCGCCGG    240
CCACCTGCCG GGGGGACGCA CGGCCCGCTG GTGCAGTGGA AGAGCCCGGC GGCCGCCGCC    300
GCAGCCTTCT CGGCCCGCGC CCCCGCCGCC TGCACCCCCA TCTGCTCTTC CCCGCGGGGG    360
CCGCGCGGCG CGGGCTGGGG GCCCGGGCAG CCGCGCTCGG GCAGCGGGGG CGCGGGGCTG    420
CCGCCTGCGC TCGCAGCTGG TGCCGGTGCG CGCGCTCGGC CTGGGCCACC GCTCCGACGA    480
GCTGGTGCGT TTCCGCTTCT GCAGCGGCTC CTGCCGCCGC GCGCGCTCTC CACACGACCT    540
CAGCCTGGCC AGCCTACTGG GCGCCGGGGC CCTGCGACCG CCCCCGGGCT CCCGGCCCGT    600
CAGCCAGCCC TGCTGCCGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG ACGTCAACAG    660
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CACCTGGAGA ACCGTGGACC GCCTCTCCGC CACCGCCTGC GGCTGCCTGG GCTGAGGGCT    720
CGCTCCAGGG CTTTGCAGAC TGGACCCTTA CCGGTGGCTC TTCCTGCCTG GGACCCCTCCC   780
GCAGAGTCCC ACTAGCCAGC GGCCTCAGCC AGGGACGAAG GCCTCAAAGC TGAGAGGCCC    840
CTACCGGTGG GTGATGGATA TCATCCCCGA ACAGGTGAAG GGACAACTGA CTAGCAGCCC    900
CAGAGCCCTC ACCCTGCGGA TCCCAGCCTA AAAGACACCA GAGACCTCAG CTATGGAGCC    960
CTTCGGACCC ACTTCTCACA GACTCTGGCA CTGGCCAGGC CTCGAACCTG GGACCCCTCC   1020
TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCCGCC CAGGCCCTGT AGGGACAGCA   1080
TTTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAAGTGCC TGTGCTGGAA CTGGCCTGTA   1140
CTCACTCATG GGAGCTGGCC CC
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Seq ID NO: 281 Protein sequence:
Protein Accession #: NP_476431.1

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1          11         21         31         41         51
|          |          |          |          |          |
MELGLGGLST LSHCPWPRRQ APLGLSAQPA LWPTLAALAL LSSVAEASLG SAPRSPAPRE     60
GPPPVLASPA GHLPGGRTAR WCSGRARRPP PQPSRPAPPP PAPPSALPRG GRAARAGGPG    120
SRARAAGARG CRLRSQLVPV RALGLGHRSD ELVRFRFCSG SCRRARSPHD LSLASLLGAG    180
ALRPPPGSRP VSQPCCRPTR YEAVSFMDVN STWRTVDRLS ATACGCLG
```

Seq ID NO: 282 DNA sequence
Nucleic Acid Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
CTACTGCACC TGCCCTCTGT TTCCTTTGGA AATCTCTTAC CTTTCATTAG GGTTTCTTTC     60
ATAGCAATTT CCTTTGGTTT TTAAGACTTC TACATTGCTT TTTCTTTTAT TATCTGTGCT    120
CCGTGAACCT TATGAATGCT GCTTAAAAAT AATGTCAAAA TATGTTTTAG CTGCCTACTC    180
AGGTAACGTT TTCTTTTGCT CTCATCTTGG TTTCCATATA CTATTTTTGG TTTTTTGTGA    240
GATCTAATCA ATGATCTAGT CAGAAGCTAC TTCACTGGCT AACAGTGATC ATGTTCATGT    300
GCTAAAAATG AACTTGAAAC ACGGAAGTAG TGGTTGGTCC AGTTTGAAAG CTCTTATTAG    360
TATTCTTCAT CCTGGCTGTA ATAATAGCCA TTATTTGTTA TGCCTTTGTT ATGTAGCAGA    420
CACTCTTAAG GATTTTATGT GTATTATTCA AATTGCTATT ACTGTTCTTT TTATAGTTGA    480
GAATCTCAGG ATACCTACAT TTATCACTTT TTCAATATAT ATGTATTTCT TATT
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Seq ID NO: 283 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 564-1481

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1          11         21         31         41         51
|          |          |          |          |          |
GAGACTTTTA ATCATCTATC CCTTGTGCTT TACGCAGACC CTACAATACA CTAGAGGCTT     60
CAAAGAGGTC AAAAATTCAC ATGTGTAGAC AAATTAGGTC CCTTAAGATG CCAGGCAAAC    120
GAAGTGCTAC CAAAACACGC AATGACTGTC CTAAAAGTGC GTTCTGGGAT ACACCTGTAA    180
ACTTGGATCA AGTTCCCTCC CCTCTCCTCA AAATATATCG ACTTGTGCTG AAAGAAATCA    240
CGACCGATGC TCACAATTCT GACCTCGTAA TTATATAGGG GGTGGTTTTG GTTTCTGCGT    300
CTTTCCCTGA TTCAGTGGCA GGTAACATAT TTCATGTACA AAATGAACTG CAACACCACG    360
GCAAACAAGG GACAGGCCCT CAAAGTTGTC GGTAGGGAGC CAGGACCCCG CCAGTGGCGT    420
GGGGAGACAC CGTACTAAAC AAGCTTGCAA ACAGCAGGCA CCTTCCTGCC ACTGAGGAGG    480
AAGGGCTGGC TAAGGGAGGC CGGGGCGGAG GAAGCCAAGC TCTGCAGGCC CTGACAAAGT    540
CCTCCCGGCC TCCACGCGTC GCCATGGCAA CGCGGGGTCT GTGCTGGCCG GGATTGGCCG    600
GCCTGGCGCG CGCAGGGCCC GCTGGGAAAG CGCGTCCCCG CCGCGGCTCC GCCAGTTTGA    660
ACTTGGCGGG CCAGATGTGG GCGGCGGGGC GCTGGGGCCC TACTTTTCCC TCTTCCTACG    720
CCGGTTTCTC TGCTGACTGC AGACCCAGGT CTCGGCCCTC CTCGGACTCC TGCTCAGTCC    780
CTATGACGGG CGCACGTGGG CAGGGGCTGG AGGTGGTGCG CTCGCCGTCG CCGCCGCTGC    840
CGCTGAGCTG CAGCAATTCC ACCAGGTCGC TGTTGTCTCC CCTTGGCCAC CAGAGCTTCC    900
AGTTTGACGA GGACGACGGT GACGGGGAGG ATGAGGAAGA CGTGGATGAT GAGGAAGACG    960
TGGATGAAGA TGCCCATGAT TCAGAGGCCA AAGTGGCGAG CCTGAGAGGA ATGGAGTTAC   1020
AGGGGTGCGC CAGCACTCAG GTTGAATCAG AAAATAACCA AGAAGAACAG AAACAGGTGC   1080
GCTTACCAGA AAGCCGCCTG ACACCATGGG AGGTGTGGTT TATTGGCAAA GAAAAAGAAG   1140
AACGTGACCG GCTGCAACTG AAAGCTCTAG AGGAATTAAA TCAACAACTA GAAAAAAGAA   1200
AAGAAATGGA AGAACGTGAA AAAAGAAAGA TAATTGCTGA AGAAAAGCAC AAGGAATGGG   1260
TTCAGAAAAA GAATGAGCAA AAAAGAAAAG AAAGAGAACA AAAAATTAAT AAAGAAATGG   1320
AGGAAAAAGC AGCAAAGGAA CTGGAGAAAG AATACTTGCA AGAAAAAGCA AAAGAAAAAT   1380
ATCAAGAATG GTTAAAGAAA AAAAATGCTG AAGAATGTGA GAGGAAGAAG AAAGAAAAGA   1440
AAAACAACAG CAAGCTGAAA TACAGGAGAA AAAGGAAATA GCAGAAAAAA AGTTTCAAGA   1500
ATGGTTGGAA AATGCGAAAC ATAAACCTCG TCCAGCTGCA AAGAGCTATG GTTATGCCAA   1560
TGGAAAACTT ACAGGTTTTT ACAGTGGAAA TTCCTATCCA GAACCAGCCT TTTATAATCC   1620
AATTCCGTGG AAACCAATTC ATATGCCACC TCCCAAAGAA GCTAAGGATC TATCAGGAAG   1680
GAAGAGTAAA AGACCTGTGA TAAGTCAGCC ACACAAGTCA TCATCTCTGG TAATTCATAA   1740
AGCCAGGAGC AATCTTTGCC TTGGAACTCT GTGCAGAATA CAAAGATAGC GTATGTGGAA   1800
AATAACATGC TTTTATCTGG AGCTATTTAA TTTAAAAATC AGAAATTGTT TTTTACTGCT   1860
CAGTCAATAA CTCAACACTT AATGTGATTA TTGACAAATA GCAATTTTTG CATTTGTATA   1920
TGGAGTCCTT AGAGTTGAGG AAGATATTTT CTGGATTTTG GTTTTTATAA ACTTTTTAAG   1980
GTTGATCTTG GCATGTTGTT TTGCAGAATA AGTGGCTGAA TATGTAAGAA TTGTGTTTGT   2040
ATTTAGCTTG TATTAAAAGT ACACTGTAAT ACCAATAAAA CTAACAATTT TTCTTG
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Seq ID NO: 284 Protein sequence:
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MATRGLCWPG LAGLARAGPA GKARPRRGSA SLNLAGQMWA AGRWGPTFPS SYAGFSADCR     60
PRSRPSSDSC SVPMTGARGQ GLEVVRSPSP PLPLSCSNST RSLLSPLGHQ SFQFDEDDGD    120
GEDEEDVDDE EDVDEDAHDS EAKVASLRGM ELQGCASTQV ESENNQEEQK QVRLPESRLT    180
PWEVWFIGKE KEERDRLQLK ALEELNQQLE KRKEMEEREK RKIIAEEKHK EWVQKKNEQK    240
RKEREQKINK EMEEKAAKEL EKEYLQEKAK EKYQEWLKKK NAEECERKKK EKKNNSKLKY    300
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RRKRK

Seq ID NO: 285 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1-1746

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1          11         21         31         41         51
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ATGCCACTGA AGCATTATCT CCTTTTGCTG GTGGGCTGCC AAGCCTGGGG TGCAGGGTTG     60
GCCTACCATG GCTGCCCTAG CGAGTGTACC TGCTCCAGGG CCTCCCAGGT GGAGTGCACC    120
GGGGCACGCA TTGTGGCGGT GCCCACCCCT CTGCCCTGGA ACGCCATGAG CCTGCAGATC    180
CTCAACACGC ACATCACTGA ACTCAATGAG TCCCCGTTCC TCAATATCTC AGCCCTCATC    240
GCCCTGAGGA TTGAGAAGAA TGAGCTGTCG CGCATCACGC CTGGGGCCTT CCGAAACCTG    300
GGCTCGCTGC GCTATCTCAG CCTCGCCAAC AACAAGCTGC AGGTTCTGCC CATCGGCCTC    360
TTCCAGGGCC TGGACAGCCT TGAGTCTCTC CTTCTGTCCA GTAACCAGCT GTTGCAGATC    420
CAGCCGGCCC ACTTCTCCCA GTGCAGCAAC CTCAAGGAGC TGCAGTTGCA CGGCAACCAC    480
CTGGAATACA TCCCTGACGG AGCCTTCGAC CACCTGGTAG GACTCACGAA GCTCAATCTG    540
GGCAAGAATA GCCTCACCCA CATCTCACCC AGGGTCTTCC AGCACCTGGG CAATCTCCAG    600
GTCCTCCGGC TGTATGAGAA CAGGCTCACG GATATCCCCA TGGGCACTTT TGATGGGCTT    660
GTTAACCTGC AGGAACTGGC TCTACAGCAG AACCAGATTG GACTGCTCTC CCCTGGTCTC    720
TTCCACAACA ACCACAACCT CCAGAGACTC TACCTGTCCA ACAACCACAT CTCCCAGCTG    780
CCACCCAGCA TCTTCATGCA GCTGCCCCAG CTCAACCGTC TTACTCTCTT TGGGAATTCC    840
CTGAAGGAGC TCTCTCTGGG GATCTTCGGG CCCATGCCCA ACCTGCGGGA GCTTTGGCTC    900
TATGACAACC ACATCTCTTC TCTACCCGAC AATGTCTTCA GCAACCTCCG CCAGTTGCAG    960
GTCCTGATTC TTAGCCGCAA TCAGATCAGC TTCATCTCCC CGGGTGCCTT CAACGGGCTA   1020
ACGGAGCTTC GGGAGCTGTC CCTCCACACC AACGCACTGC AGGACCTGGA CGGGAATGTC   1080
TTCCGCATGT TGGCCAACCT GCAGAACATC TCCCTGCAGA ACAATCGCCT CAGACAGCTC   1140
CCAGGGAATA TCTTCGCCAA CGTCAATGGC CTCATGGCCA TCCAGCTGCA GAACAACCAG   1200
CTGGAGAACT TGCCCCTCGG CATCTTCGAT CACCTGGGGA AACTGTGTGA GCTGCGGCTG   1260
TATGACAATC CCTGGAGGTG TGACTCAGAC ATCCTTCCGC TCCGCAACTG GCTCCTGCTC   1320
AACCAGCCTA GGTTAGGGAC GGACACTGTA CCTGTGTGTT TCAGCCCAGC CAATGTCCGA   1380
GGCCAGTCCC TCATTATCAT CAATGTCAAC GTTGCTGTTC CAAGCGTCCA TGTCCCTGAG   1440
GTGCCTAGTT ACCCAGAAAC ACCATGGTAC CCAGACACAC CCAGTTACCC TGACACCACA   1500
TCCGTCTCTT CTACCACTGA GCTAACCAGC CCTGTGGAAG ACTACACTGA TCTGACTACC   1560
ATTCAGGTCA CTGATGACCG CAGCGTTTGG GGCATGACCC AGGCCCAGAG CGGGCTGGCC   1620
ATTGCCGCCA TTGTAATTGG CATTGTCGCC CTGGCCTGCT CCCTGGCTGC CTGCGTCGGC   1680
TGTTGCTGCT GCAAGAAGAG GAGCCAAGCT GTCCTGATGC AGATGAAGGC ACCCAATGAG   1740
TGTTAAAGAG GCAGGCTGGA GCAGGGCTGG GGAATGATGG GACTGGAGGA CCTGGGAATT   1800
TCATCTTTCT GCCTCCACCC CTGGGTCCAT GGAGCTTTCC CGTGATTGCT CTTTCTGGCC   1860
CTAGATAAAG GTGTGCCTAC CTCTTCCTGA CTTGCCTGAT TCTCCCGTAG AGAAGCAGGT   1920
CGTGCCGGAC CTTCCTACAA TCAGGAAGAT AGATCCAACT GGCCATGGCA AAAGCCCTGG   1980
GGATTTCCGA TTCATACCCC TGGGCTTCCT TCGAGAGGGC TCTTCCTCCA AATCCTCCCC   2040
ACCTGTCCTC CAAGAACAGC CTTCCCTGCG CCCAGGCCCC CTCCGGGCCT CTGTAGACTC   2100
AGTTAGTCCA CAGCCTGCTC ACTTCGTGGG AATAGTTCTC CGCTGAGATA GCCCCTCTCG   2160
CCTAAGTATT ATGTAAGTTG ATTTCCCTTC TTTTGTTTCT CTTGTTTGTG CTATGGCTTG   2220
ACCCAGCATG TCCCCTCAAA TGAAAGTTCT CCCCTTGATT TTCTGCTCCT GAAGGCAGGG   2280
TGAGTTCTCT CCTCAAAGAA GACTTCAAAC CATTTAACTG GTTTCTTAAG AGCCGTCAAT   2340
CAGCCTGGTT TTGGGGATGC TATGAAAGAG AGAAGGAAAA TCATGCCGCT CAGTTCCTGG   2400
AGACAGAAGA GCCGTCATCA GTGTCTCACT TGTGATTTTT ATCTGGAAAA GGAAGAAACA   2460
CCCCAGCACA GCAAGCTCAG CCTTTTAGAG AAGGATATTT CCAAACTGCA AACTTTGCTT   2520
TGAAAAGTTT AGCCCTTTAA GGAATGAAAT CATGTAGAAT TTTGGACTTC TAAAAACATT   2580
AAAATCAGCT TATTAATACG GGATAGAGAA AGAAATCTGG TGCCTGGGGG TCCCTGTGTT   2640
CACCCCTAGA GTTTGTTTTA AAATTTTTAA TTGAAGCATG TGAAGTGTAC STGCAGAAAA   2700
GTGGGAACAT GATAGTGTAT GGCTTGGTGG ATTTTCACAA ACTGAACATA CCTGTGTAAT   2760
CAGCATCTAG ACCCAGACCC AGAGCATCAC AAATATCCCC CATCCTGGGC TTTTCCCAGA   2820
GGAGATGGGG GCTTCTGAAG ATGGACTTAC CTGGGACCTG CCCCCCATGA GCCAGGACGG   2880
TCCCCCCACA GTCAGCCTGT GCAAAGGCCC CGTGGCCAGG GGTGGAGGAG AATATGTGGG   2940
TGTGGACAGG ATGGGAGACT GTGGCCTGAA CAGGAGATTT TATTATATCT GGAGACCCTG   3000
AGAGACCCTG AGACCTGGGG CACCATGGCT GGCCAGGTCA GAAGCATCCT GACTGCAGAG   3060
GTCCGTGCAG CCACACCCTC TTCCCTGCCA GCAAGTTGTC TGCGGCTCAT CGGAGGCCCC   3120
TCCGCCTGGA GCCTTCTATG GACGTGATAT GCCTGTATCT GTTTTTAATT TTCATTCTTC   3180
ACTTAGGGGA AGTGAAATCG CTCAGAGATG AGATCCTTTA ATTGAAAACG AAGTGTAACG   3240
GAATCTAGTG TCTTTCTAAT GTGGTAAAAT TCTCCATCAA CATCACAGTC AGCTGGCAGC   3300
TGAACTTCAG AATCTCACTT ACAGCAGGCG ACACGGGGGT ACACCGATGG GTCACACTGG   3360
GTCTGGGGGC TCCCTGGAGC TCCTCCTGCG TGTGGTCTGG TTAGGAGTTG AGTTGTTTGC   3420
TCCAGGGTTA TTCTCCTCCT CGAGTCACAG TCACACGAAT ACCTGCCTTC TCTGGCTTTC   3480
CTGCTATACA CATATTCACA TGGCGCTCAA GAAGTTAGGC TCATGGCAAC GTGTGTCTTT   3540
CTCTGGACAA CTGGCCCAGT TTACAGTGAA ATGGAGAATT TCAGGTCTCC ACGTCTGCCC   3600
AGGAAAGAAC TTCAGCTGAC TCCACGGGGA TCTGGAAATC CACGACCAAT CCCGATCGGC   3660
TCTTATTAGC TCCCCGCTCC ACAAGACACC TGTGCTTTGG AAATCCACCA CCAATCCCGA   3720
TCGGCTCTTA TTAGCTCCCC GCTCCACAAG ACACCTGTGA TCTGGAAATC TACCACCAAT   3780
CCCGATCGGC TCTTATTAGC TCCCCGCTCC ACAAGACACC TGTGACATCC TCCAGGGCCA   3840
CAGGAGCACG TGCTGACCAG TTTTCCCTTC CAGTTCCTGC ACAAAAAGTG TCCAGAGGGC   3900
TGTTTGCAAA CACTAGTGCA CTTTGTAGCT TTTCACCCTC TGTCCCAGGG AATCTAGGAG   3960
AGATGAGGCC CGTCAGAGTC AAGAGATGTC ATCCCCCCAG GGTCTCCAAG GCATTTCCAC   4020
ACTATTGGTG GCACCTGGAG GACATGCACC AAGGCTTGCC AGAGCCAACA GGAAGTGAGC   4080
CCAGAGCATG GCACATGAGC ATCACCCGCT GATGGTGGCC TGCTGTGCCT GGTGCCAACA   4140
GGGGCATCCC GGCCCGTACC CCTCCAGACA GGAAGCATGG GTTTGCCCAC AGACCTGTCG   4200
GGTGCTCCTG TGAGTGGCCT CCAGATGTCT TTGTGCATAG GCACAAGTGG GCCAGGGCTG   4260
GAGGGAGGTG GGAAACCTCA TCATCCGGTG GGCCCTGCCA ATCTTAACCC AGAACCCTTA   4320
GGTATTCCTG GCAGTAGCCA TGACATTGGA GCACCTTCCT CTCCAGCCAG AGGCTGACCT   4380
GAGGGCCACT GTCCTCAGAT GACACCACCC AGGAGCACCC TAGGTGAGGG GTGAGGGCCC   4440
CCTTATGTGA ACCTCTTGCC TCTTCCTTTC TCCCATCAGA GTGGTTGGAT GGAGCCATTG   4500
GCCTCCTTTT CTTCAGCGGG CCCTTCAACC TCTCTGCACC ATGTTGTCTG GCTGAGGAGC   4560
TACTAGAAAA GCTGAGTGGA GTCTCCTTTC CAACAGGATG ATGCATTTGC TCAATTCTCA   4620
GGGCTGGAAT GAGCCGGCTG GTCCCCCAGA AAGCTGGAGT GGGGTACAGA GTTCAGTTTT   4680
CCTCTCTGTT TACAGCTCCT TGACAGTCCC ACGCCCATCT GGAGTGGGAG CTGGGAGTTA   4740
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GTGTTGGAGA AGAAACAACA AAAGCCAATT AGAACCACTA TTTTTAAAAA GTGCTTACTG  4800
TGCACAGATA CTCTTCAAGC ACTGGACGTG GATTCTCTCT CTAGCCCTCA GCACCCCTGC  4860
GGTAGGAGTG CCGCCTCTAC CCACTTGTGA TGGGGTACAG AGGCACTTGC TCTTCTGCAT  4920
GGTGTTCAAT AGGCTGGGAG TTTTATTTAT CTCTTCAAAC TTTGTACAAG AGCTCATGGC  4980
TTGTCTTGGG CTTTCGTCAT TAAACCAAAG GAAATGGAAG CCATTCCCCT GTTGCTCTCC  5040
TTAGTCTTGG TCATCAGAAC CTCACTTGGT ACCATATAGA TCAAAAGCTT TGTAACCACA  5100
GGAAAAAATA AACTCTTCCA TCCCTTAAAG AATAGAATAG TTTGTCCCTC TCATGGGAAT  5160
TGGGCTGTAT GTATATTGTT CTTCCTCCTT AGAATTTAGA GATACAAGAG TTCTACTTAG  5220
AACTTTTCAT GGACACAATT TCCACAACCT TTCAGATGCT GATGTAGAGC TATTGGGAAA  5280
GAACTTCCAA ACTCAGGAAG TTTGCAGAGA GCAGACAGCT AGAGATAACT CGGGACCCAG  5340
AGTTGGTCGA CAGATGTTAG ATGTATCCTA GCTTTTAGCC ATAAACCACT CAAAGATTCA  5400
GCCCCCAGAT CCCACAGTCA GAACTGAATC TGCGTTGTTG GGAAGCCAGC AGTGGCCTTG  5460
GGAAGGAAGC CATGGCTGTG GTTCAGAGAG GGTGGGCTGG CAAGCCACTT CCGGGGAAAA  5520
CTCCTTCCGC CCCAGGTTTC TTCTTCTCTT AAGGAGAGAT TGTTCTCACC AACCCGCTGC  5580
CTTCATGCTG CCTTCAAAGC TAGATCATGT TTGCCTTGCT TAGAGAATTA CTGCAAATCA  5640
GCCCCAGTGC TTGGCGATGC ATTTACAGAT TTCTAGGCCC TCAGGGTTTT GTAGAGTGTG  5700
AGCCCTGGTG GGCAGGGTTG GGGGGTCTGT CTTCTGCTGG ATGCTGCTTG TAATCCATTT  5760
GGTGTACAGA ATCAACAATA AATAATATAC ATGTAT
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Seq ID NO: 286 Protein sequence:
Protein Accession #: NP_570843.1

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1          11         21         31         41         51
|          |          |          |          |          |
MPLKHYLLLL VGCQAWGAGL AYHGCPSECT CSRASQVECT GARIVAVPTP LPWNAMSLQI    60
LNTHITELNE SPFLNISALI ALRIEKNELS RITPGAFRNL GSLRYLSLAN NKLQVLPIGL   120
FQGLDSLESL LLSSNQLLQI QPAHFSQCSN LKELQLHGNH LEYIPDGAFD HLVGLTKLNL   180
GKNSLTHISP RVFQHLGNLQ VLRLYENRLT DIPMGTFDGL VNLQELALQQ NQIGLLSPGL   240
FHNNHNLQRL YLSNNHISQL PPSIFMQLPQ LNRLTLFGNS LKELSLGIFG PMPNLRELWL   300
YDNHISSLPD NVFSNLRQLQ VLILSRNQIS FISPGAFNGL TELRELSLHT NALQDLDGNV   360
FRMLANLQNI SLQNNRLRQL PGNIFANVNG LMAIQLQNNQ LENLPLGIFD HLGKLCELRL   420
YDNPWRCDSD ILPLRNWLLL NQPRLGTDTV PVCFSPANVR GQSLIIINVN VAVPSVHVPE   480
VPSYPETPWY PDTPSYPDTT SVSSTTELTS PVEDYTDLTT IQVTDDRSVW GMTQAQSGLA   540
IAAIVIGIVA LACSLAACVG CCCCKKRSQA VLMQMKAPNE C
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Seq ID NO: 287 DNA sequence
Nucleic Acid Accession #: NM_002362
Coding sequence: 1..954

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1          11         21         31         41         51
|          |          |          |          |          |
ATGTCTTCTG AGCAGAAGAG TCAGCACTGC AAGCCTGAGG AAGGCGTTGA GGCCCAAGAA    60
GAGGCCCTGG GCCTGGTGGG TGCACAGGCT CCTACTACTG AGGAGCAGGA GGCTGCTGTC   120
TCCTCCTCCT CTCCTCTGGT CCCTGGCACC CTGGAGGAAG TGCCTGCTGC TGAGTCAGCA   180
GGTCCTCCCC AGAGTCCTCA GGGAGCCTCT GCCTTACCCA CTACCATCAG CTTCACTTGC   240
TGGAGGCAAC CCAATGAGGG TTCCAGCAGC CAAGAAGAGG AGGGGCCAAG CACCTCGCCT   300
GACGCAGAGT CCTTGTTCCG AGAAGCACTC AGTAACAAGG TGGATGAGTT GGCTCATTTT   360
CTGCTCCGCA AGTATCGAGC CAAGGAGCTG GTCACAAAGG CAGAAATGCT GGAGAGAGTC   420
ATCAAAAATT ACAAGCGCTG CTTTCCTGTG ATCTTCGGCA AAGCCTCCGA GTCCCTGAAG   480
ATGATCTTTG GCATTGACGT GAAGGAAGTG GACCCCGCCA GCAACACCTA CACCCTTGTC   540
ACCTGCCTGG GCCTTTCCTA TGATGGCCTG CTGGGTAATA ATCAGATCTT TCCCAAGACA   600
GGCCTTCTGA TAATCGTCCT GGGCACAATT GCAATGGAGG GCGACAGCGC CTCTGAGGAG   660
GAAATCTGGG AGGAGCTGGG TGTGATGGGG GTGTATGATG GGAGGGAGCA CACTGTCTAT   720
GGGGAGCCCA GGAAACTGCT CACCCAAGAT TGGGTGCAGG AAAACTACCT GGAGTACCGG   780
CAGGTACCCG GCAGTAATCC TGCGCGCTAT GAGTTCCTGT GGGGTCCAAG GGCTCTGGCT   840
GAAACCAGCT ATGTGAAAGT CCTGGAGCAT GTGGTCAGGG TCAATGCAAG AGTTCGCATT   900
GCCTACCCAT CCCTGCGTGA AGCAGCTTTG TTAGAGGAGG AAGAGGGAGT CTGA
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Seq ID NO: 288 Protein sequence:
Protein Accession #: NP_002353.1

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1          11         21         31         41         51
|          |          |          |          |          |
MSSEQKSQHC KPEEGVEAQE EALGLVGAQA PTTEEQEAAV SSSSPLVPGT LEEVPAAESA    60
GPPQSPQGAS ALPTTISFTC WRQPNEGSSS QEEEGPSTSP DAESLFREAL SNKVDELAHF   120
LLRKYRAKEL VTKAEMLERV IKNYKRCFPV IFGKASESLK MIFGIDVKEV DPASNTYTLV   180
TCLGLSYDGL LGNNQIFPKT GLLIIVLGTI AMEGDSASEE EIWEELGVMG VYDGREHTVY   240
GEPRKLLTQD WVQENYLEYR QVPGSNPARY EFLWGPRALA ETSYVKVLEH VVRVNARVRI   300
AYPSLREAAL LEEEEGV
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Seq ID NO: 289 DNA sequence
Nucleic Acid Accession #: NM_002362
Coding sequence: 46..1344

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1          11         21         31         41         51
|          |          |          |          |          |
CGGCGGCCGC GCCCTGGTTG GGTCCCCACT GCTCTCGGGG GCGCCATGGA CGAGGCCGTG    60
GGCGACCTGA AGCAGGCGCT TCCCTGTGTG GCCGAGTCGC CAACGGTCCA CGTGGAGGTG   120
CATCAGCGCG GCAGCAGCAC TGCAAAGAAA GAAGACATAA ACCTGAGTGT TAGAAAGCTA   180
CTCAACAGAC ATAATATTGT GTTTGGTGAT TACACATGGA CTGAGTTTGA TGAACCTTTT   240
TTGACCAGAA ATGTGCAGTC TGTGTCTATT ATTGACACAG AATTAAAGGT TAAAGACTCA   300
CAGCCCATCG ATTTGAGTGC ATGCACTGTT GCACTTCACA TTTTCCAGCT GAATGAAGAT   360
GGCCCCAGCA GTGAAAATCT GGAGGAAGAG ACAGAAAACA TAATTGCAGC AAATCACTGG   420
GTTCTACCTG CAGCTGAATT CCATGGGCTT TGGGACAGCT TGGTATACGA TGTGGAAGTC   480
AAATCCCATC TCCTCGATTA TGTGATGACA ACTTTACTGT TTTCAGACAA GAACGTCAAC   540
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AGCAACCTCA TCACCTGGAA CCGGGTGGTG CTGCTCCACG GTCCTGGTGG CACTGGAAAA   600
ACATCCCTGT GTAAAGCGTT AGCCCAGAAA TTGACAATTA GACTTTCAAG CAGGTACCGA   660
TATGGCCAAT TAATTGAAAT AAACAGCCAC AGCCTCTTTT CTAAGTGGTT TTCGGAAAGT   720
GGCAAGCTGG TAACCAAGAT GTTTCAGAAG ATTCAGGATT TGATTGATGA TAAAGACGCC   780
CTGGTGTTCG TGCTGATTGA TGAGGTGGAG AGTCTCACAG CCGCCCGAAA TGCCTGCAGG   840
GCGGGCACCG AGCCATCAGA TGCCATCCGC GTGGTCAATG CTGTCTTGAC CCAAATTGAT   900
CAGATTAAAA GGCATTCCAA TGTTGTGATT CTGACCACTT CTAACATCAC CGAGAAGATC   960
GACGTGGCCT TCGTGGACAG GGCTGACATC AAGCAGTACA TTGGGCCACC CTCTGCAGCA  1020
GCCATCTTCA AAATCTACCT CTCTTGTTTG GAAGAACTGA TGAAGTGTCA GATCATATAC  1080
CCTCGCCAGC AGCTGCTGAC CCTCCGAGAG CTAGAGATGA TTGGCTTCAT TGAAAACAAC  1140
GTGTCAAAAT TGAGCCTTCT TTTGAATGAC ATTTCAAGGA AGAGCGAGGG CCTCAGCGGC  1200
CGGGTCCTGA GAAAACTCCC CTTTCTGGCT CATGCGCTGT ATGTCCAGGC CCCCACCGTC  1260
ACCATAGAGG GGTTCCTCCA GGCCCTGTCT CTGGCAGTGG ACAAGCAGTT TGAAGAGAGA  1320
AAGAAGCTTG CAGCTTACAT CTGATCCTGG GCTTCCCCAT CTGGTGCTTT TCCCATGGAG  1380
AACACACAAC CAGTAAGTGA GGTTGCCCCA CACAGCCGTC TCCCAGGGAA TCCCTTCTGC  1440
AAACCAAACG TTACTTAGAC TGCAAGCTAG AAAGCCACCA AGGCCAGGCT TTGTTAAAAG  1500
AAGTGTATTC TATTTATGTT GTTTTAAAAT GCATACTGAG AGACAAACAT CTTGTCATTT  1560
TCACTGTTTG TAAAAGATAA TTCAGATTGT TTGTCTCCTT GTGAAGAACC ATCGAAACCT  1620
GTTTGTTCCC AGCCCACCCC CAGTGGATGG GATGCATAAT GCCAGCAAGT TTTGTTTAAC  1680
AGCAAAAAAG GAAGATTAAT GCAGGTGTTA TAGAAGCCAG AAGAGAAACT GTGTCACCCT  1740
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TTGCTTTCTG ATATCAGCTC GTTTGATTTA GTGCAAAAAT GTTTTCAAGA CTATTTAATG  1860
GATGTAAAAA AGCCTATTTC TACATTATAC CAACTGAGAA AAAAATGGTC GGTAAAGTGT  1920
TCTTTCATAA TAAATAATCA AGACATGGTC CCATTTGCAG GAAAAGTGCA GACTCTGAGT  1980
GTTCCAGGGA AACACATGCT GGACATCCCT TGTAACCCGG TATGGGCGCC CCTGCATTGC  2040
TGGGATGTTT CTGCCCACGG TTTTGTTTGT GCAATAACGT TATCACATTT CTAATGAGGA  2100
TTCACATTAA TATAATATAA AATAAATAGG TCAGTTACTG GTCTCTTTCT GCCGAATGTT  2160
ATGTTTTGCT TTTATCTCAC AGTAAAATAA ATATAATTAA AAA
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Seq ID NO: 290 Protein sequence:
Protein Accession #: NP_004228

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1          11         21         31         41         51
|          |          |          |          |          |
MDEAVGDLKQ ALPCVAESPT VHVEVHQRGS STAKKEDINL SVRKLLNRHN IVFGDYTWTE    60
FDEPFLTRNV QSVSIIDTEL KVKDSQPIDL SACTVALHIF QLNEDGPSSE NLEEETENII   120
AANHWVLPAA EFHGLWDSLV YDVEVKSHLL DYVMTTLLFS DKNVNSNLIT WNRVVLLHGP   180
PGTGKTSLCK ALAQKLTIRL SSRYRYGQLI EINSHSLFSK WFSESGKLVT KMFQKIQDLI   240
DDKDALVFVL IDEVESLTAA RNACRAGTEP SDAIRVVNAV LTQIDQIKRH SNVVILTTSN   300
ITEKIDVAFV DRADIKQYIG PPSAAAIFKI YLSCLEELMK CQIIYPRQQL LTLRELEMIG   360
FIENNVSKLS LLLNDISRKS EGLSGRVLRK LPFLAHALYV QAPTVTIEGF LQALSLAVDK   420
QFEERKKLAA YI
```

Seq ID NO: 291 DNA sequence
Nucleic Acid Accession #: NM_002658.1
Coding sequence: 77-1372

```
1          11         21         31         41         51
|          |          |          |          |          |
GTCCCCGCAG CGCCGTCGCG CCCTCCTGCC GCAGGCCACC GAGGCCGCCG CCGTCTAGCG    60
CCCCGACCTC GCCACCATGA GAGCCCTGCT GGCGCGCCTG CTTCTCTGCG TCCTGGTCGT   120
GAGCGACTCC AAAGGCAGCA ATGAACTTCA TCAAGTTCCA TCGAACTGTG ACTGTCTAAA   180
TGGAGGAACA TGTGTGTCCA ACAAGTACTT CTCCAACATT CACTGGTGCA ACTGCCCAAA   240
GAAATTCGGA GGGCAGCACT GTGAAATAGA TAAGTCAAAA ACCTGCTATG AGGGGAATGG   300
TCACTTTTAC CGAGGAAAGG CCAGCACTGA CACCATGGGC CGGCCCTGCC TGCCCTGGAA   360
CTCTGCCACT GTCCTTCAGC AAACGTACCA TGCCCACAGA TCTGATGCTC TTCAGCTGGG   420
CCTGGGGAAA CATAATTACT GCAGGAACCC AGACAACCGG AGGCGACCCT GGTGCTATGT   480
GCAGGTGGGC CTAAAGCCGC TTGTCCAAGA GTGCATGGTG CATGACTGCG CAGATGGAAA   540
AAAGCCCTCC TCTCCTCCAG AAGAATTAAA ATTTCAGTGT GGCCAAAAGA CTCTGAGGCC   600
CCGCTTTAAG ATTATTGGGG GAGAATTCAC CACCATCGAG AACCAGCCCT GGTTTGCGGC   660
CATCTACAGG AGGCACCGGG GGGGCTCTGT CACCTACGTG TGTGGAGGCA GCCTCATCAG   720
CCCTTGCTGG GTGATCAGCG CCACACACTG CTTCATTGAT TACCCAAAGA AGGAGGACTA   780
CATCGTCTAC CTGGGTCGCT CAAGGCTTAA CTCCAACACG CAAGGGGAGA TGAAGTTTGA   840
GGTGGAAAAC CTCATCCTAC ACAAGGACTA CAGCGCTGAC ACGCTTGCTC ACCACAACGA   900
CATTGCCTTG CTGAAGATCC GTTCCAAGGA GGGCAGGTGT GCGCAGCCAT CCCGGACTAT   960
ACAGACCATC TGCCTGCCCT CGATGTATAA CGATCCCCAG TTTGGCACAA GCTGTGAGAT  1020
CACTGGCTTT GGAAAAGAGA ATTCTACCGA CTATCTCTAT CCGGAGCAGC TGAAAATGAC  1080
TGTTGTGAAG CTGATTTCCC ACCGGGAGTG TCAGCAGCCC CACTACTACG GCTCTGAAGT  1140
CACCACCAAA ATGCTATGTG CTGCTGACCC CCAATGGAAA ACAGATTCCT GCCAGGGAGA  1200
CTCAGGGGGA CCCCTCGTCT GTTCCCTCCA AGGCCGCATG ACTTTGACTG GAATTGTGAG  1260
CTGGGGCCGT GGATGTGCCC TGAAGGACAA GCCAGGCGTC TACACGAGAG TCTCACACTT  1320
CTTACCCTGG ATCCGCAGTC ACACCAAGGA AGAGAATGGC CTGGCCCTCT GAGGGTCCCC  1380
AGGGAGGAAA CGGGCACCAC CCGCTTTCTT GCTGGTTGTC ATTTTTGCAG TAGAGTCATC  1440
TCCATCAGCT GTAAGAAGAG ACTGGGAAGA TAGGCTCTGC ACAGATGGAT TTGCCTGTGG  1500
CACCACCAGG GTGAACGACA ATAGCTTTAC CCTCACGGAT AGGCCTGGGT GCTGGCTGCC  1560
CAGACCCTCT GGCCAGGATG GAGGGGTGGT CCTGACTCAA CATGTTACTG ACCAGCAACT  1620
TGTCTTTTTC TGGACTGAAG CCTGCAGGAG TTAAAAAGGG CAGGGCATCT CCTGTGCATG  1680
GGCTCGAAGG GAGAGCCAGC TCCCCCGACC GGTGGGCATT TGTGAGGCCC ATGGTTGAGA  1740
AATGAATAAT TTCCCAATTA GGAAGTGTAA GCAGCTGAGG TCTCTTGAGG GAGCTTAGCC  1800
AATGTGGGAG CAGCGGTTTG GGGAGCAGAG ACACTAACGA CTTCAGGGCA GGGCTCTGAT  1860
ATTCCATGAA TGTATCAGGA AATATATATG TGTGTGTATG TTTGCACACT TGTTGTGTGG  1920
GCTGTGAGTG TAAGTGTGAG TAAGAGCTGG TGTCTGATTG TTAAGTCTAA ATATTTCCTT  1980
AAACTGTGTG GACTGTGATG CCACACAGAG TGGTCTTTCT GGAGAGGTTA TAGGTCACTC  2040
CTGGGGCCTC TTGGGTCCCC CACGTGACAG TGCCTGGGAA TGTACTTATT CTGCAGCATG  2100
ACCTGTGACC AGCACTGTCT CAGTTTCACT TTCACATAGA TGTCCCTTTC TTGGCCAGTT  2160
ATCCCTTCCT TTTAGCCTAG TTCATCCAAT CCTCACTGGG TGGGGTGAGG ACCACTCCTT  2220
ACACTGAATA TTTATATTTC ACTATTTTTA TTTATATTTT TGTAATTTTA AATAAAAGTG  2280
```

ATCAATAAAA TGTGATTTTT CTGA

Seq ID NO: 292 Protein sequence:
Protein Accession #:NP_002649.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MRALLARLLL CVLVVSDSKG SNELHQVPSN CDCLNGGTCV SNKYFSNIHW CNCPKKFGGQ    60
HCEIDKSKTC YEGNGHFYRG KASTDTMGRP CLPWNSATVL QQTYHAHRSD ALQLGLGKHN   120
YCRNPDNRRR PWCYVQVGLK PLVQECMVHD CADGKKPSSP PEELKFQCGQ KTLRPRFKII   180
GGEFTTIENQ PWFAAIYRRH RGGSVTYVCG GSLISPCWVI SATHCFIDYP KKEDYIVYLG   240
RSRLNSNTQG EMKFEVENLI LHKDYSADTL AHHNDIALLK IRSKEGRCAQ PSRTIQTICL   300
PSMYNDPQFG TSCEITGFGK ENSTDYLYPE QLKMTVVKLI SHRECQQPHY YGSEVTTKML   360
CAADPQWKTD SCQGDSGGPL VCSLQGRMTL TGIVSWGRGC ALKDKPGVYT RVSHFLPWIR   420
SHTKEENGLA L
```

Seq ID NO: 293 DNA sequence
Nucleic Acid Accession #: NM_001498
Coding sequence: 93..2006

```
1          11         21         31         41         51
|          |          |          |          |          |
GGCACGAGGC TGAGTGTCCG TCTCGCGCCC GGAAGCGGGC GACCGCCGTC AGCCCGGAGG    60
AGGAGGAGGA GGAGGAGGAG GAGGGGGCGG CCATGGGGCT GCTGTCCCAG GGCTCGCCGC   120
TGAGCTGGGA GGAAACCAAG CGCCATGCCG ACCACGTGCG GCGGCACGGG ATCCTCCAGT   180
TCCTGCACAT CTACCACGCC GTCAAGGACC GGCACAAGGA CGTTCTCAAG TGGGGCGATG   240
AGGTGGAATA CATGTTGGTA TCTTTTGATC ATGAAAATAA AAAAGTCCGG TTGGTCCTGT   300
CTGGGGAGAA AGTTCTTGAA ACTCTGCAAG AGAAGGGGGA AAGGACAAAC CCAAACCATC   360
CTACCCTTTG GAGACCAGAG TATGGGAGTT ACATGATTGA AGGGACACCA GGACAGCCCT   420
ACGGAGGAAC AATGTCCGAG TTCAATACAG TTGAGGCCAA CATGCGAAAA CGCCGGAAGG   480
AGGCTACTTC TATATTAGAA GAAAATCAGG CTCTTTGCAC AATAACTTCA TTTCCCAGAT   540
TAGGCTGTCC TGGGTTCACA CTGCCCGAGG TCAAACCCAA CCCAGTGGAA GGAGGAGCTT   600
CCAAGTCCCT CTTCTTTCCA GATGAAGCAA TAAACAAGCA CCCTCGCTTC AGTACCTTAA   660
CAAGAAATAT CCGACATAGG AGAGGAGAAA AGGTTGTCAT CAATGTACCA ATATTTAAGG   720
ACAAGAATAC ACCATCTCCA TTTATAGAAA CATTTACTGA GGATGATGAA GCTTCAAGGG   780
CTTCTAAGCC GGATCATATT TACATGGATG CCATGGGATT TGGAATGGGC AATTGCTGTC   840
TCCAGGTGAC ATTCCAAGCC TGCAGTATAT CTGAGGCCAG ATACCTTTAT GATCAGTTGG   900
CTACTATCTG TCCAATTGTT ATGGCTTTGA GTGCTGCATC TCCCTTTTAC CGAGGCTATG   960
TGTCAGACAT TGATTGTCGC TGGGGAGTGA TTTCTGCATC TGTAGATGAT AGAACTCGGG  1020
AGGAGCGAGG ACTGGAGCCA TTGAAGAACA ATAACTATAG GATCAGTAAA TCCCGATATG  1080
ACTCAATAGA CAGCTATTTA TCTAAGTGTG GTGAGAAATA TAATGACATC GACTTGACGA  1140
TAGATAAAGA GATCTACGAA CAGCTGTTGC AGGAAGGCAT TGATCATCTC CTGGCCCAGC  1200
ATGTTGCTCA TCTCTTTATT AGAGACCCAC TGACACTGTT TGAAGAGAAA ATACACCTGG  1260
ATGATGCTAA TGAGTCTGAC CATTTTGAGA ATATTCAGTC CACAAATTGG CAGACAATGA  1320
GATTTAAGCC CCCTCCTCCA AACTCAGACA TTGGATGGAG AGTAGAATTT CGACCCATGG  1380
AGGTGCAATT AACAGACTTT GAGAACTCTG CCTATGTGGT GTTTGTGGTA CTGCTCACCA  1440
GAGTGATCCT TTCCTACAAA TTGGATTTTC TCATTCCACT GTCAAAGGTT GATGAGAACA  1500
TGAAGGTAGC ACAGAAAAGA GATGCTGTCT TGCAGGGAAT GTTTTATTTC AGGAAAGATA  1560
TTTGCAAAGG TGGCAATGCA GTGGTGGATG GTTGTGGCAA GGCCCAGAAC AGCACGGAGC  1620
TCGCTGCAGA GGAGTACACC CTCATGAGCA TAGACACCAT CATCAATGGG AAGGAAGGTG  1680
TGTTTCCTGG ACTGATCCCA ATTCTGAACT CTTACCTTGA AAACATGGAA GTGGATGTGG  1740
ACACCAGATG TAGTATTCTG AACTACCTAA AGCTAATTAA GAAGAGAGCA TCTGGAGAAC  1800
TAATGACAGT TGCCAGATGG ATGAGGGAGT TTATCGCAAA CCATCCTGAC TACAAGCAAG  1860
ACAGTGTCAT AACTGATGAA ATGAATTATA GCCTTATTTT GAAGTGTAAC CAAATTGCAA  1920
ATGAATTATG TGAATGCCCA GAGTTACTTG GATCAGCATT TAGGAAAGTA AAATATAGTG  1980
GAAGTAAAAC TGACTCATCC AACTAGACAT TCTACAGAAA GAAAAATGCA TTATTGACGA  2040
ACTGGCTACA GTACCATGCC TCTCAGCCCG TGTGTATAAT ATGAAGACCA AATGATAGAA  2100
CTGTACTGTT TTCTGGGCCA GTGAGCCAGA AATTGATTAA GGCTTTCTTT GGTAGGTAAA  2160
TCTAGAGTTT ATACAGTGTA CATGTACATA GTAAAGTATT TTTGATTAAC AATGTATTTT  2220
AATAACATAT CTAAAGTCAT CATGAACTGG CTTGTACATT TTTAAATTCT TACTCTGGAG  2280
CAACCTACTG TCTAAGCAGT TTTGTAAATG TACTGGTAAT TGTACAATAC TTGCATTCCA  2340
GAGTTAAAAT GTTTACTGTA AATTTTTGTT CTTTTAAAGA CTACCTGGGA CCTGATTTAT  2400
TGAAATTTTT CTCTTTAAAA ACATTTTCTC TCGTTAATTT TCCTTTGTCA TTTCCTTTGT  2460
TGTCTACATT AAATCACTTG AATCCATTGA AAGTGCTTCA AGGGTAATCT TGGGTTTCTA  2520
GCACCTTATC TATGATGTTT CTTTTGCAAT TGGAATAATC ACTTGGTCAC CTTGCCCCAA  2580
GCTTTCCCCT CTGAATAAAT ACCCATTGAA CTCTGAAAAA AAAAAAAAAA AAAA
```

Seq ID NO: 294 Protein sequence:
Protein Accession #: NP_001489

```
1          11         21         31         41         51
|          |          |          |          |          |
MGLLSQGSPL SWEETKRHAD HVRRHGILQF LHIYHAVKDR HKDVLKWGDE VEYMLVSFDH    60
ENKKVRLVLS GEKVLETLQE KGERTNPNHP TLWRPEYGSY MIEGTPGQPY GGTMSEFNTV   120
EANMRKRRKE ATSILEENQA LCTITSFPRL GCPGFTLPEV KPNPVEGGAS KSLFFPDEAI   180
NKHPRFSTLT RNIRHRRGEK VVINVPIFKD KNTPSPFIET FTEDDEASRA SKPDHIYMDA   240
MGFGMGNCCL QVTFQACSIS EARYLYDQLA TICPIVMALS AASPFYRGYV SDIDCRWGVI   300
SASVDDRTRE ERGLEPLKNN NYRISKSRYD SIDSYLSKCG EKYNDIDLTI DKEIYEQLLQ   360
EGIDHLLAQH VAHLFIRDPL TLFEEKIHLD DANESDHFEN IQSTNWQTMR FKPPPPNSDI   420
GWRVEFRPME VQLTDFENSA YVVFVVLLTR VILSYKLDFL IPLSKVDENM KVAQKRDAVL   480
QGMFYFRKDI CKGGNAVVDG CGKAQNSTEL AAEEYTLMSI DTIINGKEGV FPGLIPILNS   540
YLENMEVDVD TRCSILNYLK LIKKRASGEL MTVARWMREF IANHPDYKQD SVITDEMNYS   600
LILKCNQIAN ELCECPELLG SAFRKVKYSG SKTDSSN
```

Seq ID NO: 295 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-816

```
1          11         21         31         41         51
|          |          |          |          |          |
AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG   60
GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCCAGGTGC  120
CCTAGGGGGC ACATTTCCCA CAACTCCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAGTG  180
GGGAGGCGCC ACAACTTCAC TGCCATTTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG  240
GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT  300
CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG  360
AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGA AAAGAAGCTT  420
ATGACAGGAC ATGCTATTCC ACCCAGCCAA TTGGATTCTC AGATTGATGA CTTCACTGGT  480
TTCAGCAAAG ATAGGATGAT GCAGAAACCT GGTAGCAATG CACCTGTGGG AGGAAACGTT  540
ACCAGCAGTT TCTCTGGAGA TGACCTAGAA TGCAGAGAAA CAGCCTCCTC TCCCAAAAGC  600
CAACGAGAAA TTAATGCTGA TATAAAACGT AAATTAGTGA AGGAACTCCG ATGCGTTGGA  660
CAAAAATATG AAAAAATCTT CGAAATGCTT GAAGGAGTGC AAGGACCTAC TGCAGTCAGG  720
AAGCGATTTT TTGAATCCAT CATCAAGGAA GCAGCAAGAT GTATGAGACG AGACTTTGTT  780
AAGCACCTTA AGAAGAAACT GAAACGTATG ATTTGAGAAT ACTTGTCCCT GGAGGATTAT  840
CACACCCCAA ATGCATAATC TCGTTAATGA TTGAGGAGAG AAAAGGATCA GATTGCTGTT  900
TTCTACAATG GAGCAGGATA TTGCTGAAGT CTCCTGGCAT ATGTTACCGA ATCAAATAGC  960
CTTCCAGAGG CTAAGAAATT TCTGTTAGTA AAAGATGTTC TTTTTCCCAA AGCATTTTAT 1020
TTGAAAGGAT AACTTGTGTT TTGGTTATTT TGTATTCCCA CCTGTGCTGG TAGATATTAT 1080
TAACCCATTA GGTAAATACT ATTACAGTCG TGGTTTCTGC A
```

Seq ID NO: 296 Protein sequence:
Protein Accession #: Eos sequence

```
1          11         21         31         41         51
|          |          |          |          |          |
MTDKTEKVAV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIAGS AMSKEKKLMT   60
GHAIPPSQLD SQIDDFTGFS KDRMMQKPGS NAPVGGNVTS SFSGDDLECR ETASSPKSQR  120
EINADIKRKL VKELRCVGQK YEKIFEMLEG VQGPTAVRKR FFESIIKEAA RCMRRDFVKH  180
LKKKLKRMI
```

Seq ID NO: 297 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-815

```
1          11         21         31         41         51
|          |          |          |          |          |
AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG   60
GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCCAGGTGC  120
CCTAGGGGGC ACATTTCCCA CAACTCCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAGTG  180
GGGAGGCGCC ACAACTTCAC TGCCATTTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG  240
GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT  300
CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG  360
AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGA AAAGAAGCTT  420
ATGACAGGAC ATGCTATTCC ACCCAGCCAA TTGGATTCTC AGATTGATGA CTTCACTGGT  480
TTCAGCAAAG ATAGGATGAT GCAGAAACCT GGTAGCAATG CACCTGTGGG AGGAAACGTT  540
ACCAGCAGTT TCTCTGGAGA TGACCTAGAA TGCAGAGAAA CAGCCTCCTC TCCCAAAAGC  600
CAACAAGAAA TTAATGCTGA TATAAAACGT AAATTAGTGA AGGAACTCCG ATGCGTTGGA  660
CAAAAATATG AAAAAATCTT CGAAATGCTT GAAGGAGTGC AAGGACCTAC TGCAGTCAGG  720
AAACGATTTT TTGAATCCAT CATCAAGGAA GCAGCAAGAT GTATGAGACG AGACTTTGTT  780
AAGCACCTTA AGAAGAAACT GAAACGTATG ATTTGAGAAT ACTTGTCCCT GGAGGATTAT  840
CACACCCCAA ATGCATAATC TCATTAATGA TTGAGGAGAG AAAAGGATCA GATTGCTGTT  900
TTCTACAATG GAGCAGGATA TTGCTGAAGT CTCCTGGCAT ATGTTACCGA ATCAACTGGC  960
CTTCCAGAGG CTAAGAAATT TCTGTTAGTA AAAGATGTTC TTTTTCCCAA AGCGTTTTAT 1020
TTGAAAGGAT AACTTGTGTT TTGGTTATTT TGTATTCCCA CCTGTGCTGG TAGATATTAT 1080
TAACCCATTA GGTAAATACT ATTACAGTCG TGGTTTCTGC A
```

Seq ID NO: 298 Protein sequence:
Protein Accession #: Eos sequence

```
1          11         21         31         41         51
|          |          |          |          |          |
MTDKTEKVAV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIAGS AMSKEKKLMT   60
GHAIPPSQLD SQIDDFTGFS KDRMMQKPGS NAPVGGNVTS SFSGDDLECR ETASSPKSQQ  120
EINADIKRKL VKELRCVGQK YEKIFEMLEG VQGPTAVRKR FFESIIKEAA RCMRRDFVKH  180
LKKKLKRMI
```

Seq ID NO: 299 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-815

```
1          11         21         31         41         51
|          |          |          |          |          |
AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG   60
GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCCAGGTGC  120
CCTAGGGGGC ACATTTCCCA CAACTCCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAGTG  180
GGGAGGCGCC ACAACTTCAC TGCCATTTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG  240
GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT  300
CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG  360
AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGC AAAGAGCTTA  420
TGACAGGACA TGCTATTCCA CCCAGCCAAT TGGATTCTCA GATTGATGAC TTCACTGGTT  480
```

```
TCAGCAAAGA TAGGATGATG CAGAAACCTG GTAGCAATGC ACCTGTGGGA GGAAACGTTA   540
CCAGCAGTTT CTCTGGAGAT GACCTAGAAT GCAGAGAAAC AGCCTCCTCT CCCAAAAGCC   600
AACAAGAAAT TAATGCTGAT ATAAAACGTA AATTAGTGAA GGAACTCCGA TGCGTTGGAC   660
AAAAATATGA AAAAATCTTC GAAATGCTTG AAGGAGTGCA AGGACCTACT GCAGTCAGGA   720
AACGATTTTT TGAATCCATC ATCAAGGAAG CAGCAAGATG TATGAGACGA GACTTTGTTA   780
AGCACCTTAA GAAGAAACTG AAACGTATGA TTTGAGAATA CTTGTCCCTG GAGGATTATC   840
ACACCCCAAA TGCATAATCT CATTAATGAT TGAGGAGAGA AAAGGATCAG ATTGCTGTTT   900
TCTACAATGG AGCAGGATAT TGCTGAAGTC TCCTGGCATA TGTTACCGAA TCAACTGGCC   960
TTCCAGAGGC TAAGAAATTT CTGTTAGTAA AAGATGTTCT TTTTCCCAAA GCGTTTTATT  1020
TGAAAGGATA ACTTGTGTTT TGGTTATTTT GTATTCCCAC CTGTGCTGGT AGATATTATT  1080
AACCCATTAG GTAAATACTA TTACAGTCGT GGTTTCTGCA
```

Seq ID NO: 300 Protein sequence:
Protein Accession #: Eos sequence

```
1          11         21         31         41         51
|          |          |          |          |          |
MTDKTEKVAV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIAGS AMSKAKKLMT    60
GHAIPPSQLD SQIDDFTGFS KDRMMQKPGS NAPVGGNVTS SFSGDDLECR ETASSPKSQQ   120
EINADIKRKL VKELRCVGQK YEKIFEMLEG VQGPTAVRKR FFESIIKEAA RCMRRDFVKH   180
LKKKLKRMI
```

Seq ID NO: 301 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-812

```
1          11         21         31         41         51
|          |          |          |          |          |
AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG    60
GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCCAGGTGC   120
CCTAGGGGGC ACATTTCCCA CAACTCCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAGTG   180
GGGAGGCGCC ACAACTTCAC TGCCATTTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG   240
GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT   300
CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG   360
AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGA AAAGAGCTTA   420
TGACAGGACA TGCTATTCCA CCCAGCCAAT TGGATTCTCA GATTGATGAC TTCACTGGTT   480
TCAGCAAAGA TGGGATGATG CAGAAACCTG GTAGCAATGC ACCTGTGGGA GGAAATGTTA   540
CCAGCAATTT CTCTGGAGAT GACCTAGAAT GCAGAGGAAT AGCCTCCTCT CCCAAAAGCC   600
AACAAGAAAT TAATGCTGAT ATAAAATGTC AAGTAGTGAA GGAAATCCGA TGCCTTGGAC   660
AATATGAAAA AATCTTCGAA ATGCTTGAAG GAGTGCAAGG ACCTACTGCA GTCAGGAAAC   720
GATTTTTTGA ATCCATCATC AAGGAAGCAG CAAGATGTAT GAGACGAGAC TTTGTTAAGC   780
ACCTTAAGAA GAAACTGAAA CGTATGATTT GAGAATACTT GTCCCTGGAG GATTATCACA   840
CCCCAAATGC ATAATCTCAT TAATGATTGA GGAGAGAAAA GGATCAGATT GCTGTTTTCT   900
ACAATGGAGC AGGATATTGC TGAAGTCTCC TGGCATATGT TACCGAATCA ACTGGCCTTC   960
CAGAGGCTAA GAAATTTCTG TTAGTAAAAG ATGTTCTTTT TCCCAAAGCG TTTTATTTGA  1020
AAGGATAACT TGTGTTTTGG TTATTTTGTA TTCCCACCTG TGCTGGTAGA TATTATTAAC  1080
CCATTAGGTA AATACTATTA CAGTCGTGGT TTCTGCA
```

Seq ID NO: 302 Protein sequence:
Protein Accession #: Eos sequence

```
1          11         21         31         41         51
|          |          |          |          |          |
MTDKTEKVAV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIAGS AMSKEKKLMT    60
GHAIPPSQLD SQIDDFTGFS KDGMMQKPGS NAPVGGNVTS NFSGDDLECR GIASSPKSQQ   120
EINADIKCQV VKEIRCLGQY EKIFEMLEGV QGPTAVRKRF FESIIKEAAR CMRRDFVKHL   180
KKKLKRMI
```

Seq ID NO: 303 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-815

```
1          11         21         31         41         51
|          |          |          |          |          |
AGTGTTCGGC TGGGACAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTTCC ATCCCCCTTG    60
GGCCAAACAG GATCGGTGCT TCTGGTGAGA CGTCTCCCCA TGCACATCAC TCCCAGATGC   120
CCTAGGGGGC ACATTTCCCA CAACTCCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAGTG   180
GGGAGGCGCC ACAACTTCAC TGCCATTTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG   240
GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT   300
CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG   360
AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGC AAAGAGCTTA   420
TGACAGGACA TGCTATTCCA CCCAGCCAAT TGGATTCTCA GATTGATGAC TTCACTGGTT   480
TCAGCAAAGA TAGGATGATG CAGAAACCTG GTAGCAATGC ACCTGTGGGA GGAAACGTTA   540
CCAGCAGTTT CTCTGGAGAT GACCTAGAAT GCAGAGAAAC AGCCTCCTCT CCCAAAAGCC   600
AACAAGAAAT TAATGCTGAT ATAAAACGTA AATTAGTGAA GGAACTCCGA TGCGTTGGAC   660
AAAAATATGA AAAAATCTTC GAAATGCTTG AAGGAGTGCA AGGACCTACT GCAGTCAGGA   720
AACGATTTTT TGAATCCATC ATCAAGGAAG CAGCAAGATG TATGAGACGA GACTTTGTTA   780
AGCACCTTAA GAAGAAACTG AAACGTATGA TTTGAGAATA CTTGTCCCTG GAGGATTATC   840
ACACCCCAAA TGCATAATCT CGTTAATGAT TGAGGAGAGA AAAGGATCAG ATTGCTGTTT   900
TCTACAATGG AGCAGGATAT TGCTGAAGTC TCCTGGCATA TGTTACCGAA TCAACTGGCC   960
TTCCAGAGGC TAAGAAATTT CTGTTAGTAA AAGATGTTCT TTTTCCCAAA GCGTTTTATT  1020
TGAAAGGATA ACTTGTGTTT TGGTTATTTT GTATTCCCAC CTGTGCTGGT AGATATTATT  1080
AACCCATTAG GTAAATACTA TTACAGTCGT GGTTTCTGCA
```

Seq ID NO: 304 Protein sequence:
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MTDKTEKVAV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIAGS AMSKAKKLMT    60
GHAIPPSQLD SQIDDFTGFS KDRMMQKPGS NAPVGGNVTS SFSGDDLECR ETASSPKSQQ   120
EINADIKRKL VKELRCVGQK YEKIFEMLEG VQGPTAVRKR FFESIIKEAA RCMRRDFVKH   180
LKKKLKRMI
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Seq ID NO: 305 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 87-689

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1          11         21         31         41         51
|          |          |          |          |          |
CGTGGAGGCA GCTAGCGCGA GGCTGGGGAG CGCTGAGCCG CGCGTCGTGC CCTGCGCTGC    60
CCAGACTAGC GAACAATACA GTCAGGATGG CTAAAGGTGA CCCCAAGAAA CCAAAGGGCA   120
AGATGTCCGC TTATGCCTTC TTTGTGCAGA CATGCAGAGA AGAACATAAG AAGAAAAACC   180
CAGAGGTCCC TGTCAATTTT GCGGAATTTT CCAAGAAGTG CTCTGAGAGG TGGAAGACGA   240
TGTCCGGGAA AGAGAAATCT AAATTTGATG AAATGGCAAA GGCAGATAAA GTGCGCTATG   300
ATCGGGAAAT GAAGGATTAT GGACCAGCTA AGGGAGGCAA GAAGAAGAAG GATCCTAATG   360
CTCCCAAAAG GCCACCGTCT GGATTCTTCC TGTTCTGTTC AGAATTCCGC CCCAAGATCA   420
AATCCACAAA CCCCGGCATC TCTATTGGAG ACGTGGCAAA AAAGCTGGGT GAGATGTGGA   480
ATAATTTAAA TGACAGTGAA AAGCAGCCTT ACATCACTAA GGCGGCAAAG CTGAAGGAGA   540
AGTATGAGAA GGATGTTGCT GACTATAAGT CGAAAGGAAA GTTTGATGGT GCAAAGGGTC   600
CTGCTAAAGT TGCCCGGAAA AAGGTGGAAG AGGAAGATGA AGAAGAGGAG GAGGAAGAAG   660
AGGAGGAGGA GGAGGAGGAG GATGAATAAA GAAACTGTTT ATCTGTCTCC TTGTGAATAC   720
TTAGAGTAGG GGAGCGCCGT AATTGACACA TCTCTTATTT GAGAAGTGTC TGTTGCCCTC   780
ATTAGGTTTA ATTACAAAAT TTGATCACGA TCATATTGTA GTCTCTCAAA GTGCTCTAGA   840
AATTGTCAGT GGTTTACATG AAGTGGCCAT GGGTGTCTGG AGCACCCTGA AACTGTATCA   900
AAGTTGTACA TATTTCCAAA CATTTTTAAA ATGAAAAGGC ACTCTCGTGT TCTCCTCACT   960
CTGTGCACTT TGCTGTTGGT GTGACAAGGC ATTTAAAGAT GTTTCTGGCA TTTTCTTTTT  1020
ATTTGTAAGG TGGTGGTAAC TATGGTTATT GGCTAGAAAT CCTGAGTTTT CAACTGTATA  1080
TATCTATAGT TTGTAAAAAG AACAAAACAA CCGAGACAAA CCCTTGATGC TCCTTGCTCG  1140
GCGTTGAGGC TGTGGGGAAG ATGCCTTTTG GGAGAGGCTG TAGCTCAGGG CGTGCACTGT  1200
GAGGCTGGAC CTGTTGACTC TGCAGGGGGC ATCCATTTAG CTTCAGGTTG TCTTGTTTCT  1260
GTATATAGTG ACATAGCATT CTGCTGCCAT CTTAGCTGTG GACAAAGGGG GGTCAGCTGG  1320
CATGAGAATA TTTTTTTTTT TAAGTGCGGT AGTTTTTAAA CTGTTTGTTT TTAAACAAAC  1380
TATAGAACTC TTCATTGTCA GCAAAGCAAA GAGTCACTGC ATCAATGAAA GTTCAAGAAC  1440
CTCCTGTACT TAAACACGAT TCGCAACGTT CTGTTATTTT TTTTGTATGT TTAGAATGCT  1500
GAAATGTTTT TGAAGTTAAA TAAACAGTAT TACATTTTTA AAACTCTTCT CTATTATAAC  1560
AGTCAATTTC TGACTCACAG CAGTGAACAA ACCCCCACTC CATTGTATTT GGAGACTGGC  1620
CTCCCTATAA ATGTGGTAGC TTCTTTTATT ACTCAGTGGC CAGCTCACTT AGGGCTGAGA  1680
TGAAGGAGAG GGCTACTTGA AGCTACTGTG TGATTTTGTT TGTGTCTGAG TGGCATTCAG  1740
ATGAAGTCTG GAGGAGTTAG GAGAACGACA TAGGCAAGGT TCAGCAGCCT TCCAAGGTAT  1800
AGGAAGGTGG GTGATTAGGA CTGAGGCTAT CTAGGTTTAA CTTTTGTCCC ACCTCCACCC  1860
CCTATTTTGT GGGGCCAAAT GCATTGCTAA ACAGCAATTT CAGAGTGTAT GGTGTGTCAA  1920
AAATTAAGGC CTTATTGTTT TTCTCTTTCA CCCCTACCCC CCGTGCTCCT GGCACATATC  1980
ACATTATTTG TGGTGCCCAA CATTTGGGGT CTTGAGCCTG CTGCTGGTCT CCTGGATGCC  2040
AGTGAGGGTA TGTGGGATGG GGTGGTGGGG TAGGGGACGG TATCCTTTTT TTGCTCCTAC  2100
TTGGAAACAC CAAACACCCC AAGGAAGATG ATAGGCTCCA TCTTGGGCCA CCTGAGCTAT  2160
AGGGCAGGCT AATGGAATCA ACCATTTCTG AGCACTAAAT GTATCATGAA AAGTTGAATG  2220
GCCTGCTCAT AAGTTTAGCT CATTCACTGG AAATGTAGAT TGATGTTCAA TGTTAAACTG  2280
GAAGGAGCTT GGTTTGTGTG TCAGTGGTTA TATTAGTGGG TAGTGTAACA TTTTATCCAG  2340
GTTGGGGTGA GGGGAGATGG CCACAGTAGC AAGTGGTGAC ACTAAATACC ATTTTGAAGG  2400
CTGATGTGTA TATACATCAT TACTGTCCGT AGCAATGAAG GATACAGTAC TGTGTTGTGG  2460
GTGAGTGTTG CTATTGCCCA GCATTAATAT TTGGGTGTGT ATGTTTGAGG CTATGAAACA  2520
CGCAGGAGTG TTTTTGTGCT ATTAATTTTA AGAGAAAGCA GCTTTTTCTT AAAATTCACT  2580
GTTGAGAAAC TTGCATGTCT GGAGGCGGTG TCCTCTCCGC CCTGTCGGGT CCTGGATGAG  2640
TACGAGTTAT GGTCACGGTC ACAGCCTGAT CTCTTATGTG TTCATAGCCA TTCGCTCTCC  2700
CATCAGAACT GTTTGTCCTG AATGTGTTCC TCTAGTTCTA GAAAATGACC ACTAATTTAA  2760
AAAACTCGGT TGTGAGGTTT GCCCAGAGGC ACTTGTTCCA GAATTTCCCC TCCTGCTTCA  2820
GCCATGTCCT TGTCACTTGG CATTCTAAGC TAAAGCTTTA GCTTCCCAAT TCGTGATGTG  2880
CTAGGCCAAG ATTCGGGAGC TGTTGCCAGC CTCGTCAAAT ATGGAAGAGA AACAACCTGC  2940
GGTCAAAAGG GAGTGATTTG TTAAGTGGTG CGCGTCTATC TCATAACTAG ATGTACCAAC  3000
CAGGGAAGGG CCAAGGATGG AAAGGGGTAA CTTTTGTGCT TCCAAAGTAG CTAAGCAGAA  3060
GTGGGGGAGC AGTTTAGCCA GATGATCTTT GATTAGGCAA ACATTGAGTT TTAAAGAGGC  3120
TGTCAAGTTG AGGCCACTTG GTCCATTAGC TGGGGCAGCA AGATCACTAC TCAACGTTTT  3180
CACACTGTGG CAAGATTGCT CTTCTAGTGG AATAATGCCC TAGTTTCTCT GAGATGATGT  3240
AAGTGGCATG ATGTTACCTA AGGCTTAGGC TTAGCTTGAT TTCTGGGCCC ACTGTCTGTG  3300
TTCTTAAGAT GCCAACCTGT TGCTTTTTTT TTTTTTTTCC CCCATTTAAA AGGATAGTAC  3360
CTACTCCCTC TAACCACCTC ACCCCATTCT TGAATGACAT TTTATCCTTC GGAAAGAACA  3420
AGGCTGTGAT GTAGTGACTA TTGTCTGTGT CTCCTGTGTG TGTCTGTTCT TGTCACAAAT  3480
GTATTTGGGG ACGTTGGATG CATTCATTTT CTGTAATAAA G
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Seq ID NO: 306 Protein sequence:
Protein Accession #: NP_005333.1

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1          11         21         31         41         51
|          |          |          |          |          |
MAKGDPKKPK GKMSAYAFFV QTCREEHKKK NPEVPVNFAE FSKKCSERWK TMSGKEKSKF    60
DEMAKADKVR YDREMKDYGP AKGGKKKKDP NAPKRPPSGF FLFCSEFRPK IKSTNPGISI   120
GDVAKKLGEM WNNLNDSEKQ PYITKAAKLK EKYEKDVADY KSKGKFDGAK GPAKVARKKV   180
EEEDEEEEEE EEEEEEEEDE
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Seq ID NO: 307 DNA sequence
Nucleic Acid Accession #: NM_022342
Coding sequence: 1..2178

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1          11         21         31         41         51
|          |          |          |          |          |
ATGGGTACTA GGAAAAAAGT TCATGCATTT GTCCGTGTCA AACCCACCGA TGACTTTGCT    60
CATGAAATGA TCAGATACGG AGATGACAAA AGAAGCATTG ATATTCACTT AAAAAAAGAC   120
ATTCGGAGAG GAGTTGTCAA TAACCAACAG ACAGACTGGT CGTTTAAGTT GGATGGAGTT   180
TTCACGATG CCTCCCAGGA CTTGGTTTAT GAGACAGTTG CAAAGGATGT GGTTTCTCAG    240
CCCTCGATG GCTATAATGG CACCATCATG TGTTATGGGC AGACGGGAGC TGGCAAGACA    300
ACACCATGA TGGGGGCAAC TGAGAATTAC AAGCACCGGG GGATCCTCCC TCGTGCCCTG    360
AGCAGGTTT TTAGGATGAT CGAAGAACGC CCCACACATG CCATCACTGT GCGTGTTTCC    420
ACTTGGAAA TCTATAATGA GAGCCTGTTT GATCTCCTGT CCACTCTGCC CTATGTTGGA    480
CCTCAGTCA CACCAATGAC CATCGTGGAA AACCCTCAAG GAGTCTTCAT TAAGGGCTTG    540
CAGTTCACC TCACAAGTCA GGAGGAGGAT GCATTCAGCC TCCTTTTTGA GGGTGAGACC    600
ACAGGATTA TAGCCTCCCA CACTATGAAC AAAAACTCTT CCAGATCACA CTGCATTTTC    660
CCATCTACT TAGAGGCCCA TTCCCGGACC TTATCAGAGG AAAAGTACAT CACTTCCAAA    720
TTAACTTGG TGGATCTGGC AGGCTCAGAG AGGCTGGGGA AGTCTGGGTC TGAGGGCCAA    780
TCCTGAAGG AAGCCACCTA CATCAACAAA TCGCTCTCAT TCCTGGAGCA GGCCATCATT    840
CCCTTGGGG ACCAGAAGCG GGACCACATC CCCTTTCGGC AGTGCAAGCT CACCCACGCT    900
TGAAGGACT CGTTAGGGGG AAACTGCAAT ATGGTCCTCG TGACAAACAT CTATGGAGAA    960
CTGCCCAGT TAGAAGAAAC GCTATCTTCA CTGAGATTTG CCAGCAGGAT GAAGCTAGTC   1020
CCACTGAGC CTGCCATCAA TGAAAAGTAT GATGCTGAGA GAATGGTCAA GAACCTGGAG   1080
AGGAACTAG CACTACTCAA GCAGGAGCTG GCTATCCATG ACAGCCTGAC CAACCGCACC   1140
TTGTGACCT ATGACCCCAT GGATGAAATC CAGATTGCTG AGATCAACTC CCAGGTGCGG   1200
GGTACCTGG AGGGGACACT GGACGAGATC GACATAATCA GCCTTAGACA GATCAAGGAG   1260
TGTTCAACC AGTTCCGGGT GGTTCTGAGC CAACAGGAAC AGGAAGTGGA GTCCACTTTG   1320
GCAGGAAGT ACACCCTCAT TGACAGGAAT GACTTTGCAG CCATTTCTGC TATCCAGAAG   1380
CGGGGCTTG TGGATGTTGA TGGCCACCTA GTGGGTGAGC CTGAAGGACA AAACTTTGGA   1440
TCGGAGTCG CCCCTTTCTC TACCAAACCT GGGAAGAAAG CCAAGTCCAA GAAGACATTC   1500
AAGAGCCAC TCAGGCCCGA CACCCCACCC TCCAAACCAG TGGCCTTTGA GGAGTTTAAG   1560
ATGAGCAAG GTAGTGAGAT CAACCGAATT TTCAAAGAAA ACAAATCCAT CTTGAATGAA   1620
GGAGGAAAA GGGCCAGCGA GACCACACAG CACATCAATG CCATCAAGCG GGAGATTGAT   1680
TGACCAAGG AGGCCCTGAA TTTCCAGAAG TCACTACGGG AGAAGCAAGG CAAGTACGAA   1740
ACAAGGGGC TGATGATCAT CGATGAGGAA GAATTCCTGC TGATCCTCAA GCTCAAAGAC   1800
TCAAGAAGC AGTACCGCAG CGAGTACCAG GACCTGCGTG ACCTCAGGGC TGAGATCCAG   1860
ATTGCCAGC ACCTAGTGGA TCAGTGTCGC CACCGCCTGC TCATGGAATT TGACATCTGG   1920
ACAATGAGT CCTTTGTCAT CCCTGAGGAC ATGCAGATGG CACTGAAGCC AGGCGGCAGC   1980
TCCGGCCAG GCATGGTCCC TGTGAACAGG ATTGTGTCTC TGGGAGAAGA TGACCAGGAC   2040
AATTCAGCC AGCTGCAGCA GAGGGTGCTT CCTGAGGGCC CTGATTCCAT CTCCTTCTAC   2100
ATGCCAAAG TCAAGATAGA GCAGAAGCAT AATTACTTGA AAACCATGAT GGGCCTCCAG   2160
AGGCACATA GAAAATAG
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Seq ID NO: 308 Protein sequence:
Protein Accession #: NP_071737

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1          11         21         31         41         51
|          |          |          |          |          |
MGTRKKVHAF VRVKPTDDFA HEMIRYGDDK RSIDIHLKKD IRRGVVNNQQ TDWSFKLDGV    60
LHDASQDLVY ETVAKDVVSQ ALDGYNGTIM CYGQTGAGKT YTMMGATENY KHRGILPRAL   120
QQVFRMIEER PTHAITVRVS YLEIYNESLF DLLSTLPYVG PSVTPMTIVE NPQGVFIKGL   180
SVHLTSQEED AFSLLFEGET NRIIASHTMN KNSSRSHCIF TIYLEAHSRT LSEEKYITSK   240
INLVDLAGSE RLGKSGSEGQ VLKEATYINK SLSFLEQAII ALGDQKRDHI PFRQCKLTHA   300
LKDSLGGNCN MVLVTNIYGE AAQLEETLSS LRFASRMKLV TTEPAINEKY DAERMVKNLE   360
KELALLKQEL AIHDSLTNRT FVTYDPMDEI QIAEINSQVR RYLEGTLDEI DIISLRQIKE   420
VFNQFRVVLS QQEQEVESTL RRKYTLIDRN DFAAISAIQK AGLVDVDGHL VGEPEGQNFG   480
LGVAPFSTKP GKKAKSKKTF KEPLRPDTPP SKPVAFEEFK NEQGSEINRI FKENKSILNE   540
RRKRASETTQ HINAIKREID VTKEALNFQK SLREKQGKYE NKGLMIIDEE EFLLILKLKD   600
LKKQYRSEYQ DLRDLRAEIQ YCQHLVDQCR HRLLMEFDIW YNESFVIPED MQMALKPGGS   660
IRPGMVPVNR IVSLGEDDQD KFSQLQQRVL PEGPDSISFY NAKVKIEQKH NYLKTMMGLQ   720
QAHRK
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Seq ID NO: 309 DNA sequence
Nucleic Acid Accession #: CAT cluster

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1          11         21         31         41         51
|          |          |          |          |          |
TTTTTTTTTT TTTTTTTTAA TGCCTGCTGT CATGCTCTGT CTACCAGGGT GAATTTCCAA    60
AAATTTCTGC ATAGCAATTT TAGCCAAAAC TATATATGTT CTGGGGAGGA TAGGCATAGG   120
CACATTGAAG ACCAAAGGAA AGAGTGAAGA AGTGTAGTTG GGTCATTGTG AATGGATGTT   180
TAGATTGTCA AGAAAAGTGG GCCAGAGGCC CCACCTCACA CTAGGACGGC AATTGCCTCT   240
CATTAGTATC TCAGGCACCA TGGGTCTTAT TTGGTGTCAT AAGAAACACC CTCAACAAAG   300
TAATGAACCC TCAGCCTCCA GCTTCTCTTC TTCGGGATTC TTCTTAGGGC CTCCTTTTTC   360
CTTTTATGTT TCCAGTACCC TGAATTTCTT ATTCCCATCC CCCATTAAAA TCTGCTTCAA   420
AGAAAAAACA AGAAGGACAC ATTCACTTTA AGATCCAAAT GAATGATAAG AGCTTAAAAC   480
ATTATACTTA TCAGTATTAT TTGCATTTTT ATAGAAACCA AAACCATATT TCAACAAC
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Seq ID NO: 310 DNA sequence
Nucleic Acid Accession #: NM_018622.2
Coding sequence: 1-1140

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1          11         21         31         41         51
|          |          |          |          |          |
ATGGCGTGGC GAGGCTGGGC GCAGAGAGGC TGGGGCTGCG GCCAGGCGTG GGGTGCGTCG    60
GTGGGCGGCC GCAGCTGCGA GGAGCTCACT GCGGTCCTAA CCCCGCCGCA GCTCCTCGGA   120
CGCAGGTTTA ACTTCTTTAT TCAACAAAAA TGCGGATTCA GAAAAGCACC CAGGAAGGTT   180
GAACCTCGAA GATCAGACCC AGGGACAAGT GGTGAAGCAT ACAAGAGAAG TGCTTTGATT   240
CCTCCTGTGG AAGAAACAGT CTTTTATCCT TCTCCCTATC CTATAAGGAG TCTCATAAAA   300
CCTTTATTTT TTACTGTTGG GTTTACAGGC TGTGCATTTG GATCAGCTGC TATTTGGCAA   360
```

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TATGAATCAC TGAAATCCAG GGTCCAGAGT TATTTTGATG GTATAAAAGC TGATTGGTTG   420
GATAGCATAA GACCACAAAA AGAAGGAGAC TTCAGAAAGG AGATTAACAA GTGGTGGAAT   480
AACCTAAGTG ATGGCCAGCG GACTGTGACA GGTATTATAG CTGCAAATGT CCTTGTATTC   540
TGTTTATGGA GAGTACCTTC TCTGCAGCGG ACAATGATCA GATATTTCAC ATCGAATCCA   600
GCCTCAAAGG TCCTTTGTTC TCCAATGTTG CTGTCAACAT TCAGTCACTT CTCCTTATTT   660
CACATGGCAG CAAATATGTA TGTTTTGTGG AGCTTCTCTT CCAGCATAGT GAACATTCTG   720
GGTCAAGAGC AGTTCATGGC AGTGTACCTA TCTGCAGGTG TTATTTCCAA TTTTGTCAGT   780
TACCTGGGTA AAGTTGCCAC AGGAAGATAT GGACCATCAC TTGGTGCATC TGGTGCCATC   840
ATGACAGTCC TCGCAGCTGT CTGCACTAAG ATCCCAGAAG GGAGGCTTGC CATTATTTTC   900
CTTCCGATGT TCACGTTCAC AGCAGGGAAT GCCCTGAAAG CCATTATCGC CATGGATACA   960
GCAGGAATGA TCCTGGGATG GAAATTTTTT GATCATGCGG CACATCTTGG GGGAGCTCTT  1020
TTTGGAATAT GGTATGTTAC TTACGGTCAT GAACTGATTT GGAAGAACAG GGAGCCGCTA  1080
GTGAAAATCT GGCATGAAAT AAGGACTAAT GGCCCCAAAA AAGGAGGTGG CTCTAAGTAA
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Seq ID NO: 311 Protein sequence:
Protein Accession #: NP_061092.2

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1          11         21         31         41         51
|          |          |          |          |          |
MAWRGWAQRG WGCGQAWGAS VGGRSCEELT AVLTPPQLLG RRFNFFIQQK CGFRKAPRKV    60
EPRRSDPGTS GEAYKRSALI PPVEETVFYP SPYPIRSLIK PLFFTVGFTG CAFGSAAIWQ   120
YESLKSRVQS YFDGIKADWL DSIRPQKEGD FRKEINKWWN NLSDGQRTVT GIIAANVLVF   180
CLWRVPSLQR TMIRYFTSNP ASKVLCSPML LSTFSHFSLF HMAANMYVLW SFSSSIVNIL   240
GQEQFMAVYL SAGVISNFVS YLGKVATGRY GPSLGASGAI MTVLAAVCTK IPEGRLAIIF   300
LPMFTFTAGN ALKAIIAMDT AGMILGWKFF DHAAHLGGAL FGIWYVTYGH ELIWKNREPL   360
VKIWHEIRTN GPKKGGGSK
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Seq ID NO: 312 DNA sequence
Nucleic Acid Accession #: NM_000625
Coding sequence: 195..3656

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1          11         21         31         41         51
|          |          |          |          |          |
CTCTCGGCCA CCTTTGATGA GGGGACTGGG CAGTTCTAGA CAGTCCCGAA GTTCTCAAGG    60
CACAGGTCTC TTCCTGGTTT GACTGTCCTT ACCCCGGGGA GGCAGTGCAG CCAGCTGCAA   120
GCCCCACAGT GAAGAACATC TGAGCTCAAA TCCAGATAAG TGACATAAGT GACCTGCTTT   180
GTAAAGCCAT AGAGATGGCC TGTCCTTGGA AATTTCTGTT CAAGACCAAA TTCCACCAGT   240
ATGCAATGAA TGGGGAAAAA GGCATCAACA ACAATGTGGA GAAAGCCCCC TGTGCCACCT   300
CCAGTCCAGT GACACAGGAT GACCTTCAGT ATCACAACCT CAGCAAGCAG CAGAATGAGT   360
CCCCGCAGCC CCTCGTGGAG ACGGGAAAGA AGTCTCCAGA ATCTCTGGTC AAGCTGGATG   420
CAACCCCATT GTCCTCCCCA CGGCATGTGA GGATCAAAAA CTGGGGCAGC GGGATGACTT   480
TCCAAGACAC ACTTCACCAT AAGGCCAAAG GGATTTTAAC TTGCAGGTCC AAATCTTGCC   540
TGGGGTCCAT TATGACTCCC AAAAGTTTGA CCAGAGGACC CAGGGACAAG CCTACCCCTC   600
CAGATGAGCT TCTACCTCAA GCTATCGAAT TTGTCAACCA ATATTACGGC TCCCTCAAAG   660
AGGCAAAAAT AGAGGAACAT CTGGCCAGGG TGGAAGCGGT AACAAAGGAG ATAGAAACAA   720
CAGTAACCTA CCAACTGACG GGAGATGAGC TCATCTTCGC CACCAAGCAG GCCTGGCGCA   780
ATGCCCCACG CTGCATTGGG AGGATCCAGT GGTCCAACCT GCAGGTCTTC GATGCCCGCA   840
GCTGTTCCAC TGCCCGGGAA ATGTTTGAAC ACATCTGCAG ACACGTGCGT TACTCCACCA   900
ACAATGGCAA CATCAGGTCG GCCATCACCG TGTTCCCCCA GCGGAGTGAT GGCAAGCACG   960
ACTTCCGGGT GTGGAATGCT CAGCTCATCC GCTATGCTGG CTACCAGATG CCAGATGGCA  1020
GCATCAGAGG GGACCCTGCC AACGTGGAAT TCACTCAGCT GTGCATCGAC CTGGGCTGGA  1080
AGCCCAAGTA CGGCCGCTTC GATGTGGTCC CCCTGGTCCT GCAGGCCAAT GGCCGTGACC  1140
CTGAGCTCTT CGAAATCCCA CCTGACCTTG TGCTTGAGGT GGCCATGGAA CATCCCAAAT  1200
ACGAGTGGTT TCGGGAACTG GAGCTAAAGT GGTACGCCCT GCCTGCAGTG GCCAACATGC  1260
TGCTTGAGGT GGGCGGCCTG GAGTTCCCAG GGTGCCCCTT CAATGGCTGG TACATGGGCA  1320
CAGAGATCGG AGTCCGGGAC TTCTGTGATG TCCAGCGCTA CAACATCCTG GAGGAAGTGG  1380
GCAGGAGAAT GGGCCTGGAA ACGCACAAGC TGGCCTCGCT CTGGAAAGAC CAGGCTGTCG  1440
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ACCACTCGGC TGCAGAATCC TTCATGAAGT ACATGCAGAA TGAATACCGG TCCCGTGGGG  1560
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GAGTCAGAGT CACCATCCTC TTTGCGACAG AGACAGGAAA ATCAGAGGCG CTGGCCTGGG  1860
ACCTGGGGGC CTTATTCAGC TGTGCCTTCA ACCCCAAGGT TGTCTGCATG GATAAGTACA  1920
GGCTGAGCTG CCTGGAGGAG GAACGGCTGC TGTTGGTGGT GACCAGTACG TTTGGCAATG  1980
GAGACTGCCC TGGCAATGGA GAGAAACTGA AGAAATCGCT CTTCATGCTG AAAGAGCTCA  2040
ACAACAAATT CAGGTACGCT GTGTTTGGCC TCGGCTCCAG CATGTACCCT CGGTTCTGCG  2100
CCTTTGCTCA TGACATTGAT CAGAAGCTGT CCCACCTGGG GGCCTCTCAG CTCACCCCGA  2160
TGGGAGAAGG GGATGAGCTC AGTGGGCAGG AGGACGCCTT CCGCAGCTGG GCCGTGCAAA  2220
CCTTCAAGGC AGCCTGTGAG ACGTTTGATG TCCGAGGCAA ACAGCACATT CAGATCCCCA  2280
AGCTCTACAC CTCCAATGTG ACCTGGGACC CGCACCACTA CAGGCTCGTG CAGGACTCAC  2340
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GGCTCAAATC TCGGCAGAAT CTACAAAGTC CGACATCCAG CCGTGCCACC ATCCTGGTGG  2460
AACTCTCCTG TGAGGATGGC CAAGGCCTGA ACTACCTGCC GGGGGAGCAC CTTGGGGTTT  2520
GCCCAGGCAA CCAGCCGGCC CTGGTCCAAG GCATCCTGGA GCGAGTGGTG GATGGCCCCA  2580
CACCCCACCA GGCAGTGCGC CTGGAGGCCC TGGATGAGAG TGGCAGCTAC TGGGTCAGTG  2640
ACAAGAGGCT GCCCCCCTGC TCACTCAGCC AGGCCCTCAC CTACTTCCTG GACATCACCA  2700
CACCCCCAAC CCAGCTGCTG CTCCAAAAGC TGGCCCAGGT GGCCACAGAA GAGCCTGAGA  2760
GACAGAGGCT GGAGGCCCTG TGCCAGCCCT CAGAGTACAG CAAGTGGAAG TTCACCAACA  2820
GCCCCACATT CCTGGAGGTG CTAGAGGAGT TCCCGTCCCT GCGGGTGTCT GCTGGCTTCC  2880
TGCTTTCCCA GCTCCCCATT CTGAAGCCCA GGTTCTACTC CATCAGCTCC CCCCGGGATC  2940
ACACGCCCAC GGAGATCCAC CTGACTGTGG CCGTGGTCAC CTACCACACC CGAGATGGCC  3000
AGGGTCCCCT GCACCACGGC GTCTGCAGCA CATGGCTCAA CAGCCTGAAG CCCCAAGACC  3060
CAGTGCCCTG CTTTGTGCGG AATGCCAGCG GCTTCCACCT CCCCGAGGAT CCCTCCCATC  3120
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CTTGCATCCT CATCGGGCCT GGCACAGGCA TCGCGCCCTT CCGCAGTTTC TGGCAGCAAC 3180
GGCTCCATGA CTCCCAGCAC AAGGGAGTGC GGGGAGGCCG CATGACCTTG GTGTTTGGGT 3240
GCCGCCGCCC AGATGAGGAC CACATCTACC AGGAGGAGAT GCTGGAGATG GCCCAGAAGG 3300
GGGTGCTGCA TGCGGTGCAC ACAGCCTATT CCCGCCTGCC TGGCAAGCCC AAGGTCTATG 3360
TTCAGGACAT CCTGCGGCAG CAGCTGGCCA GCGAGGTGCT CCGTGTGCTC CACAAGGAGC 3420
CAGGCCACCT CTATGTTTGC GGGGATGTGC GCATGGCCCG GGACGTGGCC CACACCCTGA 3480
AGCAGCTGGT GGCTGCCAAG CTGAAATTGA ATGAGGAGCA GGTCGAGGAC TATTTCTTTC 3540
AGCTCAAGAG CCAGAAGCGC TATCACGAAG ATATCTTTGG TGCTGTATTT CCTTACGAGG 3600
CGAAGAAGGA CAGGGTGGCG GTGCAGCCCA GCAGCCTGGA GATGTCAGCG CTCTGAGGGC 3660
CTACAGGAGG GGTTAAAGCT GCCGGCACAG AACTTAAGGA TGGAGCCAGC TCTGCATTAT 3720
CTGAGGTCAC AGGGCCTGGG GAGATGGAGG AAAGTGATAT CCCCCAGCCT CAAGTCTTAT 3780
TTCCTCAACG TTGCTCCCCA TCAAGCCCTT TACTTGACCT CCTAACAAGT AGCACCCTGG 3840
ATTGATCGGA GCCTC

Seq ID NO: 313 Protein sequence:
Protein Accession #: NP_000616

1 11 21 31 41 51
| | | | | |
MACPWKFLFK TKFHQYAMNG EKGINNNVEK APCATSSPVT QDDLQYHNLS KQQNESPQPL 60
VETGKKSPES LVKLDATPLS SPRHVRIKNW GSGMTFQDTL HHKAKGILTC RSKSCLGSIM 120
TPKSLTRGPR DKPTPPDELL PQAIEFVNQY YGSLKEAKIE EHLARVEAVT KEIETTVTYQ 180
LTGDELIFAT KQAWRNAPRC IGRIQWSNLQ VFDARSCSTA REMFEHICRH VRYSTNNGNI 240
RSAITVFPQR SDGKHDFRVW NAQLIRYAGY QMPDGSIRGD PANVEFTQLC IDLGWKPKYG 300
RFDVVPLVLQ ANGRDPELFE IPPDLVLEVA MEHPKYEWFR ELELKWYALP AVANMLLEVG 360
GLEFPGCPFN GWYMGTEIGV RDFCDVQRYN ILEEVGRRMG LETHKLASLW KDQAVVEINI 420
AVLHSFQKQN VTIMDHHSAA ESFMKYMQNE YRSRGGCPAD WIWLVPPMSG SITPVFHQEM 480
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Seq ID NO: 314 DNA sequence
Nucleic Acid Accession #: XM_087254
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Seq ID NO: 315 Protein sequence:
Protein Accession #: XP_087254

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Seq ID NO: 316 DNA sequence
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Protein Accession #: NP_004464

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CCTCGGTGAG TGACAGCATG AAGGACAATC CTCATATGCA GTACTATGCC AGCATCTACG 2880
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ACCTCAGGTT GCTGGTTGCT GTGTGGTTTG GTGTGTTCCC GCAAACCCCC TTTGTGCTGT 5640
GGGGCTGGTA GCTCAGGTGG GCGTGGTCAC TGCTGTCATC AGTTGAATGG TCAGCGTTGC 5700

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ATGTCGTGAC CAACTAGACA TTCTGTCGCC TTAGCATGTT TGCTGAACAC CTTGTGGAAG  5760
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Seq ID NO: 319 Protein sequence:
Protein Accession #: NP_005679

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LDASMHSQLR ILDEEHPKGK YHHGLSALKP IRTTSKHQHP VDNAGLFSCM TFSWLSSLAR   120
VAHKKGELSM EDVWSLSKHE SSDVNCRRLE RLWQEELNEV GPDAASLRRV VWIFCRTRLI   180
LSIVCLMITQ LAGFSGPAFM VKHLLEYTQA TESNLQYSLL LVLGLLLTEI VRSWSLALTW   240
ALNYRTGVRL RGAILTMAFK KILKLKNIKE KSLGELINIC SNDGQRMFEA AAVGSLLAGG   300
PVVAILGMIY NVIILGPTGF LGSAVFILFY PAMMFASRLT AYFRRKCVAA TDERVQKMNE   360
VLTYIKFIKM YAWVKAFSQS VQKIREEERR ILEKAGYFQG ITVGVAPIVV VIASVVTFSV   420
HMTLGFDLTA AQAFTVVTVF NSMTFALKVT PFSVKSLSEA SVAVDRFKSL FLMEEVHMIK   480
NKPASPHIKI EMKNATLAWD SSHSSIQNSP KLTPKMKKDK RASRGKKEKV RQLQRTEHQA   540
VLAEQKGHLL LDSDERPSPE EEEGKHIHLG HLRLQRTLHS IDLEIQEGKL VGICGSVGSG   600
KTSLISAILG QMTLLEGSIA ISGTFAYVAQ QAWILNATLR DNILFGKEYD EERYNSVLNS   660
CCLRPDLAIL PSSDLTEIGE RGANLSGGQR QRISLARALY SDRSIYILDD PLSALDAHVG   720
NHIFNSAIRK HLKSKTVLFV THQLQYLVDC DEVIFMKEGC ITERGTHEEL MNLNGDYATI   780
FNNLLLGETP PVEINSKKET SGSQKKSQDK GPKTGSVKKE KAVKPEEGQL VQLEEKGQGS   840
VPWSVYGVYI QAAGGPLAFL VIMALFMLNV GSTAFSTWWL SYWIKQGSGN TTVTRGNETS   900
VSDSMKDNPH MQYYASIYAL SMAVMLILKA IRGVVFVKGT LRASSRLHDE LFRRILRSPM   960
KFFDTTPTGR ILNRFSKDMD EVDVRLPFQA EMFIQNVILV FFCVGMIAGV FPWFLVAVGP  1020
LVILFSVLHI VSRVLIRELK RLDNITQSPF LSHITSSIQG LATIHAYNKG QEFLHRYQEL  1080
LDDNQAPFFL FTCAMRWLAV RLDLISIALI TTTGLMIVLM HGQIPPAYAG LAISYAVQLT  1140
GLFQFTVRLA SETEARFTSV ERINHYIKTL SLEAPARIKN KAPSPDWPQE GEVTFENAEM  1200
RYRENLPLVL KKVSFTIKPK EKIGIVGRTG SGKSSLGMAL FRLVELSGGC IKIDGVRISD  1260
IGLADLRSKL SIIPQEPVLF SGTVRSNLDP FNQYTEDQIW DALERTHMKE CIAQLPLKLE  1320
SEVMENGDNF SVGERQLLCI ARALLRHCKI LILDEATAAM DTETDLLIQE TIREAFADCT  1380
MLTIAHRLHT VLGSDRIMVL AQGQVVEFDT PSVLLSNDSS RFYAMFAAAE NKVAVKG
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Seq ID NO: 320 DNA sequence
Nucleic Acid Accession #: AK022089.1
Coding sequence: 181-1488

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ATGGCTCCCT TTGGAAGAAA CTTGCTAAAG ACTCGGCATA AAAACAGATC TCCAACTAAA   240
GACATGGATT CAGAAGAGAA GGAAATTGTG GTTTGGGTTT GCCAAGAAGA GAAGCTTGTC   300
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GAGGCTACGT TTGGAGAGAA ACGATTTCTT CTGGGGAAGC CCAGTGATTA CTGCATCATA   420
GAGAAGTGGA GAGGCTCCGA AAGGGTTCTT CCTCCACTAA CTAGAATCCT GAAGCTTTGG   480
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CTTCCAGTTC CTTTGTGGCG GACAGCTGAA GCCAAATTAG TGCAAAACAC AGAAAAATTG   600
TGGGAGCTCA GCCCAGCAAA CTACATGAAG ACTTTACCAC CAGATAAACA AAAAAGAATA   660
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GTCAAGAGAA TGAAAGAGCT GGATCTGGAA ATTGAAAAGT GTGAAGCTAA GTTCCATCTT   840
GATCGAGTAG AAAATGATGG AGAAAACTAT GTTCAGGATG CATATTTAAT GCCCAGTTTC   900
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GATAAGCTCT CTGCTGAAAT AGAAAAAGAG GTAAAAAGTG TTTGCATTGA TATAAATGAA  1080
GATGCGGAAG GGGAAGCTGC AAGTGAACTG GAAAGCTCTA ATTTAGAGAG TGTTAAGTGT  1140
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AAAGAGATTA AATACAGTGA CTCATTGCTT CAGATGAAAG CAAAAGAATA TGAACTCCTG  1260
GCCAAGGAAT TCAATTCACT TCACATTAGC AACAAAGATG GGTGCCAGTT AAAGGAAAAC  1320
AGAGCGAAGG AATCTGAGGT TCCCAGTAGC AATGGGGAGA TTCCTCCCTT TACTCAAAGA  1380
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CAGGACTCCG AAACAACAGT AGGAGATGTG GTGCTGTTGT CAACATAGTT CCAATGGCTC  1500
CTTTCTGACC TGCTTTCATG TTTTAATGTT TGTTTAATTT AATAGGAAAC CTCATTTTAA  1560
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GAAATGTGTT GTTTCTG
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Seq ID NO: 321 Protein sequence:
Protein Accession #: NP_005438.1

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EATFGEKRFL LGKPSDYCII EKWRGSERVL PPLTRILKLW KAWGDEQPNM QFVLVKADAF   120
LPVPLWRTAE AKLVQNTEKL WELSPANYMK TLPPDKQKRI VRKTFRKLAK IKQDTVSHDR   180
DNMETLVHLI ISQDHTIHQQ VKRMKELDLE IEKCEAKFHL DRVENDGENY VQDAYLMPSF   240
SEVEQNLDLQ YEENQTLEDL SESDGIEQLE ERLKYYRILI DKLSAEIEKE VKSVCIDINE   300
DAEGEAASEL ESSNLESVKC DLEKSMKAGL KIHSHLSGIQ KEIKYSDSLL QMKAKEYELL   360
AKEFNSLHIS NKDGCQLKEN RAKESEVPSS NGEIPPFTQR VFSNYTNDTD SDTGISSNHS   420
QDSETTVGDV VLLST
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Seq ID NO: 322 DNA sequence
Nucleic Acid Accession #: NM_030920.1

Coding sequence: 317-1123

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CTGGTGGTGG TAGTGGGCGT TTATATTTGC GTTCCTTTTC ATTCATTTCT AAATCTCTTA   240
AAAATTTTGG GTTGGGGGTA TTGGGGAAGG CAGGAAAGGG AAAAGGAGAG TAGTAGCTGA   300
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CCCGGAGGAG GTGACAGAGT TAGTCCTTGA TAATTGCCTG TGTGTCAATG GGGAAATTGA   420
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GAAACGAGAT GCTGAAGACG ATGGAGAGGA AGAAGATGAC TAGATCATTC TAAGACCAGA  1140
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Seq ID NO: 323 Protein sequence:
Protein Accession #: NP_112182.1

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PSLNKLRKLE LSDNIISGGL EVLAEKCPNL TYLNLSGNKI KDLSTVEALQ NLKNLKSLDL   120
FNCEITNLED YRESIFELLQ QITYLDGFDQ EDNEAPDSEE EDDEDGDEDD EEEEENEAGP   180
PEGYEEEEEE EEEEDEDEDE DEDEAGSELG EGEEEVGLSY LMKEEIQDEE DDDDYVEEGE   240
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Seq ID NO: 324 DNA sequence
Nucleic Acid Accession #: NM_003812
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Seq ID NO: 325 Protein sequence:
Protein Accession #: NP_003803

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|          |          |          |          |          |
MKPPGSSSRQ PPLAGCSLAG ASCGPQRGPA GSVPASAPAR TPPCRLLLVL LLLPPLAASS    60
RPRAWGAAAP SAPHWNETAE KNLGVLADED NTLQQNSSSN ISYSNAMQKE ITLPSRLIYY   120
INQDSESPYH VLDTKARHQQ KHNKAVHLAQ ASFQIEAFGS KFILDLILNN GLLSSDYVEI   180
HYENGKPQYS KGGEHCYYHG SIRGVKDSKV ALSTCNGLHG MFEDDTFVYM IEPLELVHDE   240
KSTGRPHIIQ KTLAGQYSKQ MKNLTMERGD QWPFLSELQW LKRRKRAVNP SRGIFEEMKY   300
LELMIVNDHK TYKKHRSSHA HTNNFAKSVV NLVDSIYKEQ LNTRVVLVAV ETWTEKDQID   360
ITTNPVQMLH EFSKYRQRIK QHADAVHLIS RVTFHYKRSS LSYFGGVCSR TRGVGVNEYG   420
LPMAVAQVLS QSLAQNLGIQ WEPSSRKPKC DCTESWGGCI MEETGVSHSR KFSKCSILEY   480
RDFLQRGGGA CLFNRPTKLF EPTECGNGYV EAGEECDCGF HVECYGLCCK KCSLSNGAHC   540
SDGPCCNNTS CLFQPRGYEC RDAVNECDIT EYCTGDSGQC PPNLHKQDGY ACNQNQGRCY   600
NGECKTRDNQ CQYIWGTKAA GSDKFCYEKL NTEGTEKGNC GKDGDRWIQC SKHDVFCGFL   660
LCTNLTRAPR IGQLQGEIIP TSFYHQGRVI DCSGAHVVLD DDTDVGYVED GTPCGPSMMC   720
LDRKCLQIQA LNMSSCPLDS KGKVCSGHGV CSNEATCICD FTWAGTDCSI RDPVRNLHPP   780
KDEGPKGPSA TNLIIGSIAG AILVAAIVLG GTGWGFKNVK KRRFDPTQQG PI
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Seq ID NO: 326 DNA sequence
Nucleic Acid Accession #: AK074418.1
Coding sequence: 244-1515

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CTTTCTCCAA GACGGCCGGC CATGCTCTCC TCCTCTGCCA GTCTCCTCCA CCACTCTCTA    60
ACCTGAGAGC CTGTGGAACC TGCCCGTCTC CCCTCCTCCA TCAGACACAC CTGCCTAGGA   120
AACAGATGGA AAAAGTGAGG GACCGGTGAG TGACTTGCTG CTAAAGTTTA TACCAGATGC   180
AAATGACAGA GCTGGAGTTC TGCTGTGCCT GGAAAGGACC TCGGAAGTCT TCTAAGGAGA   240
GTCATGGCGT ATTACCAGGA GCCTTCAGTG GAGACCTCCA TCATCAAGTT CAAAGACCAG   300
GACTTTACCA CCTTGCGGGA TCACTGCCTG AGCATGGGCC GGACGTTTAA GGATGAGACA   360
TTCCCCGCAG CAGATTCTTC CATAGGCCAG AAGCTGCTCC AGGAAAAACG CCTCTCCAAT   420
GTGATATGGA AGCGGCCACA GGATCTACCA GGGGGTCCTC CTCACTTCAT CCTGGATGAT   480
ATAAGCAGAT TTGACATCCA ACAAGGAGGC GCAGCTGACT GCTGGTTCCT GGCAGCACTG   540
GGATCCTTGA CTCAGAACCC ACAGTACAGG CAGAAGATCC TGATGGTCCA AAGCTTTTCA   600
CACCAGTATG CTGGCATTTT CCGTTTCCGG TTCTGGCAAT GTGGCCAGTG GGTGGAAGTG   660
GTGATTGATG ACCGCCTACC TGTCCAGGGA GATAAATGCC TCTTTGTGCG TCCTCGCCAC   720
CAAAACCAAG AGTTCTGGCC CTGCCTGCTG GAGAAGGCCT ATGCCAAGCT GCTCGGATCC   780
TATTCCGATC TGCACTATGG CTTCCTCGAG GATGCCCTGG TGGACCTCAC AGGAGGCGTG   840
ATCACCAACA TCCATCTGCA CTCTTCCCCT GTGGACCTGG TGAAGGCAGT GAAGACAGCG   900
ACCAAGGCAG GCTCCCTGAT AACCTGTGCC ACTCCAAGTG GGCCAACAGA TACAGCACAG   960
GCGATGGAGA ATGGGCTGGT GAGTCTCCAT GCCTACACTG TGACTGGGGC TGAGCAGATT  1020
CAATACCGAA GGGGCTGGGA AGAAATTATC TCCCTGTGGA ACCCCTGGGG CTGGGGCGAG  1080
ACCGAATGGA GAGGGCGCTG GAGTGATGGG TCTCAGGAGT GGGAGGAAAC CTGTGATCCG  1140
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CGGAAAAGCC AGCTACATAA GAAACGGGAA GATGGCGAGT TTTGGATGTC GTGTCAAGAT  1200
TTCCAACAGA AATTCATCGC CATGTTTATA TGTAGCGAAA TTCCAATTAC CCTGGACCAT  1260
GGAAACACAC TCCACGAAGG ATGGTCCCAA ATAATGTTTA GGAAGCAAGT GATTCTAGGA  1320
AACACTGCAG GAGGACCTCG GAATGATGCT CAATTCAACT TCTCTGTGCA AGAGCCAATG  1380
GAAGGCACCA ATGTTGTCGT GTGCGTCACA GTTGCTGTCA CACCATCAAA TTTGAAAGCA  1440
GAAGATGCAA AATTTCCACT CGATTTCCAA GTGATTCTGG CTGGCTCACA GAAACACTGT  1500
CCAAAGCTCA AATAATAAAT TCCGCCGCAA CTTCACCATG ACTTACCATC TGAGCCCTGG  1560
GAACTATGTT GTGGTTGCAC AGACACGGAG AAAATCAGCG GAGTTCTTGC TCCGAATCTT  1620
CCTGAAAATG CCAGACAGTG ACAGGCACCT GAGCAGCCAT TTCAACCTCA GAATGAAGGG  1680
AAGCCCTTCA GAACATGGCT CCCAACAAAG CATTTTCAAC AGATATGCTC AGCAGGTATG  1740
GTACCTAGCA CCCAGGGGCC TTACGTGGGA TTGGAGAAAG GGGACCTGAG GGAGGGACAG  1800
CCCTCACAGG CCCTTACTGG GATGCAGAGA GGAGAAGTGA CTTGATGGAC TATTTTACCT  1860
GCCTCTCTTC CTGGATCGTC TCCAGAACTG CTGTGGCTGC CAAGCTCGGT AGAGACGTGG  1920
CGCCCCACCC AGTCTCATCC GGGGGACTTC AAGCTGGAAT GCAGAGCTTA GAAAGGGAGG  1980
GGATAATTAT GGGGTGTGAG GTGCATTGCC CTCTAAATCT TTAAACAAGC AATTGGCAGT  2040
ACCCCGTGAA ACCTTTCCTT CTCCTACTCG GCCACCTCCC ACCAACCTGG CATCGTTCCT  2100
CCCGGGAGCT AGCCAGCTTC AGAAAGCACA TACAGCATCC TTGCTGCCAA ACCACCTATG  2160
TGCACACAGG ATTTCCTTAA TGGCTTAATA AACTGTTATA AAGAACTCCT TGACTTGTCA  2220
GAATAAAATA GCTGCCAGGG GCTCTGCACA ATGAGCCTCT TACCGTTAAA AAAAAAAAAA  2280
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
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Seq ID NO: 327 Protein sequence:
Protein Accession #: BAB85075.1

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1          11         21         31         41         51
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MAYYQEPSVE TSIIKFKDQD FTTLRDHCLS MGRTFKDETP PAADSSIGQK LLQEKRLSNV    60
IWKRPQDLPG GPPHFILDDI SRFDIQQGGA ADCWFLAALG SLTQNPQYRQ KILMVQSFSH   120
QYAGIFRFRF WQCGQWVEVV IDDRLPVQGD KCLFVRPRHQ NQEFWPCLLE KAYAKLLGSY   180
SDLHYGFLED ALVDLTGGVI TNIHLHSSPV DLVKAVKTAT KAGSLITCAT PSGPTDTAQA   240
MENGLVSLHA YTVTGAEQIQ YRRGWEEIIS LWNPWGWGET EWRGRWSDGS QEWEETCDPR   300
KSQLHKKRED GEFWMSCQDF QQKFIAMFIC SEIPITLDHG NTLHEGWSQI MFRKQVILGN   360
TAGGPRNDAQ FNFSVQEPME GTNVVVCVTV AVTPSNLKAE DAKFPLDFQV ILAGSQKHCP   420
KLK
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Seq ID NO: 328 DNA sequence
Nucleic Acid Accession #: BC017490.1
Coding sequence: 74-2788

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1          11         21         31         41         51
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GTGGGTCACG TGAACCACTT TTCGCGCGAA ACCTGGTTGT TGCTGTAGTG GCGGAGAGGA    60
TCGTGGTACT GCTATGGCGG AATCATCGGA ATCCTTCACC ATGGCATCCA GCCCGGCCCA   120
GCGTCGGCGA GGCAATGATC CTCTCACCTC CAGCCCTGGC CGAAGCTCCC GGCGTACTGA   180
TGCCCTCACC TCCAGCCCTG GCCGTGACCT TCCACCATTT GAGGATGAGT CCGAGGGGCT   240
CCTAGGCACA GAGGGGCCCC TGGAGGAAGA AGAGGATGGA GAGGAGCTCA TTGGAGATGG   300
CATGGAAAGG GACTACCGCG CCATCCCAGA GCTGGACGCC TATGAGGCCG AGGGACTGGC   360
TCTGGATGAT GAGGACGTAG AGGAGCTGAC GGCCAGTCAG AGGGAGGCAG CAGAGCGGGC   420
CATGCGGCAG CGTGACCGGG AGGCTGGCCG GGGCCTGGGC CGCATGCGCC GTGGGCTCCT   480
GTATGACAGC GATGAGGAGG ACGAGGAGCG CCCTGCCCGC AAGCGCCGCC AGGTGGAGCG   540
GGCCACGGAG GACGGCGAGG AGGACGAGGA GATGATCGAG AGCATCGAGA ACCTGGAGGA   600
TCTCAAAGGC CACTCTGTGC GCGAGTGGGT GAGCATGGCG GGCCCCCGGC TGGAGATCCA   660
CCACCGCTTC AAGAACTTCC TGCGCACTCA CGTCGACAGC CACGGCCACA ACGTCTTCAA   720
GGAGCGCATC AGCGACATGT GCAAAGAGAA CCGTGAGAGC CTGGTGGTGA ACTATGAGGA   780
CTTGGCAGCC AGGGAGCACG TGCTGGCCTA CTTCCTGCCT GAGGCACCGG CGGAGCTGCT   840
GCAGATCTTT GATGAGGCTG CCCTGGAGGT GGTACTGGCC ATGTACCCCA AGTACGACCG   900
CATCACCAAC CACATCCATG TCCGCATCTC CCACCTGCCT CTGGTGGAGG AGCTGCGCTC   960
GCTGAGGCAG CTGCATCTGA ACCAGCTGAT CCGCACCAGT GGGGTGGTGA CCAGCTGCAC  1020
TGGCGTCCTG CCCCAGCTCA GCATGGTCAA GTACAACTGC AACAAGTGCA ATTTCGTCCT  1080
GGGTCCTTTC TGCCAGTCCC AGAACCAGGA GGTGAAACCA GGCTCCTGTC CTGAGTGCCA  1140
GTCGGCCGGC CCCTTTGAGG TCAACATGGA GGAGACCATC TATCAGAACT ACCAGCGTAT  1200
CCGAATCCAG GAGAGTCCAG GCAAAGTGGC GGCTGGCCGG CTGCCCCGCT CCAAGGACGC  1260
CATTCTCCTC GCAGATCTGG TGGACAGCTG CAAGCCAGGA GACGAGATAG AGCTGACTGG  1320
CATCTATCAC AACAACTATG ATGGCTCCCT CAACACTGCC AATGGCTTCC CTGTCTTTGC  1380
CACTGTCATC CTAGCCAACC ACGTGGCCAA GAAGGACAAC AAGGTTGCTG TAGGGGAACT  1440
GACCGATGAA GATGTGAAGA TGATCACTAG CCTCTCCAAG GATCAGCAGA TCGGAGAGAA  1500
GATCTTTGCC AGCATTGCTC CTTCCATCTA TGGTCATGAA GACATCAAGA GAGGCCTGGC  1560
TCTGGCCCTG TTCGGAGGGG AGCCCAAAAA CCCAGGTGGC AAGCACAAGG TACGTGGTGA  1620
TATCAACGTG CTCTTGTGCG GAGACCCTGG CACAGCGAAG TCGCAGTTTC TCAAGTATAT  1680
TGAGAAAGTG TCCAGCCGAG CCATCTTCAC CACTGGCCAG GGGGCGTCGG CTGTGGGCCT  1740
CACGGCGTAT GTCCAGCGGC ACCCTGTCAG CAGGGAGTGG ACCTTGGAGG CTGGGGCCCT  1800
GGTTCTGGCT GACCGAGGAG TGTGTCTCAT TGATGAATTT GACAAGATGA ATGACCAGGA  1860
CAGAACCAGC ATCCATGAGG CCATGGAGCA ACAGAGCATC TCCATCTCGA AGGCTGGCAT  1920
CGTCACCTCC CTGCAGGCTC GCTGCACGGT CATTGCTGCC GCCAACCCCA TAGGAGGGCG  1980
CTACGACCCC TCGCTGACTT TCTCTGAGAA CGTGGACCTC ACAGAGCCCA TCATCTCACG  2040
CTTTGACATC CTGTGTGTGG TGAGGGACAC CGTGGACCCA GTCCAGGACG AGATGCTGGC  2100
CCGCTTCGTG GTGGGCAGCC ACGTCAGACA CCACCCCAGC AACAAGGAGG AGGAGGGGCT  2160
GGCCAATGGC AGCGCTGCTG AGCCCGCCAT GCCCAACACG TATGGCGTGG AGCCCCTGCC  2220
CCAGGAGGTC CTGAAGAAGT ACATCATCTA CGCCAAGGAG AGGGTCCACC CGAAGCTCAA  2280
CCAGATGGAC CAGGACAAGG TGGCCAAGAT GTACAGTGAC CTGAGGAAAG AATCTATGGC  2340
GACAGGCAGC ATCCCCATTA CGGTGCGGCA CATCGAGTCC ATGATCCGCA TGGCGGAGGC  2400
CCACGCGCGC ATCCATCTGC GGGACTATGT GATCGAAGAC GACGTCAACA TGGCCATCCG  2460
CGTGATGCTG GAGAGCTTCA TAGACACACA GAAGTTCAGC GTCATGCGCA GCATGCGCAA  2520
GACTTTTGCC CGCTACCTTT CATTCCGGCG TGACAACAAT GAGCTGTTGC TCTTCATACT  2580
GAAGCAGTTA GTGGCAGAGC AGGTGACATA TCAGCGCAAC CGCTTTGGGG CCCAGCAGGA  2640
CACTATTGAG GTCCCTGAGA AGGACTTGGT GGATAAGGCT CGTCAGATCA ACATCCACAA  2700
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CCTCTCTGCA TTTTATGACA GTGAGCTCTT CAGGATGAAC AAGTTCAGCC ACGACCTGAA  2760
AAGGAAAATG ATCCTGCAGC AGTTCTGAGG CCCTATGCCA TCCATAAGGA TTCCTTGGGA  2820
TTCTGGTTTG GGGTGGTCAG TGCCCTCTGT GCTTTATGGA CACAAAACCA GAGCACTTGA  2880
TGAACTCGGG GTACTAGGGT CAGGGCTTAT AGCAGGATGT CTGGCTGCAC CTGGCATGAC  2940
TGTTTGTTTC TCCAAGCCTG CTTTGTGCTT CTCACCTTTG GGTGGGATGC CTTGCCAGTG  3000
TGTCTTACTT GGTTGCTGAA CATCTTGCCA CCTCCGAGTG CTTTGTCTCC ACTCAGTACC  3060
TTGGATCAGA GCTGCTGAGT TCAGGATGCC TGCGTGTGGT TTAGGTGTTA GCCTTCTTAC  3120
ATGGATGTCA GGAGAGCTGC TGCCCTCTTG GCGTGAGTTG CGTATTCAGG CTGCTTTTGC  3180
TGCCTTTGGC CAGAGAGCTG GTTGAAGATG TTTGTAATCG TTTTCAGTCT CCTGCAGGTT  3240
TCTGTGCCCC TGTGGTGGAA GAGGGCACGA CAGTGCCAGC GCAGCGTTCT GGGCTCCTCA  3300
GTCGCAGGGG TGGGATGTGA GTCATGCGGA TTATCCACTC GCCACAGTTA TCAGCTGCCA  3360
TTGCTCCCTG TCTGTTTCCC CACTCTCTTA TTTGTGCATT CGGTTTGGTT TCTGTAGTTT  3420
TAATTTTTAA TAAAGTTGAA TAAAATATAA AAAAAAAAAA AAAAAA
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Seq ID NO: 329 Protein sequence:
Protein Accession #: AAH17490.1

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1          11         21         31         41         51
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MAESSESFTM ASSPAQRRRG NDPLTSSPGR SSRRTDALTS SPGRDLPPFE DESEGLLGTE    60
GPLEEEEDGE ELIGDGMERD YRAIPELDAY EAEGLALDDE DVEELTASQR EAAERAMRQR   120
DREAGRGLGR MRRGLLYDSD EEDEERPARK RRQVERATED GEEDEEMIES IENLEDLKGH   180
SVREWVSMAG PRLEIHHRFK NFLRTHVDSH GHNVFKERIS DMCKENRESL VVNYEDLAAR   240
EHVLAYFLPE APAELLQIFD EAALEVVLAM YPKYDRITNH IHVRISHLPL VEELRSLRQL   300
HLNQLIRTSG VVTSCTGVLP QLSMVKYNCN KCNFVLGPFC QSQNQEVKPG SCPECQSAGP   360
FEVNMEETIY QNYQRIRIQE SPGKVAAGRL PRSKDAILLA DLVDSCKPGD EIELTGIYHN   420
NYDGSLNTAN GFPVFATVIL ANHVAKKDNK VAVGELTDED VKMITSLSKD QQIGEKIFAS   480
IAPSIYGHED IKRGLALALF GGEPKNPGGK HKVRGDINVL LCGDPGTAKS QFLKYIEKVS   540
SRAIFTTGQG ASAVGLTAYV QRHPVSREWT LEAGALVLAD RGVCLIDEFD KMNDQDRTSI   600
HEAMEQQSIS ISKAGIVTSL QARCTVIAAA NPIGGRYDPS LTFSENVDLT EPIISRFDIL   660
CVVRDTVDPV QDEMLARFVV GSHVRHHPSN KEEEGLANGS AAEPAMPNTY GVEPLPQEVL   720
KKYIIYAKER VHPKLNQMDQ DKVAKMYSDL RKESMATGSI PITVRHIESM IRMAEAHARI   780
HLRDYVIEDD VNMAIRVMLE SFIDTQKFSV MRSMRKTFAR YLSFRRDNNE LLLFILKQLV   840
AEQVTYQRNR FGAQQDTIEV PEKDLVDKAR QINIHNLSAF YDSELFRMNK FSHDLKRKMI   900
LQQF
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Seq ID NO: 330 DNA sequence
Nucleic Acid Accession #: M17254
Coding sequence: 257-1645

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GTCCGCGCGT GTCCGCGCCC GCGTGTGCCA GCGCGCGTGC CTTGGCCGTG CGCGCCGAGC    60
CGGGTCGCAC TAACTCCCTC GGCGCCGACG GCGGCGCTAA CCTCTCGGTT ATTCCAGGAT   120
CTTTGGAGAC CCGAGGAAAG CCGTGTTGAC CAAAAGCAAG ACAAATGACT CACAGAGAAA   180
AAAGATGGCA GAACCAAGGG CAACTAAAGC CGTCAGGTTC TGAACAGCTG GTAGATGGGC   240
TGGCTTACTG AAGGACATGA TTCAGACTGT CCCGGACCCA GCAGCTCATA TCAAGGAAGC   300
CTTATCAGTT GTGAGTGAGG ACCAGTCGTT GTTTGAGTGT GCCTACGGAA CGCCACACCT   360
GGCTAAGACA GAGATGACCG CGTCCTCCTC CAGCGACTAT GGACAGACTT CCAAGATGAG   420
CCCACGCGTC CCTCAGCAGG ATTGGCTGTC TCAACCCCCA GCCAGGGTCA CCATCAAAAT   480
GGAATGTAAC CCTAGCCAGG TGAATGGCTC AAGGAACTCT CCTGATGAAT GCAGTGTGGC   540
CAAAGGCGGG AAGATGGTGG GCAGCCCAGA CACCGTTGGG ATGAACTACG GCAGCTACAT   600
GGAGGAGAAG CACATGCCAC CCCCAAACAT GACCACGAAC GAGCGCAGAG TTATCGTGCC   660
AGCAGATCCT ACGCTATGGA GTACAGACCA TGTGCGGCAG TGGCTGGAGT GGGCGGTGAA   720
AGAATATGGC CTTCCAGACG TCAACATCTT GTTATTCCAG AACATCGATG GGAAGGAACT   780
GTGCAAGATG ACCAAGGACG ACTTCCAGAG GCTCACCCCC AGCTACAACG CCGACATCCT   840
TCTCTCACAT CTCCACTACC TCAGAGAGAC TCCTCTTCCA CATTTGACTT CAGATGATGT   900
TGATAAAGCC TTACAAAACT CTCCACGGTT AATGCATGCT AGAAACACAG ATTTACCATA   960
TGAGCCCCCC AGGAGATCAG CCTGGACCGG TCACGGCCAC CCCACGCCCC AGTCGAAAGC  1020
TGCTCAACCA TCTCCTTCCA CAGTGCCCAA AACTGAAGAC CAGCGTCCTC AGTTAGATCC  1080
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GCTTTGGCAG TTCCTCCTGG AGCTCCTGTC GGACAGCTCC AACTCCAGCT GCATCACCTG  1200
GGAAGGCACC AACGGGGAGT TCAAGATGAC GGATCCCGAC GAGGTGGCCC GGCGCTGGGG  1260
AGAGCGGAAG AGCAAACCCA ACATGAACTA CGATAAGCTC AGCCGCGCCC TCCGTTACTA  1320
CTATGACAAG AACATCATGA CCAAGGTCCA TGGGAAGCGC TACGCCTACA AGTTCGACTT  1380
CCACGGGATC GCCCAGGCCC TCCAGCCCCA CCCCCCGGAG TCATCTCTGT ACAAGTACCC  1440
CTCAGACCTC CCGTACATGG GCTCCTATCA CGCCCACCCA CAGAAGATGA ACTTTGTGGC  1500
GCCCCACCCT CCAGCCCTCC CCGTGACATC TTCCAGTTTT TTTGCTGCCC CAAACCCATA  1560
CTGGAATTCA CCAACTGGGG GTATATACCC CAACACTAGG CTCCCCACCA GCCATATGCC  1620
TTCTCATCTG GGCACTTACT ACTAAAGACC TGGCGGAGGC TTTTCCCATC AGCGTGCATT  1680
CACCAGCCCA TCGCCAGAAA CTCTATCGGA GAACATGAAT CAAAAGTGCC TCAAGAGGAA  1740
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GAGGGAGTTA CTGAAGTCTT ACTACAGAAA TGAGGAGGAT GCTAAAAATG TCACGAATAT  1860
GGACATATCA TCTGTGGACT GACCTTGTAA AAGACAGTGT ATGTAGAAGC ATGAAGTCTT  1920
AAGGACAAAG TGCCAAAGAA AGTGGTCTTA AGAAATGTAT AAACTTTAGA GTAGAGTTTG  1980
AATCCCACTA ATGCAAACTG GGATGAAACT AAAGCAATAG AAACAACACA GTTTTGACCT  2040
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TCAAAAACAA GAGAAAAGAC ACGAGAGAGA CTGTGGCCCA TCAACAGACG TTGATATGCA  2160
ACTGCATGGC ATGTGCTGTT TTGGTTGAAA TCAAATACAT TCCGTTTGAT GGACAGCTGT  2220
CAGCTTTCTC AAACTGTGAA GATGACCCAA AGTTTCCAAC TCCTTTACAG TATTACCGGG  2280
ACTATGAACT AAAAGGTGGG ACTGAGGATG TGTATAGAGT GAGCGTGTGA TTGTAGACAG  2340
AGGGGTGAAG AAGGAGGAGG AAGAGGCAGA GAAGGAGGAG ACCAGGCTGG GAAAGAAACT  2400
TCTCAAGCAA TGAAGACTGG ACTCAGGACA TTTGGGGACT GTGTACAATG AGTTATGGAG  2460
ACTCGAGGGT TCATGCAGTC AGTGTTATAC CAAACCCAGT GTTAGGAGAA AGGACACAGC  2520
GTAATGGAGA AAGGGAAGTA GTAGAATTCA GAAACAAAAA TGCGCATCTC TTTCTTTGTT  2580
TGTCAAATGA AAATTTTAAC TGGAATTGTC TGATATTTAA GAGAAACATT CAGGACCTCA  2640
TCATTATGTG GGGGCTTTGT TCTCCACAGG GTCAGGTAAG AGATGGCCTT CTTGGCTGCC  2700
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ACAATCAGAA ATCACGCAGG CATTTTGGGT AGGCGGCCTC CAGTTTTCCT TTGAGTCGCG 2760
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TAGCATGGCA AATCAGATTT ATACAGGAGT CTGCATTTGC ACTTTTTTTA GTGACTAAAG 3060
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GGAACTTGTG CAAGGGAGAG CCAAGGAAAT AGGATGTTTG GCACCC
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Seq ID NO: 331 Protein sequence
Protein Accession #: AAA52398

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QDWLSQPPAR VTIKMECNPS QVNGSRNSPD ECSVAKGGKM VGSPDTVGMN YGSYMEEKHM  120
PPPNMTTNER RVIVPADPTL WSTDHVRQWL EWAVKEYGLP DVNILLFQNI DGKELCKMTK  180
DDFQRLTPSY NADILLSHLH YLRETPLPHL TSDDVDKALQ NSPRLMHARN TDLPYEPPRR  240
SAWTGHGHPT PQSKAAQPSP STVPKTEDQR PQLDPYQILG PTSSRLANPG SGQIQLWQFL  300
LELLSDSSNS SCITWEGTNG EFKMTDPDEV ARRWGERKSK PNMNYDKLSR ALRYYYDKNI  360
MTKVHGKRYA YKFDFHGIAQ ALQPHPPESS LYKYPSDLPY MGSYHAHPQK MNFVAPHPPA  420
LPVTSSSFFA APNPYWNSPT GGIYPNTRLP TSHMPSHLGT YY                   462
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Seq ID NO: 332 DNA sequence
Nucleic Acid Accession #: NM_000020
Coding sequence: 283-1794

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CCAGCGCTGG CGGTGCAACT GCGGCCGCGC GGTGGAGGGG AGGTGGCCCC GGTCCGCCGA  240
AGGCTAGCGC CCCGCCACCC GCAGAGCGGG CCCAGAGGGA CCATGACCTT GGGCTCCCCC  300
AGGAAAGGCC TTCTGATGCT GCTGATGGCC TTGGTGACCC AGGGAGACCC TGTGAAGCCG  360
TCTCGGGGCC CGCTGGTGAC CTGCACGTGT GAGAGCCCAC ATTGCAAGGG GCCTACCTGC  420
CGGGGGGCCT GGTGCACAGT AGTGCTGGTG CGGGAGGAGG GGAGGCACCC CCAGGAACAT  480
CGGGGCTGCG GGAACTTGCA CAGGGAGCTC TGCAGGGGGC GCCCCACCGA GTTCGTCAAC  540
CACTACTGCT GCGACAGCCA CCTCTGCAAC CACAACGTGT CCCTGGTGCT GGAGGCCACC  600
CAACCTCCTT CGGAGCAGCC GGGAACAGAT GGCCAGCTGG CCCTGATCCT GGGCCCCGTG  660
CTGGCCTTGC TGGCCCTGGT GGCCCTGGGT GTCCTGGGCC TGTGGCATGT CCGACGGAGG  720
CAGGAGAAGC AGCGTGGCCT GCACAGCGAG CTGGGAGAGT CCAGTCTCAT CCTGAAAGCA  780
TCTGAGCAGG GCGACACGAT GTTGGGGGAC CTCCTGGACA GTGACTGCAC CACAGGGAGT  840
GGCTCAGGGC TCCCCTTCCT GGTGCAGAGG ACAGTGGCAC GGCAGGTTGC CTTGGTGGAG  900
TGTGTGGGAA AAGGCCGCTA TGGCGAAGTG TGGCGGGGCT TGTGGCACGG TGAGAGTGTG  960
GCCGTCAAGA TCTTCTCCTC GAGGGATGAA CAGTCCTGGT TCCGGGAGAC TGAGATCTAT 1020
AACACAGTAT TGCTCAGACA CGACAACATC CTAGGCTTCA TCGCCTCAGA CATGACCTCC 1080
CGCAACTCGA GCACGCAGCT GTGGCTCATC ACGCACTACC ACGAGCACGG CTCCCTCTAC 1140
GACTTTCTGC AGAGACAGAC GCTGGAGCCC CATCTGGCTC TGAGGCTAGC TGTGTCCGCG 1200
GCATGCGGCC TGGCGCACCT GCACGTGGAG ATCTTCGGTA CACAGGGCAA ACCAGCCATT 1260
GCCCACCGCG ACTTCAAGAG CCGCAATGTG CTGGTCAAGA GCAACCTGCA GTGTTGCATC 1320
GCCGACCTGG GCCTGGCTGT GATGCACTCA CAGGGCAGCG ATTACCTGGA CATCGGCAAC 1380
AACCCGAGAG TGGGCACCAA GCGGTACATG GCACCCGAGG TGCTGGACGA GCAGATCCGC 1440
ACGGACTGCT TTGAGTCCTA CAAGTGGACT GACATCTGGG CCTTTGGCCT GGTGCTGTGG 1500
GAGATTGCCC GCCGGACCAT CGTGAATGGC ATCGTGGAGG ACTATAGACC ACCCTTCTAT 1560
GATGTGGTGC CCAATGACCC CAGCTTTGAG GACATGAAGA AGGTGGTGTG TGTGGATCAG 1620
CAGACCCCCA CCATCCCTAA CCGGCTGGCT GCAGACCCGG TCCTCTCAGG CCTAGCTCAG 1680
ATGATGCGGG AGTGCTGGTA CCCAAACCCC TCTGCCCGAC TCACCGCGCT GCGGATCAAG 1740
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TGCTCGGCCC CCAGCCCACC CAGCCAAAAA TACAGCTGGG CTGAAACCTG ATCCCCTGCT 1980
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CAGCATGGTG CACCCCCTAC CACTCCCGGG ACAGGATGCA AAAGAGGCTC CAGAGTCAGA 2100
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CAGGGTTTCA CCATGCTGGC CATGCTGGTT CTCGAACTCC TGACCTCAGG TGTTCCACCT 2880
ACCTCAGCCT CCCAAAGTGC TGGGGTTACA GGTGTGAGCC ATCGCGCCTG GCCAGGACCT 2940
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CTAGTTCTCT GACACTTCAG CCTATATCAC AGCTAACTTC YTCAGTCTCA TCTATTCCTT 3060
ATGCTCCAGC CCCTGGCAAT TTGCCTCAAG ATGGGGGTTT GAAAATAACT TTACCTGACT 3120
CAAGGAGTGT CTGGAGCACC TCCTAGTCTA AGTCTGCAAG CTCCAGTTCT TGCCTAAAAC 3180
CATGCCAGTG GCCACCCTTG GGCTCAGACA GCTCTGGGCC TTTTGACCAC AAGCCAGCCC 3240
CTCGCCCTCT CTGTGGCATA GTCTTCTCTG CCCCAGGACT GCAGGGCGGC TTCCTCCAAG 3300
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ATGGGCTCTA GAGAGACACA CAGAAAGTTT GGGCATTTGG GAAATTTTCA AGGRTGTATG 3480
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GACAAGGACA GCCCCAAGGT TGGGAAGACC TGGCCTTAGT CGTCCTCAGC CTAGGGCAGG 3660
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CATTGTGCAA GGCTCGGAAG AGAACCAGGA AGTGAAACTG GGTGAAAACA GAAAGCTCAA 3840
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GAGAAGGGGG CCCAATGGCC AGGGAGTGAA GGAGGTGGCG TTGCTGAGAG CAGTCTGCAC 4140
ATGCTTCTGT CTGAGTGCAG GAAGGTGTTC CAGGGTCGAA ATTACACTTC TCGTACCTGG 4200
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Seq ID NO: 333 Protein sequence
Protein Accession #: NP_000011

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RHPQEHRGCG NLHRELCRGR PTEFVNHYCC DSHLCNHNVS LVLEATQPPS EQPGTDGQLA 120
LILGPVLALL ALVALGVLGL WHVRRRQEKQ RGLHSELGES SLILKASEQG DTMLGDLLDS 180
DCTTGSGSGL PFLVQRTVAR QVALVECVGK GRYGEVWRGL WHGESVAVKI FSSRDEQSWF 240
RETEIYNTVL LRHDNILGFI ASDMTSRNSS TQLWLITHYH EHGSLYDFLQ RQTLEPHLAL 300
RLAVSAACGL AHLHVEIFGT QGKPAIAHRD FKSRNVLVKS NLQCCIADLG LAVMHSQGSD 360
YLDIGNNPRV GTKRYMAPEV LDEQIRTDCF ESYKWTDIWA FGLVLWEIAR RTIVNGIVED 420
YRPPFYDVVP NDPSFEDMKK VVCVDQQTPT IPNRLAADPV LSGLAQMMRE CWYPNPSARL 480
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Seq ID NO: 334 DNA sequence
Nucleic Acid Accession #: NM_004126.1
Coding sequence: 108-329

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ACATCGAAGA TTTGCCAGAG AAGGAAAAAC TGAAAATGGA AGTTGAGCAG CTTCGCAAAG 180
AAGTGAAGTT GCAGAGACAA CAAGTGTCTA AATGTTCTGA AGAAATAAAG AACTATATTG 240
AAGAACGTTC TGGAGAGGAT CCTCTAGTAA AGGGAATTCC AGAAGACAAG AACCCCTTTA 300
AAGAAAAAGG CAGCTGTGTT ATTTCATAAA TAACTTGGGA GAAACTGCAT CCTAAGTGGA 360
AGAACTAGTT TGTTTTAGTT TTCCCAGATA AAACCAACAT GCTTTTTAAG GAAGGAAGAA 420
TGAAATTAAA AGGAGACTTT CTTAAGCACC ATATAGATAG GGTTATGTAT AAAAGCATAT 480
GTGCTACTCA TCTTTGCTCA CTATGCAGTC TTTTTTAAGA GAGCAGAGAG TATCAGATGT 540
ACAATTATGG AAATAAGAAC ATTACTTGAG CATGACACTT CTTTCAGTAT ATTGCTTGAT 600
GCTTCAAATA AAGTTTTGTC TT

Seq ID NO: 335 Protein sequence
Protein Accession #: NP_004117.1

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KNPFKEKGSC VIS

Seq ID NO: 336 DNA sequence
Nucleic Acid Accession #: NM_005795
Coding sequence: 555-1940

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TTCCCACCTT GCTTGTGGGT AAATCTCTTC TGCGGAATCT CAGAAAGTAA AGTTCCATCC 180
TGAGAATATT TCACAAAGAA TTTCCTTAAG AGCTGGACTG GGTCTTGACC CCTGGAATTT 240
AAGAAATTCT TAAAGACAAT GTCAAATATG ATCCAAGAGA AAATGTGATT TGAGTCTGGA 300
GACAATTGTG CATATCGTCT AATAATAAAA ACCCATACTA GCCTATAGAA AACAATATTT 360
GAATAATAAA AACCCATACT AGCCTATAGA AAACAATATT TGAAAGATTG CTACCACTAA 420
AAAGAAAACT ACTACAACTT GACAAGACTG CTGCAAACTT CAATTGGTCA CCACAACTTG 480
ACAAGGTTGC TATAAAACAA GATTGCTACA ACTTCTAGTT TATGTTATAC AGCATATTTC 540
ATTTGGGCTT AATGATGGAG AAAAAGTGTA CCCTGTATTT TCTGGTTCTC TTGCCTTTTT 600
TTATGATTCT TGTTACAGCA GAATTAGAAG AGAGTCCTGA GGACTCAATT CAGTTGGGAG 660
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CCATTCAACA AGCAGAAGGC GTTTACTGCA ACAGAACCTG GGATGGATGG CTCTGCTGGA 780
ACGATGTTGC AGCAGGAACT GAATCAATGC AGCTCTGCCC TGATTACTTT CAGGACTTTG 840
ATCCATCAGA AAAAGTTACA AAGATCTGTG ACCAAGATGG AAACTGGTTT AGACATCCAG 900
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TGCTTATCTC GCTTGGCATA TTCTTTTATT TCAAGAGCCT AAGTTGCCAA AGGATTACCT 1080
TACACAAAAA TCTGTTCTTC TCATTTGTTT GTAACTCTGT TGTAACAATC ATTCACCTCA 1140
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AGTTCATTCA TCTTTACCTG ATGGGCTGTA ATTACTTTTG GATGCTCTGT GAAGGCATTT 1260
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ATTTTCTTGG CTGGGGATTT CCACTGATTC CTGCTTGTAT ACATGCCATT GCTAGAAGCT 1380

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ATCTTGTGGC ATATCCATTG TGGAAACTGG ATGAACAGGA TGTATAATAT GCAATCTTAC  2640
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TGTCTTACCA AACAGTGGGA GGGAATTCCT AGCTGTAAAT ATAAATTTTG CCCTTCCATT  2760
TCTACTGTAT AAACAAATTA GCAATCATTT TATATAAAGA AAATCAATGA AGGATTTCTT  2820
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TTTATTTTAT AGTCTCAAAT CAAATACATA CAACCTATGT AATTTTTAAA GCAAATATAT  2940
AATGCAACAA TGTGTGTATG TTAATATCTG ATACTGTATC TGGGCTGATT TTTTAAATAA  3000
AATAGAGTCT GGAATGCT
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Seq ID NO: 337 protein sequence
Protein Accession #: NP_005786.1

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EGVYCNRTWD GWLCWNDVAA GTESMQLCPD YFQDFDPSEK VTKICDQDGN WFRHPASNRT   120
WTNYTQCNVN THEKVKTALN LFYLTIIGHG LSIASLLISL GIFFYFKSLS CQRITLHKNL   180
FFSFVCNSVV TIIHLTAVAN NQALVATNPV SCKVSQFIHL YLMGCNYFWM LCEGIYLHTL   240
IVVAVFAEKQ HLMWYYFLGW GFPLIPACIH AIARSLYYND NCWISSDTHL LYIIHGPICA   300
ALLVNLFFLL NIVRVLITKL KVTHQAESNL YMKAVRATLI LVPLLGIEFV LIPWRPEGKI   360
AEEVYDYIMH ILMHFQGLLV STIFCFFNGE VQAILRRNWN QYKIQFGNSF SNSEALRSAS   420
YTVSTISDGP GYSHDCPSEH LNGKSIHDIE NVLLKPENLY N
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Seq ID NO: 338 DNA sequence
Nucleic Acid Accession #: NM_001795
Coding sequence: 25-2379

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GCCTGCCTGG GCCTGCTGGC AGTGGCAGCA GTGGCAGCAG CAGGTGCTAA CCCTGCCCAA   120
CGGGACACCC ACAGCCTGCT GCCCACCCAC CGGCGCCAAA AGAGAGATTG GATTTGGAAC   180
CAGATGCACA TTGATGAAGA GAAAAACACC TCACTTCCCC ATCATGTAGG CAAGATCAAG   240
TCAAGCGTGA GTCGCAAGAA TGCCAAGTAC CTGCTCAAAG GAGAATATGT GGGCAAGGTC   300
TTCCGGGTCG ATGCAGAGAC AGGAGACGTG TTCGCCATTG AGAGGCTGGA CCGGGAGAAT   360
ATCTCAGAGT ACCACCTCAC TGCTGTCATT GTGGACAAGG ACACTGGTGA AAACCTGGAG   420
ACTCCTTCCA GCTTCACCAT CAAAGTTCAT GACGTGAACG ACAACTGGCC TGTGTTCACG   480
CATCGGTTGT TCAATGCGTC CGTGCCTGAG TCGTCGGCTG TGGGGACCTC AGTCATCTCT   540
GTGACAGCAG TGGATGCAGA CGACCCCACT GTGGGAGACC ACGCCTCTGT CATGTACCAA   600
ATCCTGAAGG GGAAAGAGTA TTTTGCCATC GATAATTCTG GACGTATTAT CACAATAACG   660
AAAAGCTTGG ACCGAGAGAA GCAGGCCAGG TATGAGATCG TGGTGGAAGC GCGAGATGCC   720
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GACAACTTCC CCTTCTTCAC CCAGACCAAG TACACATTTG TCGTGCCTGA AGACACCCGT   840
GTGGGCACCT CTGTGGGCTC TCTGTTTGTT GAGGACCCAG ATGAGCCCCA GAACCGGATG   900
ACCAAGTACA GCATCTTGCG GGGCGACTAC CAGGACGCTT TCACCATTGA GACAAACCCC   960
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TACAGCTTCA TCGTCGAGGC CACAGACCCC ACCATCGACC TCCGATACAT GAGCCCTCCC  1080
GCGGGAAACA GAGCCCAGGT CATTATCAAC ATCACAGATG TGGACGAGCC CCCCATTTTC  1140
CAGCAGCCTT TCTACCACTT CCAGCTGAAG GAAAACCAGA AGAAGCCTCT GATTGGCACA  1200
GTGCTGGCCA TGGACCCTGA TGCGGCTAGG CATAGCATTG GATACTCCAT CCGCAGGACC  1260
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TACGAGGGCT CCGAGTCCAT AGCCGAGTCC CTCAGCTCCC TGGGCACCGA CTCATCCGAC  2280
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CACCTTGCAG AAGGAAGGCC CTGCCCTGCC CAACCTCTGT GGTCACCCAT GCATCATTCC 3540
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Seq ID NO: 339 Protein sequence
Protein Accession #: NP_001786

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PTVGDHASVM YQILKGKEYF AIDNSGRIIT ITKSLDREKQ ARYEIVVEAR DAQGLRGDSG  240
TATVLVTLQD INDNFPFFTQ TKYTFVVPED TRVGTSVGSL FVEDPDEPQN RMTKYSILRG  300
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INITDVDEPP IFQQPFYHFQ LKENQKKPLI GTVLAMDPDA ARHSIGYSIR RTSDKGQFFR  420
VTKKGDIYNE KELDREVYPW YNLTVEAKEL DSTGTPTGKE SIVQVHIEVL DENDNAPEFA  480
KPYQPKVCEN AVHGQLVLQI SAIDKDITPR NVKFKFTLNT ENNFTLTDNH DNTANITVKY  540
GQFDREHTKV HFLPVVISDN GMPSRTGTST LTVAVCKCNE QGEFTFCEDM AAQVGVSIQA  600
VVAILLCILT ITVITLLIFL RRRLRKQARA HGKSVPEIHE QLVTYDEEGG GEMDTTSYDV  660
SVLNSVRRGG AKPPRPALDA RPSLYAQVQK PPRHAPGAHG GPGEMAAMIE VKKDEADHDG  720
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ELLY
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Seq ID NO: 340 DNA sequence
Nucleic Acid Accession #: NM_003088
Coding sequence: 112-1593

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CTGACGGCCG AGGCGTTCGG GTTCAAGGTG AACGCGTCCG CCAGCAGCCT GAAGAAGAAG  240
CAGATCTGGA CGCTGGAGCA GCCCCCTGAC GAGGCGGGCA GCGCGGCCGT GTGCCTGCGC  300
AGCCACCTGG GCCGCTACCT GGCGGCGGAC AAGGACGGCA ACGTGACCTG CGAGCGCGAG  360
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CAGTCCGAGG CGCACCGGCG CTACTTCGGC GGCACCGAGG ACCGCCTGTC CTGCTTCGCG  480
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GCCGTGGACC GCGACGTGCC CTGGGGCGTC GACTCGCTCA TCACCCTCGC CTTCCAGGAC  660
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GCGCGCCCCG AGCCGGCCAC TGGCTACACG CTGGAGTTCC GCTCCGGCAA GGTGGCCTTC  780
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AACATCAAAG ACTCCACAGG CAAATACTGG ACGGTGGGCA GTGACTCCGC GGTCACCAGC 1440
AGCGGCGACA CTCCTGTGGA CTTCTTCTTC GAGTTCTGCG ACTATAACAA GGTGGCCATC 1500
AAGGTGGGCG GGCGCTACCT GAAGGGCGAC CACGCAGGCG TCCTGAAGGC CTCGGCGGAA 1560
ACCGTGGACC CCGCCTCGCT CTGGGAGTAC TAGGGCCGGC CCGTCCTTCC CCGCCCCTGC 1620
CCACATGGCG GCTCCTGCCA ACCCTCCCTG CTAACCCCTT CTCCGCCAGG TGGGCTCCAG 1680
GGCGGGAGGC AAGCCCCCTT GCCTTTCAAA CTGGAAACCC CAGAGAAAAC GGTGCCCCCA 1740
CCTGTCGCCC CTATGGACTC CCCACTCTCC CCTCCGCCCG GGTTCCCTAC TCCCCTCGGG 1800
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TCAGCGGCTG CGGCCTGGCC CTGGGAGGGA TTTCAGATGC CCCTGCCCTC TTGTCTGCCA  1860
CGGGGCGAGT CTGGCACCTC TTTCTTCTGA CCTCAGACGG CTCTGAGCCT TATTTCTCTG  1920
GAAGCGGCTA AGGGACGGTT GGGGGCTGGG AGCCCTGGGC GTGTAGTGTA ACTGGAATCT  1980
TTTGCCTCTC CCAGCCACCT CCTCCCAGCC CCCCAGGAGA GCTGGGCACA TGTCCCAAGC  2040
CTGTCAGTGG CCCTCCCTGG TGCACTGTCC CCGAAACCCC TGCTTGGGAA GGGAAGCTGT  2100
CGGGAGGGCT AGGACTGACC CTTGTGGTGT TTTTTTGGGT GGTGGCTGGA AACAGCCCCT  2160
CTCCCACGTG GGAGAGGCTC AGCCTGGCTC CCTTCCCTGG AGCGGCAGGG CGTGACGGCC  2220
ACAGGGTCTG CCCGCTGCAC GTTCTGCCAA GGTGGTGGTG GCGGGCGGGT AGGGGTGTGG  2280
GGGCCGTCTT CCTCCTGTCT CTTTCCTTTC ACCCTAGCCT GACTGGAAGC AGAAAATGAC  2340
CAAATCAGTA TTTTTTTTAA TGAAATATTA TTGCTGGAGG CGTCCCAGGC AAGCCTGGCT  2400
GTAGTAGCGA GTGATCTGGC GGGGGGCGTC TCAGCACCCT CCCCAGGGGG TGCATCTCAG  2460
CCCCCTCTTT CCGTCCTTCC CGTCCAGCCC CAGCCCTGGG CCTGGGCTGC CGACACCTGG  2520
GCCAGAGCCC CTGCTGTGAT TGGTGCTCCC TGGGCCTCCC GGGTGGATGA AGCCAGGCGT  2580
CGCCCCCTCC GGGAGCCCTG GGGTGAGCCG CCGGGGCCCC CCTGCTGCCA GCCTCCCCCG  2640
TCCCCAACAT GCATCTCACT CTGGGTGTCT TGGTCTTTTA TTTTTTGTAA GTGTCATTTG  2700
TATAACTCTA AACGCCCATG ATAGTAGCTT CAAACTGGAA ATAGCGAAAT AAAATAACTC  2760
AGTCTGC
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Seq ID NO: 341 Protein sequence
Protein Accession #: NP_003079

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1          11         21         31         41         51
|          |          |          |          |          |
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CLRSHLGRYL AADKDGNVTC EREVPGPDCR FLIVAHDDGR WSLQSEAHRR YFGGTEDRLS  120
CFAQTVSPAE KWSVHIAMHP QVNIYSVTRK RYAHLSARPA DEIAVDRDVP WGVDSLITLA  180
FQDQRYSVQT ADHRFLRHDG RLVARPEPAT GYTLEFRSGK VAFRDCEGRY LAPSGPSGTL  240
KAGKATKVGK DELFALEQSC AQVVLQAANE RNVSTRQGMD LSANQDEETD QETFQLEIDR  300
DTKKCAFRTH TGKYWTLTAT GGVQSTASSK NASCYFDIEW RDRRITLRAS NGKFVTSKKN  360
GQLAASVETA GDSELFLMKL INRPIIVFRG EHGFIGCRKV TGTLDANRSS YDVFQLEFND  420
GAYNIKDSTG KYWTVGSDSA VTSSGDTPVD FFFEFCDYNK VAIKVGGRYL KGDHAGVLKA  480
SAETVDPASL WEY
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Seq ID NO: 342 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence:660..1705

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1          11         21         31         41         51
|          |          |          |          |          |
CGCTCCGCAC ACATTTCCTG TCGCGGCCTA AGGGAAACTG TTGGCCGCTG GGCCCGCGGG   60
GGGATTCTTG GCAGTTGGGG GGTCCGTCGG GAGCGAGGGC GGAGGGGAAG GGAGGGGGAA  120
CCGGGTTGGG GAAGCCAGCT GTAGAGGGCG GTGACCGCGC TCCAGACACA GCTCTGCGTC  180
CTCGAGCGGG ACAGATCCAA GTTGGGAGCA GCTCTGCGTG CGGGGCCTCA GAGAATGAGG  240
CCGGCGTTCG CCCTGTGCCT CCTCTGGCAG GCGCTCTGGC CCGGGCCGGG CGGCGGCGAA  300
CACCCCACTG CCGACCGTGC TGGCTGCTCG GCCTCGGGGG CCTGCTACAG CCTGCACCAC  360
GCTACCATGA AGCGGCAGGC GGCCGAGGAG GCCTGCATCC TGCGAGGTGG GGCGCTCAGC  420
ACCGTGCGTG CGGGCGCCGA GCTGCGCGCT GTGCTCGCGC TCCTGCGGGC AGGCCCAGGG  480
CCCGGAGGGG GCTCCAAAGA CCTGCTGTTC TGGGTCGCAC TGGAGCGCAG GCGTTCCCAC  540
TGCACCCTGG AGAACGAGCC TTTGCGGGGT TTCTCCTGGC TGTCCTCCGA CCCCGGCGGT  600
CTCGAAAGCG ACACGCTGCA GTGGGTGGAG GAGCCCCAAC GCTCCTGCAC CGCGCGGAGA  660
TGCGCGGTAC TCCAGGCCAC CGGTGGGGTC GAGCCCGCAG CTGGAAGGAG ATGCGATGCC  720
ACCTGCGCGC CAACGGCTAC CTGTGCAAGT ACCAGTTTGA GGTCTTGTGT CCTGCGCCGC  780
GCCCCGGGGC CGCCTCTAAC TTGAGCTATC GCGCGCCCTT CCAGCTGCAC AGCGCCGCTC  840
TGGACTTCAG TCCACCTGGG ACCGAGGTGA GTGCGCTCTG CCGGGGACAG CTCCCGATCT  900
CAGTTACTTG CATCGCGGAC GAAATCGGCG CTCGCTGGGA CAAACTCTCG GGCGATGTGT  960
TGTGTCCCTG CCCCGGGAGG TACCTCCGTG CTGGCAAATG CGCAGAGCTC CCTAACTGCC 1020
TAGACGACTT GGGAGGCTTT GCCTGCGAAT GTGCTACGGG CTTCGAGCTG GGGAAGGACG 1080
GCCGCTCTTG TGTGACCAGT GGGGAAGGAC AGCCGACCCT TGGGGGGACC GGGGTGCCCA 1140
CCAGGCGCCC GCCGGCCACT GCAACCAGCC CCGTGCCGCA GAGAACATGG CCAATCAGGG 1200
TCGACGAGAA GCTGGGAGAG ACACCACTTG TCCCTGAACA AGACAATTCA GTAACATCTA 1260
TTCCTGAGAT TCCTCGATGG GGATCACAGA GCACGATGTC TACCCTTCAA ATGTCCCTTC 1320
AAGCCGAGTC AAAGGCCACT ATCACCCCAT CAGGGAGCGT GATTTCCAAG TTTAATTCTA 1380
CGACTTCCTC TGCCACTCCT CAGGCTTTCG ACTCCTCCTC TGCCGTGGTC TTCATATTTG 1440
TGAGCACAGC AGTAGTAGTG TTGGTGATCT TGACCATGAC AGTACTGGGG CTTGTCAAGC 1500
TCTGCTTTCA CGAAAGCCCC TCTTCCCAGC CAAGGAAGGA GTCTATGGGC CCGCCGGGCC 1560
TGGAGAGTGA TCCTGAGCCC GCTGCTTTGG GCTCCAGTTC TGCACATTGC ACAAACAATG 1620
GGGTGAAAGT CGGGGACTGT GATCTGCGGG ACAGAGCAGA GGGTGCCTTG CTGGCGGAGT 1680
CCCCTCTTGG CTCTAGTGAT GCATAG
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Seq ID NO: 343 Protein sequence
Protein Accession #: FGENESH predicted

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1          11         21         31         41         51
|          |          |          |          |          |
MGKDFMTKTP KAFATKAKID KWDLIKLKSF CTAKETIIRV NSQPTDWQKT FAIYPSDKGV   60
IARIYKELEQ IYKKKKPTKT LRTHFLSRPK GNCWPLGPRG DSWQLGGPSG ARAEGKGGGT  120
GLGKPAVEGG DRAPDTALRP RAGQIQVGSS SACGASENEA GVRPVPPLAG ALARAGRRRT  180
PHCRPCWLLG LGGLLQPAPR YHEAAGGRGG LHPARWGAQH RACGRRAARC ARAPAGRPRA  240
RRGLQRPAVL GRTGAQAFPL HPGERAFAGF LLAVLRPRRS RKRHAAVGGG APTLLHRAEM  300
RGTPGHRWGR ARSWKEMRCH LRANGYLCKY QFEVLCPAPR PGAASNLSYR APFQLHSAAL  360
DFSPPGTEVS ALCRGQLPIS VTCIADEIGA RWDKLSGDVL CPCPGRYLRA GKCAELPNCL  420
DDLGGFACEC ATGFELGKDG RSCVTSGEGQ PTLGGTGVPT RRPPATATSP VPQRTWPIRV  480
DEKLGETPLV PEQDNSVTSI PEIPRWGSQS TMSTLQMSLQ AESKATITPS GSVISKFNST  540
TSSATPQAFD SSSAVVFIFV STAVVVLVIL TMTVLGLVKL CFHESPSSQP RKESMGPPGL  600
ESDPEPAALG SSSAHCTNNG VKVGDCDLRD RAEGALLAES PLGSSDA
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Seq ID NO: 344 DNA sequence
Nucleic Acid Accession #: NM_012072
Coding sequence: 149-2107

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AAAGCCCTCA GCCTTTGTGT CCTTCTCTGC GCCGGAGTGG CTGCAGCTCA CCCCTCAGCT   60
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TCCCGCAGAG GGCCACACAG AGACCGGGAT GGCCACCTCC ATGGGCCTGC TGCTGCTGCT  180
GCTGCTGCTC CTGACCCAGC CCGGGGCGGG GACGGGAGCT GACACGGAGG CGGTGGTCTG  240
CGTGGGGACC GCCTGCTACA CGGCCCACTC GGGCAAGCTG AGCGCTGCCG AGGCCCAGAA  300
CCACTGCAAC CAGAACGGGG GCAACCTGGC CACTGTGAAG AGCAAGGAGG AGGCCCAGCA  360
CGTCCAGCGA GTACTGGCCC AGCTCCTGAG GCGGGAGGCA GCCCTGACGG CGAGGATGAG  420
CAAGTTCTGG ATTGGGCTCC AGCGAGAGAA GGGCAAGTGC CTGGACCCTA GTCTGCCGCT  480
GAAGGGCTTC AGCTGGGTGG GCGGGGGGGA GGACACGCCT TACTCTAACT GGCACAAGGA  540
GCTCCGGAAC TCGTGCATCT CCAAGCGCTG TGTGTCTCTG CTGCTGGACC TGTCCCAGCC  600
GCTCCTTCCC AACCGCCTGC CCAAGTGGTC TGAGGGCCCC TGTGGGAGCC CAGGCTCCCC  660
CGGAAGTAAC ATTGAGGGCT TCGTGTGCAA GTTCAGCTTC AAAGGCATGT GCCGGCCTCT  720
GGCCCTGGGG GGCCCAGGTC AGGTGACCTA CACCACCCCC TTCCAGACCA CCAGTTCCTC  780
CTTGGAGGCT GTGCCCTTTG CCTCTGCGGC CAATGTAGCC TGTGGGGAAG GTGACAAGGA  840
CGAGACTCAG AGTCATTATT TCCTGTGCAA GGAGAAGGCC CCCGATGTGT TCGACTGGGG  900
CAGCTCGGGC CCCCTCTGTG TCAGCCCCAA GTATGGCTGC AACTTCAACA ATGGGGGCTG  960
CCACCAGGAC TGCTTTGAAG GGGGGGATGG CTCCTTCCTC TGCGGCTGCC GACCAGGATT 1020
CCGGCTGCTG GATGACCTGG TGACCTGTGC CTCTCGAAAC CCTTGCAGCT CCAGCCCATG 1080
TCGTGGGGGG GCCACGTGCG TCCTGGGACC CCATGGGAAA AACTACACGT GCCGCTGCCC 1140
CCAAGGGTAC CAGCTGGACT CGAGTCAGCT GGACTGTGTG GACGTGGATG AATGCCAGGA 1200
CTCCCCCTGT GCCCAGGAGT GTGTCAACAC CCCTGGGGGC TTCCGCTGCG AATGCTGGGT 1260
TGGCTATGAG CCGGGCGGTC CTGGAGAGGG GGCCTGTCAG GATGTGGATG AGTGTGCTCT 1320
GGGTCGCTCG CCTTGCGCCC AGGGCTGCAC CAACACAGAT GGCTCATTTC ACTGCTCCTG 1380
TGAGGAGGGC TACGTCCTGG CCGGGGAGGA CGGGACTCAG TGCCAGGACG TGGATGAGTG 1440
TGTGGGCCCG GGGGGCCCCC TCTGCGACAG CTTGTGCTTC AACACACAAG GGTCCTTCCA 1500
CTGTGGCTGC CTGCCAGGCT GGGTGCTGGC CCCAAATGGG GTCTCTTGCA CCATGGGGCC 1560
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GAGCACCGTG CCCCGCGCTG CAACAGCCAG TCCCACAAGG GGCCCCGAGG GCACCCCCAA 1680
GGCTACACCC ACCACAAGTA GACCTTCGCT GTCATCTGAC GCCCCCATCA CATCTGCCCC 1740
ACTCAAGATG CTGGCCCCCA GTGGGTCCTC AGGCGTCTGG AGGGAGCCCA GCATCCATCA 1800
CGCCACAGCT GCCTCTGGCC CCCAGGAGCC TGCAGGTGGG GACTCCTCCG TGGCCACACA 1860
AAACAACGAT GGCACTGACG GGCAAAAGCT GCTTTTATTC TACATCCTAG GCACCGTGGT 1920
GGCCATCCTA CTCCTGCTGG CCCTGGCTCT GGGGCTACTG GTCTATCGCA AGCGGAGAGC 1980
GAAGAGGGAG GAGAAGAAGG AGAAGAAGCC CCAGAATGCG GCAGACAGTT ACTCCTGGGT 2040
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CTGCTGAAAG TGAGGTGGCC CTAGAGACAC TAGAGTCACC AGCCACCATC CTCAGAGCTT 2160
TGAACTCCCC ATTCCAAAGG GGCACCCACA TTTTTTTGAA AGACTGGACT GGAATCTTAG 2220
CAAACAATTG TAAGTCTCCT CCTTAAAGGC CCCTTGGAAC ATGCAGGTAT TTTCTACGGG 2280
TGTTTGATGT TCCTGAAGTG GAAGCTGTGT GTTGGCGTGC CACGGTGGGG ATTTCGTGAC 2340
TCTATAATGA TTGTTACTCC CCCTCCCTTT TCAAATTCCA ATGTGACCAA TTCCGGATCA 2400
GGGTGTGAGG AGGCTGGGGC TAAGGGGCTC CCCTGAATAT CTTCTCTGCT CACTTCCACC 2460
ATCTAAGAGG AAAAGGTGAG TTGCTCATGC TGATTAGGAT TGAAATGATT TGTTTCTCTT 2520
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CAGGTGTTTG TGAAGTCACA TAATCTACGG GGCTAGGGCG AGAGAGGCCA GGGATTTGTT 2880
CACAGATACT TGAATTAATT CATCCAAATG TACTGAGGTT ACCACACACT TGACTACGGA 2940
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CCTCAGACAC CCTGCCTGTG GCCCCGCCTC CACTTCATCC TGCCCGGAAT GCCAGTGCTC 3060
CGAGCTCAGA CAGAGGAAGC CCTGCAGAAA GTTCCATCAG GCTGTTTCCT AAAGGATGTG 3120
TGAACGGGAG ATGATGCACT GTGTTTTGAA AGTTGTCATT TTAAAGCATT TTAGCACAGT 3180
TCATAGTCCA CAGTTGATGC AGCATCCTGA GATTTTAAAT CCTGAAGTGT GGGTGGCGCA 3240
CACACCAAGT AGGGAGCTAG TCAGGCAGTT TGCTTAAGGA ACTTTTGTTC TCTGTCTCTT 3300
TTCCTTAAAA TTGGGGGTAA GGAGGGAAGG AAGAGGGAAA GAGATGACTA ACTAAAATCA 3360
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TTGCAAATAT TTCTCCCTAT GATAATGCAG TCGATAGTGT GCACTCTTTC TCTCTCTCTC 3480
TCTCTCTCAC ACACACACAC ACACACACAC ACACACACAC AGAGACACGG CACCATTCTG 3540
CCTGGGGCAC TGGAACACAT TCCTGGGGGT CACCGATGGT CAGAGTCACT AGAAGTTACC 3600
TGAGTATCTC TGGGAGGCCT CATGTCTCCT GTGGGCTTTT TACCACCACT GTGCAGGAGA 3660
ACAGACAGAG GAAATGTGTC TCCCTCCAAG GCCCCAAAGC CTCAGAGAAA GGGTGTTTCT 3720
GGTTTTGCCT TAGCAATGCA TCGGTCTCTG AGGTGACACT CTGGAGTGGT TGAAGGGCCA 3780
CAAGGTGCAG GGTTAATACT CTTGCCAGTT TTGAAATATA GATGCTATGG TTCAGATTGT 3840
TTTTAATAGA AAACTAAAGG GGCAGGGGAA GTGAAAGGAA AGATGGAGGT TTTGTGCGGC 3900
TCGATGGGGC ATTTGGAACT TCTTTTTAAA GTCATCTCAT GGTCTCCAGT TTTCAGTTGG 3960
AACTCTGGTG TTTAACACTT AAGGGAGACA AAGGCTGTGT CCATTTGGCA AAACTTCCTT 4020
GGCCACGAGA CTCTAGGTGA TGTGTGAAGC TGGGCAGTCT GTGGTGTGGA GAGCAGCCAT 4080
CTGTCTGGCC ATTCAGAGGA TTCTAAAGAC ATGGCTGGAT GCGCTGCTGA CCAACATCAG 4140
CACTTAAATA AATGCAAATG CAACATTTCT CCCTCTGGGC CTTGAAAATC CTTGCCCTTA 4200
TCATTTGGGG TGAAGGAGAC ATTTCTGTCC TTGGCTTCCC ACAGCCCCAA CGCAGTCTGT 4260
GTATGATTCC TGGGATCCAA CGAGCCCTCC TATTTTCACA GTGTTCTGAT TGCTCTCACA 4320
GCCCAGGCCC ATCGTCTGTT CTCTGAATGC AGCCCTGTTC TCAACAACAG GGAGGTCATG 4380
GAACCCCTCT GTGGAACCCA CAAGGGGAGA AATGGGTGAT AAAGAATCCA GTTCCTCAAA 4440
ACCTTCCCTG GCAGGCTGGG TCCCTCTCCT GCTGGGTGGT GCTTTCTCTT GCACACCACT 4500
CCCACCACGG GGGGAGAGCC AGCAACCCAA CCAGACAGCT CAGGTTGTGC ATCTGATGGA 4560
AACCACTGGG CTCAAACACG TGCTTTATTC TCCTGTTTAT TTTTGCTGTT ACTTTGAAGC 4620
ATGGAAATTC TTGTTTGGGG GATCTTGGGG CTACAGTAGT GGGTAAACAA ATGCCCACCG 4680
GCCAAGAGGC CATTAACAAA TCGTCCTTGT CCTGAGGGGC CCCAGCTTGC TCGGGCGTGG 4740
CACAGTGGGG AATCCAAGGG TCACAGTATG GGGAGAGGTG CACCCTGCCA CCTGCTAACT 4800
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TCTCGCTAGA CACAGTGTTT CTGCCCAGGT GACCTGTTCA GCAGCAGAAC AAGCCAGGGC  4860
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CCAAATAGGT CAATAATTCT GGGAGACTCT TGGAAAAAAC TGAATATATT CAGGACCAAC  4980
TCTCTCCCTC CCCTCATCCC ACATCTCAAA GCAGACAATG TAAAGAGAGA ACATCTCACA  5040
CACCCAGCTC GCCATGCCTA CTCATTCCTG AATTTCAGGT GCCATCACTG CTCTTTCTTT  5100
CTTCTTTGTC ATTTGAGAAA GGATGCAGGA GGACAATTCC CACAGATAAT CTGAGGAATG  5160
CAGAAAAACC AGGGCAGGAC AGTTATCGAC AATGCATTAG AACTTGGTGA GCATCCTCTG  5220
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CTCTGCCTTC GGTGGCCCAC ACACCTAAGC GTCATCGTCA TTGCCATAGC ATCATGATGC  5340
AACACATCTA CGTGTAGCAC TACGACGTTA TGTTTGGGTA ATGTGGGGAT GAACTGCATG  5400
AGGCTCTGAT TAAGGATGTG GGGAAGTGGG CTGCGGTCAC TGTCGGCCTT GCAAGGCCAC  5460
CTGGAGGCCT GTCTGTTAGC CAGTGGTGGA GGAGCAAGGC TTCAGGAAGG GCCAGCCACA  5520
TGCCATCTTC CCTGCGATCA GGCAAAAAAG TGGAATTAAA AAGTCAAACC TTTATATGCA  5580
TGTGTTATGT CCATTTTGCA GGATGAACTG AGTTTAAAAG AATTTTTTTT TCTCTTCAAG  5640
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TCTTTCGATG GATGGAGATG ATCATTAGGT ACTTTTGTTT CAACCTTTAT TCCTGTAAAT  5760
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TTAATGCCCC CTACATATTT CCATCACCTT GAACAATAGC TTTAGCTTGG GAATCTGAGA  6000
TATGATCCCA GAAAACATCT GTCTCTACTT CGGCTGCAAA ACCCATGGTT TAAATCTATA  6060
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TTTAAAAATA AATTGTGTTT TGGTCTGTTC TTGTAGATAA TGCCCTTCTA TTTTAGGTAG  6240
AAGCTCTGGA ATCCCTTTAT TGTGCTGTTG CTCTTATCTG CAAGGTGGCA AGCAGTTCTT  6300
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GCTTGAATTA GATCCCTGCA AAGGCTTGCT CTGTGATGTC AGATGTAATT GTAAATGTCA  6420
GTAATCACTT CATGAATGCT AAATGAGAAT GTAAGTATTT TTAAATGTGT GTATTTCAAA  6480
TTTGTTTGAC TAATTCTGGA ATTACAAGAT TTCTATGCAG GATTTACCTT CATCCTGTGC  6540
ATGTTTCCCA AACTGTGAGG AGGGAAGGCT CAGAGATCGA GCTTCTCCTC TGAGTTCTAA  6600
CAAAATGGTG CTTTGAGGGT CAGCCTTTAG GAAGGTGCAG CTTTGTTGTC CTTTGAGCTT  6660
TCTGTTATGT GCCTATCCTA ATAAACTCTT AAACACATT
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Seq ID NO: 345 Protein sequence
Protein Accession #: NP_036204

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ATVKSKEEAQ HVQRVLAQLL RREAALTARM SKFWIGLQRE KGKCLDPSLP LKGFSWVGGG   120
EDTPYSNWHK ELRNSCISKR CVSLLLDLSQ PLLPNRLPKW SEGPCGSPGS PGSNIEGFVC   180
KFSFKGMCRP LALGGPGQVT YTTPFQTTSS SLEAVPFASA ANVACGEGDK DETQSHYFLC   240
KEKAPDVFDW GSSGPLCVSP KYGCNFNNGG CHQDCFEGGD GSFLCGCRPG FRLLDDLVTC   300
ASRNPCSSSP CRGGATCVLG PHGKNYTCRC PQGYQLDSSQ LDCVDVDECQ DSPCAQECVN   360
TPGGFRCECW VGYEPGGPGE GACQDVDECA LGRSPCAQGC TNTDGSFHCS CEEGYVLAGE   420
DGTQCQDVDE CVGPGGPLCD SLCFNTQGSF HCGCLPGWVL APNGVSCTMG PVSLGPPSGP   480
PDEEDKGEKE GSTVPRAATA SPTRGPEGTP KATPTTSRPS LSSDAPITSA PLKMLAPSGS   540
SGVWREPSIH HATAASGPQE PAGGDSSVAT QNNDGTDGQK LLLFYILGTV VAILLLLALA   600
LGLLVYRKRR AKREEKKEKK PQNAADSYSW VPERAESRAM ENQYSPTPGT DC
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Seq ID NO: 346 DNA sequence
Nucleic Acid Accession #: Z31560
Coding sequence: <1-966

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AGCCCGGACC GCGTCAAGCG GCCCATGAAT GCCTTCATGG TGTGGTCCCG CGGGCAGCGG   180
CGCAAGATGG CCCAGGAGAA CCCCAAGATG CACAACTCGG AGATCAGCAA GCGCCTGGGC   240
GCCGAGTGGA AACTTTTGTC GGAGACGGAG AAGCGGCCGT TCATCGACGA GGCTAAGCGG   300
CTGCGAGCGC TGCACATGAA GGAGCACCCG GATTATAAAT ACCGGCCCCG GCGGAAAACC   360
AAGACGCTCA TGAAGAAGGA TAAGTACACG CTGCCCGGCG GGCTGCTGGC CCCCGGCGGC   420
AATAGCATGG CGAGCGGGGT CGGGGTGGGC GCCGGCCTGG GCGCGGGCGT GAACCAGCGC   480
ATGGACAGTT ACGCGCACAT GAACGGCTGG AGCAACGGCA GCTACAGCAT GATGCAGGAC   540
CAGCTGGGCT ACCCGCAGCA CCCGGGCCTC AATGCGCACG GCGCAGCGCA GATGCAGCCC   600
ATGCACCGCT ACGACGTGAG CGCCCTGCAG TACAACTCCA TGACCAGCTC GCAGACCTAC   660
ATGAACGGCT CGCCCACCTA CAGCATGTCC TACTCGCAGC AGGGCACCCC TGGCATGGCT   720
CTTGGCTCCA TGGGTTCGGT GGTCAAGTCC GAGGCCAGCT CCAGCCCCCC TGTGGTTACC   780
TCTTCCTCCC ACTCCAGGGC GCCCTGCCAG GCCGGGGACC TCCGGGACAT GATCAGCATG   840
TATCTCCCCG GCGCCGAGGT GCCGGAACCC GCCGCCCCCA GCAGACTTCA CATGTCCCAG   900
CACTACCAGA GCGGCCCGGT GCCCGGCACG GCCATTAACG GCACACTGCC CCTCTCACAC   960
ATGTGAGGGC CGGACAGCGA ACTGGAGGGG GGAGAAATTT TCAAAGAAAA ACGAGGGAAA  1020
TGGGAGGGGT GCAAAAGAGG AGAGTAAGAA ACAGCATGGA GAAAACCCGG TACGCTCAAA  1080
AAAAA
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Seq ID NO: 347 Protein sequence
Protein Accession #: CAA83435

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1          11         21         31         41         51
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HSARMYNMME TELKPPGPQQ TSGGGGGNST AAAAGGNQKN SPDRVKRPMN AFMVWSRGQR    60
RKMAQENPKM HNSEISKRLG AEWKLLSETE KRPFIDEAKR LRALHMKEHP DYKYRPRRKT   120
KTLMKKDKYT LPGGLLAPGG NSMASGVGVG AGLGAGVNQR MDSYAHMNGW SNGSYSMMQD   180
QLGYPQHPGL NAHGAAQMQP MHRYDVSALQ YNSMTSSQTY MNGSPTYSMS YSQQGTPGMA   240
LGSMGSVVKS EASSSPPVVT SSSHSRAPCQ AGDLRDMISM YLPGAEVPEP AAPSRLHMSQ   300
HYQSGPVPGT AINGTLPLSH M
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Seq ID NO: 348 DNA sequence
Nucleotide Accession #: NM_002638
Coding sequence: 120-473

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GCTGGACTGC ATAAAGATTG GTATGGCCTT AGCTCTTAGC CAAACACCTT CCTGACACCA   120
TGAGGGCCAG CAGCTTCTTG ATCGTGGTGG TGTTCCTCAT CGCTGGGACG CTGGTTCTAG   180
AGGCAGCTGT CACGGGAGTT CCTGTTAAAG GTCAAGACAC TGTCAAAGGC CGTGTTCCAT   240
TCAATGGACA AGATCCCGTT AAAGGACAAG TTTCAGTTAA AGGTCAAGAT AAAGTCAAAG   300
CGCAAGAGCC AGTCAAAGGT CCAGTCTCCA CTAAGCCTGG CTCCTGCCCC ATTATCTTGA   360
TCCGGTGCGC CATGTTGAAT CCCCCTAACC GCTGCTTGAA AGATACTGAC TGCCCAGGAA   420
TCAAGAAGTG CTGTGAAGGC TCTTGCGGGA TGGCCTGTTT CGTTCCCCAG TGAAGGGAGC   480
CGGTCCTTGC TGCACCTGTG CCGTCCCCAG AGCTACAGGC CCCATCTGGT CCTAAGTCCC   540
TGCTGCCCTT CCCCTTCCCA CACTGTCCAT TCTTCCTCCC ATTCAGGATG CCCACGGCTG   600
GAGCTGCCTC TCTCATCCAC TTTCCAATAA A
```

Seq ID NO: 349 Protein sequence:
Protein Accession #: NP_002629

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1          11         21         31         41         51
|          |          |          |          |          |
MRASSFLIVV VFLIAGTLVL EAAVTGVPVK GQDTVKGRVP FNGQDPVKGQ VSVKGQDKVK    60
AQEPVKGPVS TKPGSCPIIL IRCAMLNPPN RCLKDTDCPG IKKCCEGSCG MACFVPQ
```

Seq ID NO: 350 DNA sequence
Nucleic Acid Accession #: NM_007183
Coding sequence: 75-2468

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1          11         21         31         41         51
|          |          |          |          |          |
GAATTCCGGA CAGGACGTGA AGATAGTTGG GTTTGGAGGC GGCCGCCAGG CCCAGGCCCG    60
GTGGACCTGC CGCCATGCAG GACGGTAACT TCCTGCTGTC GGCCCTGCAG CCTGAGGCCG   120
GCGTGTGCTC CCTGGCGCTG CCCTCTGACC TGCAGCTGGA CCGCCGGGGC GCCGAGGGGC   180
CGGAGGCCGA GCGGCTGCGG GCAGCCCGCG TCCAGGAGCA GGTCCGCGCC CGCCTCTTGC   240
AGCTGGGACA GCAGCCGCGG CACAACGGGG CCGCTGAGCC CGAGCCTGAG GCCGAGACTG   300
CCAGAGGCAC ATCCAGGGGG CAGTACCACA CCCTGCAGGC TGGCTTCAGC TCTCGCTCTC   360
AGGGCCTGAG TGGGGACAAG ACCTCGGGCT TCCGGCCCAT CGCCAAGCCG GCCTACAGCC   420
CAGCCTCCTG GTCCTCCCGC TCCGCCGTGG ATCTGAGCTG CAGTCGGAGG CTGAGTTCAG   480
CCCACAATGG GGGCAGCGCC TTTGGGGCCG CTGGGTACGG GGGTGCCCAG CCCACCCCTC   540
CCATGCCCAC CAGGCCCGTG TCCTTCCATG AGCGCGGTGG GGTTGGGAGC CGGGCCGACT   600
ATGACACACT CTCCCTGCGC TCGCTGCGGC TGGGGCCCGG GGGCCTGGAC GACCGCTACA   660
GCCTGGTGTC TGAGCAGCTG GAGCCCGCGG CCACCTCCAC CTACAGGGCC TTTGCGTACG   720
AGCGCCAGGC CAGCTCCAGC TCCAGCCGGG CAGGGGGGCT GGACTGGCCC GAGGCCACTG   780
AGGTTTCCCC GAGCCGGACC ATCCGTGCCC CTGCCGTGCG GACCCTGCAG CGATTCCAGA   840
GCAGCCACCG GAGCCGCGGG GTAGGCGGGG CAGTGCCGGG GGCCGTCCTG GAGCCAGTGG   900
CTCGAGCGCC ATCTGTGCGC AGCCTCAGCC TCAGCCTGGC TGACTCGGGC CACCTGCCGG   960
ACGTGCATGG GTTCAACAGC TACGGTAGCC ACCGAACCCT GCAGAGACTC AGCAGCGGTT  1020
TTGATGACAT TGACCTGCCC TCAGCAGTCA AGTACCTCAT GGCTTCAGAC CCCAACCTGC  1080
AGGTGCTGGG AGCGGCCTAC ATCCAGCACA AGTGCTACAG CGATGCAGCC GCCAAGAAGC  1140
AGGCCCGCAG CCTTCAGGCC GTGCCTAGGC TGGTGAAGCT CTTCAACCAC GCCAACCAGG  1200
AAGTGCAGCG CCATGCCACA GGTGCCATGC GCAACCTCAT CTACGACAAC GCTGACAACA  1260
AGCTGGCCCT GGTGGAGGAG AACGGGATCT TCGAGCTGCT GCGGACACTG CGGGAGCAGG  1320
ATGATGAGCT TCGCAAAAAT GTCACAGGGA TCCTGTGGAA CCTTTCATCC AGCGACCACC  1380
TGAAGGACCG CCTGGCCAGA GACACGCTGG AGCAGCTCAC GGACCTGGTG TTGAGCCCCC  1440
TGTCGGGGGC TGGGGGTCCC CCCCTCATCC AGCAGAACGC CTCGGAGGCG GAGATCTTCT  1500
ACAACGCCAC CGGCTTCCTC AGGAACCTCA GCTCAGCCTC TCAGGCCACT CGCCAGAAGA  1560
TGCGGGAGTG CCACGGGCTG GTGGACGCCC TGGTCACCTC TATCAACCAC GCCCTGGACG  1620
CGGGCAAATG CGAGGACAAG AGCGTGGAGA ACGCGGTGTG CGTCCTGCGG AACCTGTCCT  1680
ACCGCCTCTA CGACGAGATG CCGCCGTCCG CGCTGCAGCG GCTGGAGGGT CGCGGCCGCA  1740
GGGACCTGGC GGGGGCGCCG CCGGGAGAGG TCGTGGGCTG CTTCACGCCG CAGAGCCGGC  1800
GGCTGCGCGA GCTGCCCCTC GCCGCCGATG CGCTCACCTT CGCGGAGGTG TCCAAGGACC  1860
CCAAGGGCCT CGAGTGGCTG TGGAGCCCCC AGATCGTGGG GCTGTACAAC CGGCTGCTGC  1920
AGCGCTGCGA GCTCAACCGG CACACGACGG AGGCGGCCGC CGGGGCGCTG CAGAACATCA  1980
CGGCAGGCGA CCGCAGGTGG GCGGGGGTGC TGAGCCGCCT GGCCCTGGAG CAGGAGCGTA  2040
TTCTGAACCC CCTGCTAGAC CGTGTCAGGA CCGCCGACCA CCACCAGCTG CGCTCACTGA  2100
CTGGCCTCAT CCGAAACCTG TCTCGGAACG CTAGGAACAA GGACGAGATG TCCACGAAGG  2160
TGGTGAGCCA CCTGATCGAG AAGCTGCCAG GCAGCGTGGG TGAGAAGTCG CCCCCAGCCG  2220
AGGTGCTGGT CAACATCATA GCTGTGCTCA ACAACCTGGT GGTGGCCAGC CCCATCGCTG  2280
CCCGAGACCT GCTGTATTTT GACGGACTCC GAAAGCTCAT CTTCATCAAG AAGAAGCGGG  2340
ACAGCCCCGA CAGTGAGAAG TCCTCCCGGG CAGCATCCAG CCTCCTGGCC AACCTGTGGC  2400
AGTACAACAA GCTCCACCGT GACTTTCGGG CGAAGGGCTA TCGGAAGGAG GACTTCCTGG  2460
GCCCATAGGT GAAGCCTTCT GGAGGAGAAG GTGACGTGGC CCAGCGTCCA AGGGACAGAC  2520
TCAGCTCCAG GCTGCTTGGC AGCCCAGCCT GGAGGAGAAG GCTAATGACG GAGGGGCCCC  2580
TCGCTGGGGC CCCTGTGTGC ATCTTTGAGG GTCCTGGGCC ACCAGGAGGG GCAGGGTCTT  2640
ATAGCTGGGG ACTTGGCTTC CGCAGGGCAG GGGGTGGGGC AGGGCTCAAG GCTGCTCTGG  2700
TGTATGGGGT GGTGACCCAG TCACATTGGC AGAGGTGGGG GTTGGCTGTG GCCTGGCAGT  2760
ATCTTGGGAT AGCCAGCACT GGGAATAAAG ATGGCCATGA ACAGTCACAA AAAAAAAAAA  2820
AAAAGGAATT C
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Seq ID NO: 351 Protein sequence
Protein Accession #: NP_009114.1

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1          11         21         31         41         51
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|          |          |          |          |          |
MQDGNFLLSA LQPEAGVCSL ALPSDLQLDR RGAEGPEAER LRAARVQEQV RARLLQLGQQ    60
PRHNGAAEPE PEAETARGTS RGQYHTLQAG FSSRSQGLSG DKTSGFRPIA KPAYSPASWS   120
SRSAVDLSCS RRLSSAHNGG SAFGAAGYGG AQPTPPMPTR PVSFHERGGV GSRADYDTLS   180
LRSLRLGPGG LDDRYSLVSE QLEPAATSTY RAFAYERQAS SSSSRAGGLD WPEATEVSPS   240
RTIRAPAVRT LQRFQSSHRS RGVGGAVPGA VLEPVARAPS VRSLSLSLAD SGHLPDVHGF   300
NSYGSHRTLQ RLSSGFDDID LPSAVKYLMA SDPNLQVLGA AYIQHKCYSD AAAKKQARSL   360
QAVPRLVKLF NHANQEVQRH ATGAMRNLIY DNADNKLALV EENGIFELLR TLREQDDELR   420
KNVTGILWNL SSSDHLKDRL ARDTLEQLTD LVLSPLSGAG GPPLIQQNAS EAEIFYNATG   480
FLRNLSSASQ ATRQKMRECH GLVDALVTSI NHALDAGKCE DKSVENAVCV LRNLSYRLYD   540
EMPPSALQRL EGRGRRDLAG APPGEVVGCF TPQSRRLREL PLAADALTFA EVSKDPKGLE   600
WLWSPQIVGL YNRLLQRCEL NRHTTEAAAG ALQNITAGDR RWAGVLSRLA LEQERILNPL   660
LDRVRTADHH QLRSLTGLIR NLSRNARNKD EMSTKVVSHL IEKLPGSVGE KSPPAEVLVN   720
IIAVLNNLVV ASPIAARDLL YFDGLRKLIF IKKKRDSPDS EKSSRAASSL LANLWQYNKL   780
HRDFRAKGYR KEDFLGP
```

Seq ID NO: 352 DNA sequence
Nucleic Acid Accession #: M31469
Coding sequence: 1-651

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGGCTGCGC AGGGAGAGCC CCAGGTCCAG TTCAAACTTG TATTGGTTGG TGATGGTGGT    60
ACTGGAAAAA CGACCTTCGT GAAACGTCAT TTGACTGGTG AATTTGAGAA GAAGTATGTA   120
GCCACCTTGG GTGTTGAGGT TCATCCCCTA GTGTTCCACA CCAACAGAGG ACCTATTAAG   180
TTCAATGTAT GGGACACAGC CGGCCAGGAG AAATTCGGTG GACTGAGAGA TGGCTATTAT   240
ATCCAAGCCC AGTGTGCCAT CATAATGTTT GATGTAACAT CGAGAGTTAC TTACAAGAAT   300
GTGCCTAACT GGCATAGAGA TCTGGTACGA GTGTGTGAAA ACATCCCCAT TGTGTTGTGT   360
GGCAACAAAG TGGATATTAA GGACAGGAAA GTGAAGGCGA AATCCATTGT CTTCCACCGA   420
AAGAAGAATC TTCAGTACTA CGACATTTCT GCCAAAAGTA ACTACAACTT TGAAAAGCCC   480
TTCCTCTGGC TTGCTAGGAA GCTCATTGGA GACCCTAACT TGGAATTTGT TGCCATGCCT   540
GCTCTCGCCC CACCAGAAGT TGTCATGGAC CCAGCTTTGG CAGCACAGTA TGAGCACGAC   600
TTAGAGGTTG CTCAGACAAC TGCTCTCCCG GATGAGGATG ATGACCTGTG A
```

Seq ID NO: 353 Protein sequence
Protein Accession #: AAA36546

```
1          11         21         31         41         51
|          |          |          |          |          |
MAAQGEPQVQ FKLVLVGDGG TGKTTFVKRH LTGEFEKKYV ATLGVEVHPL VFHTNRGPIK    60
FNVWDTAGQE KFGGLRDGYY IQAQCAIIMF DVTSRVTYKN VPNWHRDLVR VCENIPIVLC   120
GNKVDIKDRK VKAKSIVFHR KKNLQYYDIS AKSNYNFEKP FLWLARKLIG DPNLEFVAMP   180
ALAPPEVVMD PALAAQYEHD LEVAQTTALP DEDDDL
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Seq ID NO: 354 DNA sequence
Nucleic Acid Accession #: NM_002820
Coding sequence: 304-831

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1          11         21         31         41         51
|          |          |          |          |          |
CCGGTTCGCA AAGAAGCTGA CTTCAGAGGG GGAAACTTTC TTCTTTTAGG AGGCGGTTAG    60
CCCTGTTCCA CGAACCCAGG AGAACTGCTG GCCAGATTAA TTAGACATTG CTATGGGAGA   120
CGTGTAAACA CACTACTTAT CATTGATGCA TATATAAAAC CATTTTATTT TCGCTATTAT   180
TTCAGAGGAA GCGCCTCTGA TTTGTTTCTT TTTTCCCTTT TTGCTCTTTC TGGCTGTGTG   240
GTTTGGAGAA AGCACAGTTG GAGTAGCCGG TTGCTAAATA AGTCCCGAGC GCGAGCGGAG   300
ACGATGCAGC GGAGACTGGT TCAGCAGTGG AGCGTCGCGG TGTTCCTGCT GAGCTACGCG   360
GTGCCCTCCT GCGGGCGCTC GGTGGAGGGT CTCAGCCGCC GCCTCAAAAG AGCTGTGTCT   420
GAACATCAGC TCCTCCATGA CAAGGGGAAG TCCATCCAAG ATTTACGGCG ACGATTCTTC   480
CTTCACCATC TGATCGCAGA AATCCACACA GCTGAAATCA GAGCTACCTC GGAGGTGTCC   540
CCTAACTCCA AGCCCTCTCC CAACACAAAG AACCACCCCG TCCGATTTGG GTCTGATGAT   600
GAGGGCAGAT ACCTAACTCA GGAAACTAAC AAGGTGGAGA CGTACAAAGA GCAGCCGCTC   660
AAGACACCTG GGAAGAAAAA GAAAGGCAAG CCCGGGAAAC GCAAGGAGCA GGAAAAGAAA   720
AAACGGCGAA CTCGCTCTGC CTGGTTAGAC TCTGGAGTGA CTGGGAGTGG GCTAGAAGGG   780
GACCACCTGT CTGACACCTC CACAACGTCG CTGGAGCTCG ATTCACGGTA ACAGGCTTCT   840
CTGGCCCGTA GCCTCAGCGG GGTGCTCTCA GCTGGGTTTT GGAGCCTCCC TTCTGCCTTG   900
GCTTGGACAA ACCTAGAATT TTCTCCCTTT ATGTATCTCT ATCGATTGTG TAGCAATTGA   960
CAGAGAATAA CTCAGAATAT TGTCTGCCTT AAAGCAGTAC CCCCCTACCA CACACACCCC  1020
TGTCCTCCAG CACCATAGAG AGGCGCTAGA GCCCATTCCT CTTTCTCCAC CGTCACCCAA  1080
CATCAATCCT TTACCACTCT ACCAAATAAT TTCATATTCA AGCTTCAGAA GCTAGTGACC  1140
ATCTTCATAA TTTGCTGGAG AAGTGTATTT CTTCCCCTTA CTCTCACACC TGGGCAAACT  1200
TTCTTCAGTG TTTTTCATTT CTTACGTTCT TTCACTTCAA GGGAGAATAT AGAAGCATTT  1260
GATATTATCT ACAAACACTG CAGAACAGCA TCATGTCATA AACGATTCTG AGCCATTCAC  1320
ACTTTTTATT TAATTAAATG TATTTAATTA AATCTCAAAT TTATTTTAAT GTAAAGAACT  1380
TAAATTATGT TTTAAACACA TGCCTTAAAT TTGTTTAATT AAATTTAACT CTGGTTTCTA  1440
CCAGCTCATA CAAAATAAAT GGTTTCTGAA AATGTTAAAG TATTAACTTA CAAGGATATA  1500
GGTTTTTCTC ATGTATCTTT TTGTTCATTG GCAAGATGAA ATAATTTTTC TAGGGTAATG  1560
CCGTAGGAAA AATAAAACTT CACATTTAAA AAAAA
```

Seq ID NO: 355 Protein sequence
Protein Accession #: NM_002820

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1          11         21         31         41         51
|          |          |          |          |          |
MQRRLVQQWS VAVFLLSYAV PSCGRSVEGL SRRLKRAVSE HQLLHDKGKS IQDLRRRFFL    60
HHLIAEIHTA EIRATSEVSP NSKPSPNTKN HPVRFGSDDE GRYLTQETNK VETYKEQPLK   120
```

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TPGKKKKGKP GKRKEQEKKK RRTRSAWLDS GVTGSGLEGD HLSDTSTTSL ELDSR
```

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Seq ID NO: 356 DNA sequence
Nucleic Acid Accession #: NM_017522
Coding sequence:          1-2100

1          11         21         31         41         51
|          |          |          |          |          |
ATGGGCCTCC CCGAGCCGGG CCCTCTCCGG CTTCTGGCGC TGCTGCTGCT GCTGCTGCTG     60
CTGCTGCTGC TGCGGCTCCA GCATCTTGCG GCGGCAGCGG CTGATCCGCT GCTCGGCGGC    120
CAAGGGCCGG CCAAGGAGTG CGAAAAGGAC CAATTCCAGT GCCGGAACGA GCGCTGCATC    180
CCCTCTGTGT GGAGATGCGA CGAGGACGAT GACTGCTTAG ACCACAGCGA CGAGGACGAC    240
TGCCCCAAGA AGACCTGTGC AGACAGTGAC TTCACCTGTG ACAACGGCCA CTGCATCCAC    300
GAACGGTGGA AGTGTGACGG CGAGGAGGAG TGTCCTGATG GCTCCGATGA GTCCGAGGCC    360
ACTTGCACCA AGCAGGTGTG TCCTGCAGAG AAGCTGAGCT GTGGACCCAC CAGCCACAAG    420
TGTGTACCTG CCTCGTGGCG CTGCGACGGG GAGAAGGACT GCGAGGGTGG AGCGGATGAG    480
GCCGGCTGTG CTACCTCACT GGGCACCTGC CGTGGGGACG AGTTCCAGTG TGGGGATGGG    540
ACATGTGTCC TTGCAATCAA GCACTGCAAC CAGGAGCAGG ACTGTCCAGA TGGGAGTGAT    600
GAAGCTGGCT GCCTACAGGG GCTGAACGAG TGTCTGCACA ACAATGGCGG CTGCTCACAC    660
ATCTGCACTG ACCTCAAGAT TGGCTTTGAA TGCACGTGCC CAGCAGGCTT CCAGCTCCTG    720
GACCAGAAGA CTTGTGGCGA CATTGATGAG TGCAAGGACC CAGATGCCTG CAGCCAGATC    780
TGTGTCAATT ACAAGGGCTA TTTTAAGTGT GAGTGCTACC CTGGCTGCGA GATGGACCTA    840
CTGACCAAGA ACTGCAAGGC TGCTGCTGGC AAGAGCCCAT CCCTAATCTT CACCAACCGC    900
ACGAGTGCGG AGGATCGACC TGTGAAGCGG AACTATTCAC GCCTCATCCC CATGCTCAAG    960
AATGTCGTGG CACTAGATGT GGAAGTTGCC ACCAATCGCA TCTACTGGTG TGACCTCTCC   1020
TACCGTAAGA TCTATAGCGC CTACATGGAC AAGGCCAGTG ACCCGAAAGA GCGGGAGGTC   1080
CTCATTGACG AGCAGTTGCA CTCTCCAGAG GGCCTGGCAG TGGACTGGGT CCACAAGCAC   1140
ATCTACTGGA CTGACTCGGG CAATAAGACC ATCTCAGTGG CCACAGTTGA TGGTGGCCGC   1200
CGACGCACTC TCTTCAGCCG TAACCTCAGT GAACCCCGGG CCATCGCTGT TGACCCCCTG   1260
CGAGGGTTCA TGTATTGGTC TGACTGGGGG GACCAGGCCA AGATTGAGAA ATCTGGGCTC   1320
AACGGTGTGG ACCGGCAAAC ACTGGTGTCA GACAATATTG AATGGCCCAA CGGAATCACC   1380
CTGGATCTGC TGAGCCAGCG CTTGTACTGG GTAGACTCCA AGCTACACCA ACTGTCCAGC   1440
ATTGACTTCA GTGGAGGCAA CAGAAAGACG CTGATCTCCT CCACTGACTT CCTGAGCCAC   1500
CCTTTTGGGA TAGCTGTGTT TGAGGACAAG GTGTTCTGGA CAGACCTGGA GAACGAGGCC   1560
ATTTTCAGTG CAAATCGGCT CAATGGCCTG GAAATCTCCA TCCTGGCTGA GAACCTCAAC   1620
AACCCACATG ACATTGTCAT CTTCCATGAG CTGAAGCAGC CAAGAGCTCC AGATGCCTGT   1680
GAGCTGAGTG TCCAGCCTAA TGGAGGCTGT GAATACCTGT GCCTTCCTGC TCCTCAGATC   1740
TCCAGCCACT CTCCCAAGTA CACATGTGCC TGTCCTGACA CAATGTGGCT GGGTCCAGAC   1800
ATGAAGAGGT GCTACCGAGA TGCAAATGAA GACAGTAAGA TGGGCTCAAC AGTCACTGCC   1860
GCTGTTATCG GGATCATCGT GCCCATAGTG GTGATAGCCC TCCTGTGCAT GAGTGGATAC   1920
CTGATCTGGA GAAACTGGAA GCGGAAGAAC ACCAAAAGCA TGAATTTTGA CAACCCAGTC   1980
TACAGGAAAA CAACAGAAGA AGAAGATGAA GATGAGCTCC ATATAGGGAG AACTGCTCAG   2040
ATTGGCCATG TCTATCCTGC ACGAGTGGCA TTAAGCCTTG AAGATGATGG ACTACCCTGA   2100
GGATGGGATC ACCCCCTTCG TGCCTCATGG AATTCAGTCC CATGCACTAC ACTCCGGATG   2160
GTGTATGACT GGATGAATGG GTTTCTATAT ATGGGTCTGT GTGAGTGTAT GTGTGTGTGT   2220
GATTTTTTTT TTTAAATTTA TGTTGCGGAA AGGTAACCAC AAAGTTATGA TGAACTGCAA   2280
ACATCCAAAG GATGTGAGAG TTTTTCTATG TATAATGTTT TATACACTTT TTAACTGGTT   2340
GCACTACCCA TGAGGAATTC GTGGAATGGC TACTGCTGAC TAACATGATG CACATAACCA   2400
AATGGGGGCC AATGGCACAG TACCTTACTC ATCATTTAAA AACTATATTT ACAGAAGATG   2460
TTTGGTTGCT GGGGGGCTTT TTTAGGTTTT GGGCATTTGT TTTTTGTAAA TAAGATGATT   2520
ATGCTTTGTG GCTATCCATC AACATAAGT
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Seq ID NO: 357 Protein sequence
Protein Accession #:      NP_059992

1          11         21         31         41         51
|          |          |          |          |          |
MGLPEPGPLR LLALLLLLLL LLLLRLQHLA AAAADPLLGG QGPAKECEKD QFQCRNERCI     60
PSVWRCDEDD DCLDHSDEDD CPKKTCADSD FTCDNGHCIH ERWKCDGEEE CPDGSDESEA    120
TCTKQVCPAE KLSCGPTSHK CVPASWRCDG EKDCEGGADE AGCATSLGTC RGDEFQCGDG    180
TCVLAIKHCN QEQDCPDGSD EAGCLQGLNE CLHNNGGCSH ICTDLKIGFE CTCPAGFQLL    240
DQKTCGDIDE CKDPDACSQI CVNYKGYFKC ECYPGCEMDL LTKNCKAAAG KSPSLIFTNR    300
TSAEDRPVKR NYSRLIPMLK NVVALDVEVA TNRIYWCDLS YRKIYSAYMD KASDPKEREV    360
LIDEQLHSPE GLAVDWVHKH IYWTDSGNKT ISVATVDGGR RRTLFSRNLS EPRAIAVDPL    420
RGFMYWSDWG DQAKIEKSGL NGVDRQTLVS DNIEWPNGIT LDLLSQRLYW VDSKLHQLSS    480
IDFSGGNRKT LISSTDFLSH PFGIAVFEDK VFWTDLENEA IFSANRLNGL EISILAENLN    540
NPHDIVIFHE LKQPRAPDAC ELSVQPNGGC EYLCLPAPQI SSHSPKYTCA CPDTMWLGPD    600
MKRCYRDANE DSKMGSTVTA AVIGIIVPIV VIALLCMSGY LIWRNWKRKN TKSMNFDNPV    660
YRKTTEEEDE DELHIGRTAQ IGHVYPARVA LSLEDDGLP
```

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Seq ID NO: 358 DNA sequence
Nucleic Acid Accession #: M27826
Coding sequence:  <1-503

1          11         21         31         41         51
|          |          |          |          |          |
AGCCCAAGAA ACATCTCACC AATTTCAAAT CTGATCTATT CGGCTTAGCG ACTGAAGATT     60
GACGCTGCCC GATCGCCTCG GAAGTCCCCT GGACCATCAC AGAAGCCGAG CTTCGGGTAA    120
CTCTCACAGT GGAGGGTAAG TCCATCCCCT GTTTAATCGA TACGGGGGCT ACCCACTCCA    180
CGTTGCCTTC TTTTCAAGGG CCTGTTTCCC TTGCCCCCAT AACTGTTGTG GGTATTGACG    240
GCCAAGCTTC AAAACCCCTG AAAACTCCCC CACTCTGGTG CCAACTTGGA CAACACTCTT    300
TTATGCACTC TTTTTTAGTT ATCCCCACCT GCCCACTTCC CTTATTAGGC CGAAATATTT    360
TAACCAAATT ATCTGCTTCC CTGACTATTC CTGGAGTACA GCTACATCTC ATTGCTGCCC    420
TTCTTCCCAA TCCAAAGCCT CCTTTGTGTC CTCTAACATC CCCACAATAT CAGCCCTTAC    480
CACAAGACCT CCCTTCAGCT TAATCTCTCC CACTCTAGGT TCCCACGCCG CCCCTAATCC    540
CACTTGAAGC AGCCCTGAGA AACATCGCCC ATTCTCTCTC CATACCACCC CCCAAAAATT    600
TTCGCCGCTC CAACACTTCA ACACTATTTT GTTTTATTTG TCTTATTAAT ATCAGAAGGC    660
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AGGAATGTCA GGCCTCTGAG CCCAGGCCAG GCCATCGCAT CCCCTGTGAC TTGCACGTAT   720
ACATCCAGAT GGCCTGAAGT AACTGAAGAT CCACAAAAGA AGTAAAAACA GCCTTAACTG   780
ATGACATTCC ACCATTGTGA TTTGTTCCTG CCCCACCCTA ACTGATCAAT GTACTTTGTA   840
ATCTCCCCCA CCCTTAAGAA GGTTCTTTGT AATTCTCCCC ACCCTTGAGA ATGTACTTTG   900
TGAGATCCAC CCCTGCCCAC CAGAGAACAA CCCCCTTTGA TTGTAATTTT TTATTACCTT   960
CCCAAATCCT ATAAAACAGC CCCACCCCTA TCTTCCTTCA CTGACTCTCT TTTCGGACTC  1020
AGCCACCGGC ACCCAGGTGA AATAAACAGC TTTATTGCTC AC
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Seq ID NO: 359 Protein sequence
Protein Accession #: AAA65999

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1          11         21         31         41         51
|          |          |          |          |          |
PKKHLTNFKS DLFGLATEDW RCPIASEVPW TITEAELRVT LTVEGKSIPC LIDTGATHST    60
LPSFQGPVSL APITVVGIDG QASKPLKTPP LWCQLGQHSF MHSFLVIPTC PLPLLGRNIL   120
TKLSASLTIP GVQLHLIAAL LPNPKPPLCP LTSPQYQPLP QDLPSA
```

Seq ID NO: 360 DNA sequence
Nucleic Acid Accession #: NM_001854
Coding sequence: 162-5582

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1          11         21         31         41         51
|          |          |          |          |          |
AACCATCAAA TTTAGAAGAA AAAGCCCTTT GACTTTTTCC CCCTCTCCCT CCCCAATGGC    60
TGTGTAGCAA ACATCCCTGG CGATACCTTG GAAAGGACGA AGTTGGTCTG CAGTCGCAAT   120
TTCGTGGGTT GAGTTCACAG TTGTGAGTGC GGGGCTCGGA GATGGAGCCG TGGTCCTCTA   180
GGTGGAAAAC GAAACGGTGG CTCTGGGATT TCACCGTAAC AACCCTCGCA TTGACCTTCC   240
TCTTCCAAGC TAGAGAGGTC AGAGGAGCTG CTCCAGTTGA TGTACTAAAA GCACTAGATT   300
TTCACAATTC TCCAGAGGGA ATATCAAAAA CAACGGGATT TTGCACAAAC AGAAAGAATT   360
CTAAAGGCTC AGATACTGCT TACAGAGTTT CAAAGCAAGC ACAACTCAGT GCCCCAACAA   420
AACAGTTATT TCCAGGTGGA ACTTTCCCAG AAGACTTTTC AATACTATTT ACAGTAAAAC   480
CAAAAAAAGG AATTCAGTCT TTCCTTTTAT CTATATATAA TGAGCATGGT ATTCAGCAAA   540
TTGGTGTTGA GGTTGGGAGA TCACCTGTTT TTCTGTTTGA AGACCACACT GGAAAACCTG   600
CCCCAGAAGA CTATCCCCTC TTCAGAACTG TTAACATCGC TGACGGGAAG TGGCATCGGG   660
TAGCAATCAG CGTGGAGAAG AAAACTGTGA CAATGATTGT TGATTGTAAG AAGAAAACCA   720
CGAAACCACT TGATAGAAGT GAGAGAGCAA TTGTTGATAC CAATGGAATC ACGGTTTTTG   780
GAACAAGGAT TTTGGATGAA GAAGTTTTTG AGGGGGACAT TCAGCAGTTT TTGATCACAG   840
GTGATCCCAA GGCAGCATAT GACTACTGTG AGCATTATAG TCCAGACTGT GACTCTTCAG   900
CACCCAAGGC TGCTCAAGCT CAGGAACCTC AGATAGATGA GTATGCACCA GAGGATATAA   960
TCGAATATGA CTATGAGTAT GGGGAAGCAG AGTATAAAGA GGCTGAAAGT GTAACAGAGG  1020
GACCCACTGT AACTGAGGAG ACAATAGCAC AGACGGAGGC AAACATCGTT GATGATTTTC  1080
AAGAATACAA CTATGGAACA ATGGAAAGTT ACCAGACAGA AGCTCCTAGG CATGTTTCTG  1140
GGACAAATGA GCCAAATCCA GTTGAAGAAA TATTTACTGA AGAATATCTA ACGGGAGAGG  1200
ATTATGATTC CCAGAGGAAA AATTCTGAGG ATACACTATA TGAAAACAAA GAAATAGACG  1260
GCAGGGATTC TGATCTTCTG GTAGATGGAG ATTTAGGCGA ATATGATTTT TATGAATATA  1320
AAGAATATGA AGATAAACCA ACAAGCCCCC CTAATGAAGA ATTTGGTCCA GGTGTACCAG  1380
CAGAAACTGA TATTACAGAA ACAAGCATAA ATGGCCATGG TGCATATGGA GAGAAAGGAC  1440
AGAAAGGAGA ACCAGCAGTG GTTGAGCCTG GTATGCTTGT CGAAGGACCA CCAGGACCAG  1500
CAGGACCTGC AGGTATTATG GGTCCTCCAG GTCTACAAGG CCCCACTGGA CCCCCTGGTG  1560
ACCCTGGCGA TAGGGGCCCC CCAGGACGTC CTGGCTTACC AGGGGCTGAT GGTCTACCTG  1620
GTCCTCCTGG TACTATGTTG ATGTTACCGT TCCGTTATGG TGGTGATGGT TCCAAAGGAC  1680
CAACCATCTC TGCTCAGGAA GCTCAGGCTC AAGCTATTCT TCAGCAGGCT CGGATTGCTC  1740
TGAGAGGCCC ACCTGGCCCA ATGGGTCTAA CTGGAAGACC AGGTCCTGTG GGGGGGCCTG  1800
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AGGGTCCCCC TGGTCCAACG GGAAAACCTG GAAAAAGGGG TCGTCCAGGT GCAGATGGAG  1920
GAAGAGGAAT GCCAGGAGAA CCTGGGGCAA AGGGAGATCG AGGGTTTGAT GGACTTCCGG  1980
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CCAGAGGCTT CCCTGGACCT CCTGGTCCAA TAGGTCTTCA GGGTCTGCCA GGCCCACCTG  3780
GTGAAAAAGG TGAAAATGGG GATGTTGGTC CATGGGGGCC ACCTGGTCCT CCAGGCCCAA  3840
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Seq ID NO: 361 Protein sequence
Protein Accession #: NP_001845

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DCKKKTTKPL DRSERAIVDT NGITVFGTRI LDEEVFEGDI QQFLITGDPK AAYDYCEHYS   240
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GPPGPAGEKG APGEKGPQGP AGRDGVQGPV GLPGPAGPAG SPGEDGDKGE IGEPGQKGSK  1140
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EYWIDPNQGC SGDSFKVYCN FTSGGETCIY PDKKSEGVRI SSWPKEKPGS WFSEFKRGKL  1680
LSYLDVEGNS INMVQMTFLK LLTASARQNF TYHCHQSAAW YDVSSGSYDK ALRFLGSNDE  1740
EMSYDNNPFI KTLYDGCTSR KGYEKTVIEI NTPKIDQVPI VDVMISDFGD QNQKFGFEVG  1800
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Seq ID NO: 362 DNA sequence
Nucleic Acid Accession #: NM_003107
Coding sequence: 351-1775

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GGAACTATAA CTCCTCTGCG AGAGGCGGAG AACTCCTTCC CCAAATCTTT TGGGGACTTT   180
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AAACCAACAA TGCCGAGAAC ACGGAAGCGC TGCTGGCCGG CGAGAGCTCG GACTCGGGCG   420
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GCAAGGCCGA CGACCCGAGC TGGTGCAAGA CCCCGAGTGG GCACATCAAG CGACCCATGA   540
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Seq ID NO: 363 Protein sequence
Protein Accession #: NP_003098

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ADYPDYKYRP RKKVKSGNAN SSSSAAASSK PGEKGDKVGG SGGGGHGGGG GGGSSNAGGG   180
GGGASGGGAN SKPAQKKSCG SKVAGGAGGG VSKPHAKLIL AGGGGGGKAA AAAASFAAE   240
QAGAAALLPL GAAADHHSLY KARTPSASAS ASSAASASAA LAAPGKHLAE KKVKRVYLFG   300
GLGTSSSPVG GVGAGADPSD PLGLYEEEGA GCSPDAPSLS GRSSAASSPA AGRSPADHRG   360
YASLRAASPA PSSAPSHASS SASSHSSSSS SSGSSSSDDE FEDDLLDLNP SSNFESMSLG   420
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Seq ID NO: 364 DNA sequence
Nucleic Acid Accession #: U10860
Coding sequence: 123-2204

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Seq ID NO: 365 Protein sequence
Protein Accession #: AAA60331

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KSVREDGVFN ISVDNTCSLF RGLQKEEVVL LTHGDSVDKV ADGFKVVARS GNIVAGIANE  180
SKKLYGAQFH PEVGLTENGK VILKNFLYDI AGCSGTFTVQ NRELECIREI KERVGTSKVL  240
VLLSGGVDST VCTALLNRAL NQEQVIAVHI DNGFMRKRES QSVEEALKKL GIQVKVINAA  300
HSFYNGTTTL PISDEDRTPR KRISKTLNMT TSPEEKRKII GDTFVKIANE VIGEMNLKPE  360
EVFLAQGTLR PDLIESASLV ASGKAELIKT HHNDTELIRK LREEGKVIEP LKDFHKDEVR  420
ILGRELGLPE ELVSRHPFPG PGLAIRVICA EEPYICKDFP ETNNILKIVA DFSASVKKPH  480
TLLQRVKACT TEEDQEKLMQ ITSLHSLNAF LLPIKTVGVQ GDCRSYSYVC GISSKDEPDW  540
ESLIFLARLI PRMCHNVNRV VYIFGPPVKE PPTDVTPTFL TTGVLSTLRQ ADFEAHNILR  600
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Seq ID NO: 366 DNA sequence
Nucleic Acid Accession #: NM_004219
Coding sequence: 46-654

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CCTGTGAAGA TGCCCTCTCC ACCATGGGAA TCCAATCTGT TGCAGTCTCC TTCAAGCATT  600
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Seq ID NO: 367 Protein sequence
Protein Accession #: NP_004210

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|          |          |          |          |          |
MATLIYVDKE NGEPGTRVVA KDGLKLGSGP SIKALDGRSQ VSTPRFGKTF DAPPALPKAT   60
RKALGTVNRA TEKSVKTKGP LKQKQPSFSA KKMTEKTVKA KSSVPASDDA YPEIEKFFPF  120
NPLDFESFDL PEEHQIAHLP LSGVPLMILD EERELEKLFQ LGPPSPVKMP SPPWESNLLQ  180
SPSSILSTLD VELPPVCCDI DI
```

Seq ID NO: 368 DNA sequence
Nucleic Acid Accession #: NM_000597
Coding sequence: 118-1104

```
1          11         21         31         41         51
|          |          |          |          |          |
ATTCGGGGCG AGGGAGGAGG AAGAAGCGGA GGAGGCGGCT CCCGCTCGCA GGGCCGTGCA   60
CCTGCCCGCC CGCCCGCTCG CTCGCTCGCC CGCCGCGCCG CGCTGCCGAC CGCCAGCATG  120
CTGCCGAGAG TGGGCTGCCC CGCGCTGCCG CTGCCGCCGC CGCCGCTGCT GCCGCTGCTG  180
CCGCTGCTGC TGCTGCTACT GGGCGCGAGT GGCGGCGGCG GCGGGGCGCG CGCGGAGGTG  240
CTGTTCCGCT GCCCGCCCTG CACACCCGAG CGCCTGGCCG CCTGCGGGCC CCCGCCGGTT  300
GCGCCGCCCG CCGCGGTGGC CGCAGTGGCC GGAGGCGCCC GCATGCCATG CGCGGAGCTC  360
GTCCGGGAGC CGGGCTGCGG CTGCTGCTCG GTGTGCGCCC GGCTGGAGGG CGAGGCGTGC  420
GGCGTCTACA CCCCGCGCTG CGGCCAGGGG CTGCGCTGCT ATCCCCACCC GGGCTCCGAG  480
CTGCCCCTGC AGGCGCTGGT CATGGGCGAG GGCACTTGTG AGAAGCGCCG GGACGCCGAG  540
TATGGCGCCA GCCCGGAGCA GGTTGCAGAC AATGGCGATG ACCACTCAGA AGGAGGCCTG  600
GTGGAGAACC ACGTGGACAG CACCATGAAC ATGTTGGGCG GGGGAGGCAG TGCTGGCCGG  660
AAGCCCCTCA AGTCGGGTAT GAAGGAGCTG GCCGTGTTCC GGGAGAAGGT CACTGAGCAG  720
CACCGGCAGA TGGGCAAGGG TGGCAAGCAT CACCTTGGCC TGGAGGAGCC CAAGAAGCTG  780
CGACCACCCC CTGCCAGGAC TCCCTGCCAA CAGGAACTGG ACCAGGTCCT GGAGCGGATC  840
```

TCCACCATGC GCCTTCCGGA TGAGCGGGGC CCTCTGGAGC ACCTCTACTC CCTGCACATC 900
CCCAACTGTG ACAAGCATGG CCTGTACAAC CTCAAACAGT GCAAGATGTC TCTGAACGGG 960
CAGCGTGGGG AGTGCTGGTG TGTGAACCCC AACACCGGGA AGCTGATCCA GGGAGCCCCC 1020
ACCATCCGGG GGGACCCCGA GTGTCATCTC TTCTACAATG AGCAGCAGGA GGCTTGCGGG 1080
GTGCACACCC AGCGGATGCA GTAGACCGCA GCCAGCCGGT GCCTGGCGCC CCTGCCCCCC 1140
GCCCCTCTCC AAACACCGGC AGAAAACGGA GAGTGCTTGG GTGGTGGGTG CTGGAGGATT 1200
TTCCAGTTCT GACACACGTA TTTATATTTG GAAAGAGACC AGCACCGAGC TCGGCACCTC 1260
CCCGGCCTCT CTCTTCCCAG CTGCAGATGC CACACCTGCT CCTTCTTGCT TTCCCCGGGG 1320
GAGGAAGGGG GTTGTGGTCG GGGAGCTGGG GTACAGGTTT GGGGAGGGGG AAGAGAAATT 1380
TTTATTTTTG AACCCCTGTG TCCCTTTTGC ATAAGATTAA AGGAAGGAAA AGT

Seq ID NO: 369 Protein sequence
Protein Accession #: NP_000588

1 11 21 31 41 51
| | | | | |
MLPRVGCPAL PLPPPPLLPL LPLLLLLLGA SGGGGGARAE VLFRCPPCTP ERLAACGPPP 60
VAPPAAVAAV AGGARMPCAE LVREPGCGCC SVCARLEGEA CGVYTPRCGQ GLRCYPHPGS 120
ELPLQALVMG EGTCEKRRDA EYGASPEQVA DNGDDHSEGG LVENHVDSTM NMLGGGGSAG 180
RKPLKSGMKE LAVPREKVTE QHRQMGKGGK HHLGLEEPKK LRPPPARTPC QQELDQVLER 240
ISTMRLPDER GPLEHLYSLH IPNCDKHGLY NLKQCKMSLN GQRGECWCVN PNTGKLIQGA 300
PTIRGDPECH LFYNEQQEAC GVHTQRMQ

Seq ID NO: 370 DNA sequence
Nucleic Acid Accession #: NM_004264
Coding sequence: 6-440

1 11 21 31 41 51
| | | | | |
GGAACATGGC GGATCGGCTC ACGCAGCTTC AGGACGCTGT GAATTCGCTT GCAGATCAGT 60
TTTGTAATGC CATTGGAGTA TTGCAGCAAT GTGGTCCTCC TGCCTCTTTC AATAATATTC 120
AGACAGCAAT TAACAAAGAC CAGCCAGCTA ACCCTACAGA AGAGTATGCC CAGCTTTTTG 180
CAGCACTGAT TGCACGAACA GCAAAAGACA TTGATGTTTT GATAGATTCC TTACCCAGTG 240
AAGAATCTAC AGCTGCTTTA CAGGCTGCTA GCTTGTATAA GCTAGAAGAA GAAAACCATG 300
AAGCTGCTAC ATGTGTGGAG GATGTTGTTT ATCGAGGAGA CATGCTTCTG GAGAAGATAC 360
AAAGCGCACT TGCTGATATT GCACAGTCAC AGCTGAAGAC AAGAAGTGGT ACCCATAGCC 420
AGTCTCTTCC AGACTCATAG CATCAGTGGA TACCATGTGG CTGAGAAAAG AACTGTTTGA 480
GTGCCATTAA GAATTCTGCA TCAGACTTAG ATACAAGCCT TACCAACAAT TACAGAAACA 540
TTAAACACTA TGACACATTA CCTTTTTAGC TATTTTTAAT AGTCTTCTAT TTTCACTCTT 600
GATAAGCTTA TAAATCATGA TTGAATCAGC TTTAAAGCAT CATACCATCA TTTTTTAACT 660
GAGTGAAATT ATTAAGGCAT GTAATACATT AATGAACATA ATATAAGGAA ACATATGTAA 720
AATTCTGTTA TGACATAATT TATGTCTCCA TTTTGTTGTA TTGGCCAGTA CTTTTACAAT 780
C

Seq ID NO: 371 Protein sequence
Protein Accession #: NP_004255

1 11 21 31 41 51
| | | | | |
MADRLTQLQD AVNSLADQFC NAIGVLQQCG PPASFNNIQT AINKDQPANP TEEYAQLFAA 60
LIARTAKDID VLIDSLPSEE STAALQAASL YKLEEENHEA ATCVEDVVYR GDMLLEKIQS 120
ALADIAQSQL KTRSGTHSQS LPDS

Seq ID NO: 372 DNA sequence
Nucleic Acid Accession #: AJ271091
Coding sequence: 1-1113

1 11 21 31 41 51
| | | | | |
ATGGAGAATC AGGTGTTGAC GCCGCATGTC TACTGGGCTC AGCGACACCG CGAGCTATAT 60
CTGCGCGTGG AGCTGAGTGA CGTACAGAAC CCTGCCATCA GCATCACTGA AAACGTGCTG 120
CATTTCAAAG CTCAAGGACA TGGTGCCAAA GGAGACAATG TCTATGAATT TCACCTGGAG 180
TTCTTAGACC TTGTGAAACC AGAGCCTGTT TACAAACTGA CCCAGAGGCA GGTAAACATT 240
ACAGTACAGA AGAAAGTGAG TCAGTGGTGG GAGAGACTCA CAAAGCAGGA AAAGCGACCA 300
CTGTTTTTGG CTCCTGACTT TGATCGTTGG CTGGATGAAT CTGATGCGGA AATGGAGCTC 360
AGAGCTAAGG AAGAAGAGCG CCTAAATAAA CTCCGACTGG AAAGCGAAGG CTCTCCTGAA 420
ACTCTTACAA ACTTAAGGAA AGGATACCTG TTTATGTATA ATCTTGTGCA ATTCTTGGGA 480
TTCTCCTGGA TCTTTGTCAA CCTGACTGTG CGATTCTGTA TCTTGGGAAA AGAGTCCTTT 540
TATGACACAT TCCATACTGT GGCTGACATG ATGTATTTCT GCCAGATGCT GGCAGTTGTG 600
GAAACTATCA ATGCAGCAAT TGGAGTCACT ACGTCACCGG TGCTGCCTTC TCTGATCCAG 660
CTTCTTGGAA GAAATTTTAT TTTGTTTATC ATCTTTGGCA CCATGGAAGA AATGCAGAAC 720
AAAGCTGTGG TTTTCTTTGT GTTTTATTTG TGGAGTGCAA TTGAAATTTT CAGGTACTCT 780
TTCTACATGC TGACGTGCAT TGACATGGAT TGGAAGGTGC TCACATGGCT TCGTTACACT 840
CTGTGGATTC CCTTATATCC ACTGGGATGT TTGGCGGAAG CTGTCTCAGT GATTCAGTCC 900
ATTCCAATAT TCAATGAGAC CGGACGATTC AGTTTCACAT TGCCATATCC AGTGAAAATC 960
AAAGTTAGAT TTTCCTTTTT TCTTCAGATT TATCTTATAA TGATATTTTT AGGTTTATAC 1020
ATAAATTTTC GTCACCTTTA TAAACAGCGC AGACTGAAAA TGAGGGCAGG CGCAGTGGCT 1080
CATGCCTGTG ATCCCAGCGC TTTGGGAGGC TGA

Seq ID NO: 373 Protein sequence
Protein Accession #: CAB69070

1 11 21 31 41 51
| | | | | |
MENQVLTPHV YWAQRHRELY LRVELSDVQN PAISITENVL HFKAQGHGAK GDNVYEFHLE 60
FLDLVKPEPV YKLTQRQVNI TVQKKVSQWW ERLTKQEKRP LFLAPDFDRW LDESDAEMEL 120
RAKEEERLNK LRLESEGSPE TLTNLRKGYL FMYNLVQFLG FSWIFVNLTV RFCILGKESF 180

```
YDTFHTVADM MYFCQMLAVV ETINAAIGVT TSPVLPSLIQ LLGRNFILFI IFGTMEEMQN   240
KAVVFFVFYL WSAIEIFRYS FYMLTCIDMD WKVLTWLRYT LWIPLYPLGC LAEAVSVIQS   300
IPIFNETGRF SFTLPYPVKI KVRFSFFLQI YLIMIFLGLY INFRHLYKQR RLKMRAGAVA   360
HACDPSALGG
```

Seq ID NO: 374 DNA sequence
Nucleic Acid Accession #: NM_016395
Coding sequence: 1-1113

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1          11         21         31         41         51
|          |          |          |          |          |
ATGGAGAATC AGGTGTTGAC GCCGCATGTC TACTGGGCTC AGCGACACCG CGAGCTATAT    60
CTGCGCGTGG AGCTGAGTGA CGTACAGAAC CCTGCCATCA GCATCACTGA AAACGTGCTG   120
CATTTCAAAG CTCAAGGACA TGGTGCCAAA GGAGACAATG TCTATGAATT TCACCTGGAG   180
TTCTTAGACC TTGTGAAACC AGAGCCTGTT TACAAACTGA CCCAGAGGCA GGTAAACATT   240
ACAGTACAGA AGAAAGTGAG TCAGTGGTGG GAGAGACTCA CAAAGCAGGA AAAGCGACCA   300
CTGTTTTTGG CTCCTGACTT TGATCGTTGG CTGGATGAAT CTGATGCGGA AATGGAGCTC   360
AGAGCTAAGG AAGAAGAGCG CCTAAATAAA CTCCGACTGG AAAGCGAAGG CTCTCCTGAA   420
ACTCTTACAA ACTTAAGGAA AGGATACCTG TTTATGTATA ATCTTGTGCA ATTCTTGGGA   480
TTCTCCTGGA TCTTTGTCAA CCTGACTGTG CGATTCTGTA TCTTGGGAAA AGAGTCCTTT   540
TATGACACAT TCCATACTGT GGCTGACATG ATGTATTTCT GCCAGATGCT GGCAGTTGTG   600
GAAACTATCA ATGCAGCAAT TGGAGTCACT ACGTCACCGG TGCTGCCTTC TCTGATCCAG   660
CTTCTTGGAA GAAATTTTAT TTTGTTTATC ATCTTTGGCA CCATGGAAGA AATGCAGAAC   720
AAAGCTGTGG TTTTCTTTGT GTTTTATTTG TGGAGTGCAA TTGAAATTTT CAGGTACTCT   780
TTCTACATGC TGACGTGCAT TGACATGGAT TGGAAGGTGC TCACATGGCT TCGTTACACT   840
CTGTGGATTC CCTTATATCC ACTGGGATGT TTGGCGGAAG CTGTCTCAGT GATTCAGTCC   900
ATTCCAATAT TCAATGAGAC CGGACGATTC AGTTTCACAT TGCCATATCC AGTGAAAATC   960
AAAGTTAGAT TTTCCTTTTT TCTTCAGATT TATCTTATAA TGATATTTTT AGGTTTATAC  1020
ATAAATTTTC GTCACCTTTA TAAACAGCGC AGACTGAAAA TGAGGGCAGG CGCAGTGGCT  1080
CATGCCTGTG ATCCCAGCGC TTTGGGAGGC TGA
```

Seq ID NO: 375 Protein sequence
Protein Accession #: NP_057479

```
1          11         21         31         41         51
|          |          |          |          |          |
MENQVLTPHV YWAQRHRELY LRVELSDVQN PAISITENVL HFKAQGHGAK GDNVYEFHLE    60
FLDLVKPEPV YKLTQRQVNI TVQKKVSQWW ERLTKQEKRP LFLAPDFDRW LDESDAEMEL   120
RAKEEERLNK LRLESEGSPE TLTNLRKGYL FMYNLVQFLG FSWIFVNLTV RFCILGKESF   180
YDTFHTVADM MYFCQMLAVV ETINAAIGVT TSPVLPSLIQ LLGRNFILFI IFGTMEEMQN   240
KAVVFFVFYL WSAIEIFRYS FYMLTCIDMD WKVLTWLRYT LWIPLYPLGC LVEAVSVIQS   300
IPIFNETGRF SFTLPYPVKI KVRFSFFLQI YLIMIFLGLY INFRHLYKQR RRRYGKKRKR   360
STKKKDLDGF LPV
```

Seq ID NO: 376 DNA sequence
Nucleic Acid Accession #: NM_005987
Coding sequence: 1-270

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGAATTCTC AGCAGCAGAA GCAGCCTTGC ACCCCACCCC CTCAGCCTCA GCAGCAGCAG    60
GTGAAACAAC CTTGCCAGCC TCCACCCCAG GAACCATGCA TCCCCAAAAC CAAGGAGCCC   120
TGCCAACCCA AGGTGCCTGA GCCCTGCCAC CCCAAAGTGC CTGAGCCCTG CCAGCCCAAG   180
ATTCCAGAGC CCTGCCAGCC CAAGGTGCCT GAGCCCTGCC CTTCAACGGT CACTCCAGCA   240
CCAGCCCAGC AGAAGACCAA GCAGAAGTAA
```

Seq ID NO: 377 Protein sequence
Protein Accession #: NP_005978

```
1          11         21         31         41         51
|          |          |          |          |          |
MNSQQQKQPC TPPPQPQQQQ VKQPCQPPPQ EPCIPKTKEP CQPKVPEPCH PKVPEPCQPK    60
IPEPCQPKVP EPCPSTVTPA PAQQKTKQK
```

Seq ID NO: 378 DNA sequence
Nucleic Acid Accession #: NM_002105
Coding sequence: 74-505

```
1          11         21         31         41         51
|          |          |          |          |          |
ACAGCAGTTA CACTGCGGCG GGCGTCTGTT CTAGTGTTTG AGCCGTCGTG CTTCACCGGT    60
CTACCTCGCT AGCATGTCGG GCCGCGGCAA GACTGGCGGC AAGGCCCGCG CCAAGGCCAA   120
GTCGCGCTCG TCGCGCGCCG GCCTCCAGTT CCCAGTGGGC CGTGTACACC GGCTGCTGCG   180
GAAGGGCCAC TACGCCGAGC GCGTTGGCGC CGGCGCGCCA GTGTACCTGG CGGCAGTGCT   240
GGAGTACCTC ACCGCTGAGA TCCTGGAGCT GGCGGGCAAT GCGGCCCGCG ACAACAAGAA   300
GACGCGAATC ATCCCCCGCC ACCTGCAGCT GGCCATCCGC AACGACGAGG AGCTCAACAA   360
GCTGCTGGGC GGCGTGACGA TCGCCCAGGG AGGCGTCCTG CCCAACATCC AGGCCGTGCT   420
GCTGCCCAAG AAGACCAGCG CCACCGTGGG GCCGAAGGCG CCCTCGGGCG GCAAGAAGGC   480
CACCCAGGCC TCCCAGGAGT ACTAAGAGGG CCCGCGCCGC GGCCGGCCGC CCCAGCTCCC   540
CATGCCACCA CAAAGGCCCT TTTAAGGGCC ACCACCGCCC TCATGGAAAG AGCTGAGCCG   600
CTTCAGACTG CGGGGCAAGC GGGCCGCGGC TCCCTTCCCC TCCCCTCCCC TCGCCCGCCT   660
TCGCCGCCCG GCCTCGAGTC CCCGCCCGCC CCCGCTCCCG TCCCGCACCG CCTGCCGCGT   720
CGGCCTCGGG CCTGCCCTGT CCGCCGTCCG CCCTCCGGTA GGGTTCGGGC CTTCCGGATG   780
CGGCTTGGGC GCTCTTCGGG GACCTCCGTG GCGCGGAAGA CCCGAGCCTG CCGGGGGGAG   840
```

```
GCCGGCGGCG CCGCACCTGC CCGCCTCGGC GTTCGTGACT CAGCCGCCCC ATCCCGAGTC   900
GCTAAGGGGC TGCGGGGAGG CCGCAGCACC TTCTGGAAGA CTTGGCCTTC CGCTCTGACG   960
CAGGGCCGAG GTGGGCAGTC CAGGCCGAGA GCCGGCGGCC CTGAAGGTGA GTGAGGCCCT  1020
CGGCAGCTGC AGCCGGGGTG TCTGGTACCC CCCCGGCGTG GTGCTTAGCC CAGGACTTTC  1080
AGACGGCCGC TGGCCGGGAG GCTTTGGTGG GAGAGACGCG ATCGCCGATT TCGGTCTGGC  1140
GCCCCTTCTG CGGCCGGGAC CCAGGCCTTT CACATCAGCT CTCCCTCCAT CTTCATTCAT  1200
AGGTCTGCGC TGGGGCCGGG ACGAAGCACT TGGTAACAGG CACATCTTCC TCCCGAGTGA  1260
CTGCCTCCTA GGAGGACATT TAGGGGAGGG CAGAGGCCTG CAGTTTGGCT TCACGGCTGG  1320
CTATGTGGAC AGCAAGAGTC GTTTTGCGGA ACGCGACTGG CAGCCAGGCC TGTCGGGCCC  1380
CCGACGCCGC CCCATTTCCC TTCCAGCAAA CTCAACTCGG CAATCCAAGC ACCTAGATAC  1440
CAGCACAAGT CGGTTAATCC CTGTCTGGAC TGAGCCTCCG TTGGCTTCTG AACTGGAATT  1500
CTGCAGCTAA CCCTTCCACG ACTAGAACCT TAGGCATTGG GGAGTTTTAG ATGGACTAAT  1560
TTTATTAAAG GATTGTTTTT TTTTT
```

Seq ID NO: 379 Protein sequence
Protein Accession #: NP_002096

```
1          11         21         31         41         51
|          |          |          |          |          |
MSGRGKTGGK ARAKAKSRSS RAGLQFPVGR VHRLLRKGHY AERVGAGAPV YLAAVLEYLT    60
AEILELAGNA ARDNKKTRII PRHLQLAIRN DEELNKLLGG VTIAQGGVLP NIQAVLLPKK   120
TSATVGPKAP SGGKKATQAS QEY
```

Seq ID NO: 380 DNA sequence
Nucleic Acid Accession #: AL136942
Coding sequence: 184-864

```
1          11         21         31         41         51
|          |          |          |          |          |
ACGCGTCCGG CAGAAGCTCG GAGCTCTCGG GGTATCGAGG AGGCAGGCCC GCGGGCGCAC    60
GGGCGAGCGG GCCGGGAGCC GGAGCGGCGG AGGAGCCGGC AGCAGCGGCG CGGCGGGCTC   120
CAGGCGAGGC GGTCGACGCT CCTGAAAACT TGCGCGCGCG CTCGCGCCAC TGCGCCCGGA   180
GCGATGAAGA TGGTCGCGCC CTGGACGCGG TTCTACTCCA ACAGCTGCTG CTTGTGCTGC   240
CATGTCCGCA CCGGCACCAT CCTGCTCGGC GTCTGGTATC TGATCATCAA TGCTGTGGTA   300
CTGTTGATTT TATTGAGTGC CCTGGCTGAT CCGGATCAGT ATAACTTTTC AAGTTCTGAA   360
CTGGGAGGTG ACTTTGAGTT CATGGATGAT GCCAACATGT GCATTGCCAT TGCGATTTCT   420
CTTCTCATGA TCCTGATATG TGCTATGGCT ACTTACGGAG CGTACAAGCA ACGCGCAGCC   480
TGGATCATCC CATTCTTCTG TTACCAGATC TTTGACTTTG CCCTGAACAT GTTGGTTGCA   540
ATCACTGTGC TTATTTATCC AAACTCCATT CAGGAATACA TACGGCAACT GCCTCCTAAT   600
TTTCCCTACA GAGATGATGT CATGTCAGTG AATCCTACCT GTTTGGTCCT TATTATTCTT   660
CTGTTTATTA GCATTATCTT GACTTTTAAG GGTTACTTGA TTAGCTGTGT TTGGAACTGC   720
TACCGATACA TCAATGGTAG GAACTCCTCT GATGTCCTGG TTTATGTTAC CAGCAATGAC   780
ACTACGGTGC TGCTACCCCC GTATGATGAT GCCACTGTGA ATGGTGCTGC CAAGGAGCCA   840
CCGCCACCTT ACGTGTCTGC CTAAGCCTTC AAGTGGGCGG AGCTGAGGGC AGCAGCTTGA   900
CTTTGCAGAC ATCTGAGCAA TAGTTCTGTT ATTTCACTTT TGCCATGAGC CTCTCTGAGC   960
TTGTTTGTTG CTGAAATGCT ACTTTTTAAA ATTTAGATGT TAGATTGAAA ACTGTAGTTT  1020
TCAACATATG CTTTGCTAGA ACACTGTGAT AGATTAACTG TAGAATTCTT CCTGTACGAT  1080
TGGGGATATA ACGGGCTTCA CTAACCTTCC CTAGGCATTG AAACTTCCCC CAAATCTGAT  1140
GGACCTAGAA GTCTGCTTTT GTACCTGCTG GGCCCCAAAG TTGGGCATTT TTCTCTCTGT  1200
TCCCTCTCTT TTGAAAATGT AAAATAAAAC CAAAAATAGA CAACTTTTTC TTCAGCCATT  1260
CCAGCATAGA GAACAAAACC TTATGGAAAC AGGAATGTCA ATTGTGTAAT CATTGTTCTA  1320
ATTAGGTAAA TAGAAGTCCT TATGTATGTG TTACAAGAAT TTCCCCCACA ACATCCTTTA  1380
TGACTGAAGT TCAATGACAG TTTGTGTTTG GTGGTAAAGG ATTTTCTCCA TGGCCTGAAT  1440
TAAGACCATT AGAAAGCACC AGGCCGTGGG AGCAGTGACC ATCTACTGAC TGTTCTTGTG  1500
GATCTTGTGT CCAGGGACAT GGGGTGACAT GCCTCGTATG TGTTAGAGGG TGGAATGGAT  1560
GTGTTTGGCG CTGCATGGGA TCTGGTGCCC CTCTTCTCCT GGATTCACAT CCCCACCCAG  1620
GGCCCGCTTT TACTAAGTGT TCTGCCCTAG ATTGGTTCAA GGAGGTCATC CAACTGACTT  1680
TATCAAGTGG AATTGGGATA TATTTGATAT ACTTCTGCCT AACAACATGG AAAAGGGTTT  1740
TCTTTTCCCT GCAAGCTACA TCCTACTGCT TTGAACTTCC AAGTATGTCT AGTCACCTTT  1800
TAAAATGTAA ACATTTTCAG AAAAATGAGG ATTGCCTTCC TTGTATGCGC TTTTTACCTT  1860
GACTACCTGA ATTGCAAGGG ATTTTTATAT ATTCATATGT TACAAAGTCA GCAACTCTCC  1920
TGTTGGTTCA TTATTGAATG TGCTGTAAAT TAAGTCGTTT GCAATTAAAA CAAGGTTTGC  1980
CCACATCCAA AAAAAAAAAA AAAAA
```

Seq ID NO: 381 Protein sequence
Protein Accession #: CAB66876

```
1          11         21         31         41         51
|          |          |          |          |          |
MKMVAPWTRF YSNSCCLCCH VRTGTILLGV WYLIINAVVL LILLSALADP DQYNFSSSEL    60
GGDFEFMDDA NMCIAIAISL LMILICAMAT YGAYKQRAAW IIPFFCYQIF DFALNMLVAI   120
TVLIYPNSIQ EYIRQLPPNF PYRDDVMSVN PTCLVLIILL FISIILTFKG YLISCVWNCY   180
RYINGRNSSD VLVYVTSNDT TVLLPPYDDA TVNGAAKEPP PPYVSA
```

Seq ID NO: 382 DNA sequence
Nucleic Acid Accession #: NM_002510
Coding sequence: 92-1774

```
1          11         21         31         41         51
|          |          |          |          |          |
CAGATGCCAG AAGAACACTG TTGCTCTTGG TGGACGGGCC CAGAGGAATT CAGAGTTAAA    60
CCTTGAGTGC CTGCGTCCGT GAGAATTCAG CATGGAATGT CTCTACTATT TCCTGGGATT   120
TCTGCTCCTG GCTGCAAGAT TGCCACTTGA TGCCGCCAAA CGATTTCATG ATGTGCTGGG   180
CAATGAAAGA CCTTCTGCTT ACATGAGGGA GCACAATCAA TTAAATGGCT GGTCTTCTGA   240
TGAAAATGAC TGGAATGAAA AACTCTACCC AGTGTGGAAG CGGGGAGACA TGAGGTGGAA   300
AAACTCCTGG AAGGGAGGCC GTGTGCAGGC GGTCCTGACC AGTGACTCAC CAGCCCTCGT   360
```

```
GGGCTCAAAT ATAACATTTG CGGTGAACCT GATATTCCCT AGATGCCAAA AGGAAGATGC   420
CAATGGCAAC ATAGTCTATG AGAAGAACTG CAGAAATGAG GCTGGTTTAT CTGCTGATCC   480
ATATGTTTAC AACTGGACAG CATGGTCAGA GGACAGTGAC GGGGAAAATG GCACCGGCCA   540
AAGCCATCAT AACGTCTTCC CTGATGGGAA ACCTTTTCCT CACCACCCCG GATGGAGAAG   600
ATGGAATTTC ATCTACGTCT TCCACACACT TGGTCAGTAT TTCCAGAAAT TGGGACGATG   660
TTCAGTGAGA GTTTCTGTGA ACACAGCCAA TGTGACACTT GGGCCTCAAC TCATGGAAGT   720
GACTGTCTAC AGAAGACATG GACGGGCATA TGTTCCCATC GCACAAGTGA AAGATGTGTA   780
CGTGGTAACA GATCAGATTC CTGTGTTTGT GACTATGTTC CAGAAGAACG ATCGAAATTC   840
ATCCGACGAA ACCTTCCTCA AAGATCTCCC CATTATGTTT GATGTCCTGA TTCATGATCC   900
TAGCCACTTC CTCAATTATT CTACCATTAA CTACAAGTGG AGCTTCGGGG ATAATACTGG   960
CCTGTTTGTT TCCACCAATC ATACTGTGAA TCACACGTAT GTGCTCAATG GAACCTTCAG  1020
CCTTAACCTC ACTGTGAAAG CTGCAGCACC AGGACCTTGT CCGCCACCGC CACCACCACC  1080
CAGACCTTCA AAACCCACCC CTTCTTTAGG ACCTGCTGGT GACAACCCCC TGGAGCTGAG  1140
TAGGATTCCT GATGAAAACT GCCAGATTAA CAGATATGGC CACTTTCAAG CCACCATCAC  1200
AATTGTAGAG GGAATCTTAG AGGTTAACAT CATCCAGATG ACAGACGTCC TGATGCCGGT  1260
GCCATGGCCT GAAAGCTCCC TAATAGACTT TGTCGTGACC TGCCAAGGGA GCATTCCCAC  1320
GGAGGTCTGT ACCATCATTT CTGACCCCAC CTGCGAGATC ACCCAGAACA CAGTCTGCAG  1380
CCCTGTGGAT GTGGATGAGA TGTGTCTGCT GACTGTGAGA CGAACCTTCA ATGGGTCTGG  1440
GACGTACTGT GTGAACCTCA CCCTGGGGGA TGACACAAGC CTGGCTCTCA CGAGCACCCT  1500
GATTTCTGTT CCTGACAGAG ACCCAGCCTC GCCTTTAAGG ATGGCAAACA GTGCCCTGAT  1560
CTCCGTTGGC TGCTTGGCCA TATTTGTCAC TGTGATCTCC CTCTTGGTGT ACAAAAAACA  1620
CAAGGAATAC AACCCAATAG AAAATAGTCC TGGGAATGTG GTCAGAAGCA AAGGCCTGAG  1680
TGTCTTTCTC AACCGTGCAA AAGCCGTGTT CTTCCCGGGA AACCAGGAAA AGGATCCGCT  1740
ACTCAAAAAC CAAGAATTTA AAGGAGTTTC TTAAATTTCG ACCTTGTTTC TGAAGCTCAC  1800
TTTTCAGTGC CATTGATGTG AGATGTGCTG GAGTGGCTAT TAACCTTTTT TTCCTAAAGA  1860
TTATTGTTAA ATAGATATTG TGGTTTGGGG AAGTTGAATT TTTTATAGGT TAAATGTCAT  1920
TTTAGAGATG GGGAGAGGGA TTATACTGCA GGCAGCTTCA GCCATGTTGT GAAACTGATA  1980
AAAGCAACTT AGCAAGGCTT CTTTTCATTA TTTTTTATGT TTCACTTATA AAGTCTTAGG  2040
TAACTAGTAG GATAGAAACA CTGTGTCCCG AGAGTAAGGA GAGAAGCTAC TATTGATTAG  2100
AGCCTAACCC AGGTTAACTG CAAGAAGAGG CGGGATACTT TCAGCTTTCC ATGTAACTGT  2160
ATGCATAAAG CCAATGTAGT CCAGTTTCTA AGATCATGTT CCAAGCTAAC TGAATCCCAC  2220
TTCAATACAC ACTCATGAAC TCCTGATGGA ACAATAACAG GCCCAAGCCT GTGGTATGAT  2280
GTGCACACTT GCTAGACTCA GAAAAAATAC TACTCTCATA AATGGGTGGG AGTATTTTGG  2340
TGACAACCTA CTTTGCTTGG CTGAGTGAAG GAATGATATT CATATATTCA TTTATTCCAT  2400
GGACATTTAG TTAGTGCTTT TTATATACCA GGCATGATGC TGAGTGACAC TCTTGTGTAT  2460
ATTTCCAAAT TTTTGTATAG TCGCTGCACA TATTTGAAAT CATATATTAA GACTTTCCAA  2520
AGATGAGGTC CCTGGTTTTT CATGGCAACT TGATCAGTAA GGATTTCACC TCTGTTTGTA  2580
ACTAAAACCA TCTACTATAT GTTAGACATG ACATTCTTTT TCTCTCCTTC CTGAAAAATA  2640
AAGTGTGGGA AGAGACAAAA AAAAAAAAA
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Seq ID NO: 383 Protein sequence
Protein Accession #: NP_002501

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1          11         21         31         41         51
|          |          |          |          |          |
MECLYYFLGF LLLAARLPLD AAKRFHDVLG NERPSAYMRE HNQLNGWSSD ENDWNEKLYP    60
VWKRGDMRWK NSWKGGRVQA VLTSDSPALV GSNITFAVNL IFPRCQKEDA NGNIVYEKNC   120
RNEAGLSADP YVYNWTAWSE DSDGENGTGQ SHHNVFPDGK PFPHHPGWRR WNFIYVFHTL   180
GQYFQKLGRC SVRVSVNTAN VTLGPQLMEV TVYRRHGRAY VPIAQVKDVY VVTDQIPVFV   240
TMFQKNDRNS SDETFLKDLP IMFDVLIHDP SHFLNYSTIN YKWSFGDNTG LFVSTNHTVN   300
HTYVLNGTFS LNLTVKAAAP GPCPPPPPPP RPSKPTPSLG PAGDNPLELS RIPDENCQIN   360
RYGHFQATIT IVEGILEVNI IQMTDVLMPV PWPESSLIDF VVTCQGSIPT EVCTIISDPT   420
CEITQNTVCS PVDVDEMCLL TVRRTFNGSG TYCVNLTLGD DTSLALTSTL ISVPDRDPAS   480
PLRMANSALI SVGCLAIFVT VISLLVYKKH KEYNPIENSP GNVVRSKGLS VFLNRAKAVF   540
FPGNQEKDPL LKNQEFKGVS
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Seq ID NO: 384 DNA sequence
Nucleic Acid Accession #: NM_001134
Coding sequence: 48-1877

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1          11         21         31         41         51
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TCCATATTGT GCTTCCACCA CTGCCAATAA CAAAATAACT AGCAACCATG AAGTGGGTGG    60
AATCAATTTT TTTAATTTTC CTACTAAATT TTACTGAATC CAGAACACTG CATAGAAATG   120
AATATGGAAT AGCTTCCATA TTGGATTCTT ACCAATGTAC TGCAGAGATA AGTTTAGCTG   180
ACCTGGCTAC CATATTTTTT GCCCAGTTTG TTCAAGAAGC CACTTACAAG GAAGTAAGCA   240
AAATGGTGAA AGATGCATTG ACTGCAATTG AGAAACCCAC TGGAGATGAA CAGTCTTCAG   300
GGTGTTTAGA AAACCAGCTA CCTGCCTTTC TGGAAGAACT TTGCCATGAG AAAGAAATTT   360
TGGAGAAGTA CGGACATTCA GACTGCTGCA GCCAAAGTGA AGAGGGAAGA CATAACTGTT   420
TTCTTGCACA CAAAAAGCCC ACTCCAGCAT CGATCCCACT TTTCCAAGTT CCAGAACCTG   480
TCACAAGCTG TGAAGCATAT GAAGAAGACA GGGAGACATT CATGAACAAA TTCATTTATG   540
AGATAGCAAG AAGGCATCCC TTCCTGTATG CACCTACAAT TCTTCTTTGG GCTGCTCGCT   600
ATGACAAAAT AATTCCATCT TGCTGCAAAG CTGAAAATGC AGTTGAATGC TTCCAAACAA   660
AGGCAGCAAC AGTTACAAAA GAATTAAGAG AAAGCAGCTT GTTAAATCAA CATGCATGTG   720
CAGTAATGAA AAATTTTGGG ACCCGAACTT TCCAAGCCAT AACTGTTACT AAACTGAGTC   780
AGAAGTTTAC CAAAGTTAAT TTTACTGAAA TCCAGAAACT AGTCCTGGAT GTGGCCCATG   840
TACATGAGCA CTGTTGCAGA GGAGATGTGC TGGATTGTCT GCAGGATGGG GAAAAAATCA   900
TGTCCTACAT ATGTTCTCAA CAAGACACTC TGTCAAACAA AATAACAGAA TGCTGCAAAC   960
TGACCACGCT GGAACGTGGT CAATGTATAA TTCATGCAGA AAATGATGAA AAACCTGAAG  1020
GTCTATCTCC AAATCTAAAC AGGTTTTTAG GAGATAGAGA TTTTAACCAA TTTTCTTCAG  1080
GGGAAAAAAA TATCTTCTTG GCAAGTTTTG TTCATGAATA TTCAAGAAGA CATCCTCAGC  1140
TTGCTGTCTC AGTAATTCTA AGAGTTGCTA AAGGATACCA GGAGTTATTG GAGAAGTGTT  1200
TCCAGACTGA AAACCCTCTT GAATGCCAAG ATAAAGGAGA AGAAGAATTA CAGAAATACA  1260
TCCAGGAGAG CCAAGCATTG GCAAAGCGAA GCTGCGGCCT CTTCCAGAAA CTAGGAGAAT  1320
ATTACTTACA AAATGCGTTT CTCGTTGCTT ACACAAAGAA AGCCCCCCAG CTGACCTCGT  1380
CGGAGCTGAT GGCCATCACC AGAAAAATGG CAGCCACAGC AGCCACTTGT TGCCAACTCA  1440
GTGAGGACAA ACTATTGGCC TGTGGCGAGG GAGCGGCTGA CATTATTATC GGACACTTAT  1500
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GTATCAGACA TGAAATGACT CCAGTAAACC CTGGTGTTGG CCAGTGCTGC ACTTCTTCAT  1560
ATGCCAACAG GAGGCCATGC TTCAGCAGCT TGGTGGTGGA TGAAACATAT GTCCCTCCTG  1620
CATTCTCTGA TGACAAGTTC ATTTTCCATA AGGATCTGTG CCAAGCTCAG GGTGTAGCGC  1680
TGCAAACGAT GAAGCAAGAG TTTCTCATTA ACCTTGTGAA GCAAAAGCCA CAAATAACAG  1740
AGGAACAACT TGAGGCTGTC ATTGCAGATT TCTCAGGCCT GTTGGAGAAA TGCTGCCAAG  1800
GCCAGGAACA GGAAGTCTGC TTTGCTGAAG AGGGACAAAA ACTGATTTCA AAAACTCGTG  1860
CTGCTTTGGG AGTTTAAATT ACTTCAGGGG AAGAGAAGAC AAAACGAGTC TTTCATTCGG  1920
TGTGAACTTT TCTCTTTAAT TTTAACTGAT TTAACACTTT TTGTGAATTA ATGAAATGAT  1980
AAAGACTTTT ATGTGAGATT TCCTTATCAC AGAAATAAAA TATCTCCAAA TG
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Seq ID NO: 385 Protein sequence
Protein Accession #: NP_001125

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1          11         21         31         41         51
|          |          |          |          |          |
MKWVESIFLI FLLNFTESRT LHRNEYGIAS ILDSYQCTAE ISLADLATIF FAQFVQEATY    60
KEVSKMVKDA LTAIEKPTGD EQSSGCLENQ LPAFLEELCH EKEILEKYGH SDCCSQSEEG   120
RHNCFLAHKK PTPASIPLFQ VPEPVTSCEA YEEDRETFMN KFIYEIARRH PFLYAPTILL   180
WAARYDKIIP SCCKAENAVE CFQTKAATVT KELRESSLLN QHACAVMKNF GTRTFQAITV   240
TKLSQKFTKV NFTEIQKLVL DVAHVHEHCC RGDVLDCLQD GEKIMSYICS QQDTLSNKIT   300
ECCKLTTLER GQCIIHAEND EKPEGLSPNL NRFLGDRDFN QFSSGEKNIF LASFVHEYSR   360
RHPQLAVSVI LRVAKGYQEL LEKCFQTENP LECQDKGEEE LQKYIQESQA LAKRSCGLFQ   420
KLGEYYLQNA FLVAYTKKAP QLTSSELMAI TRKMAATAAT CCQLSEDKLL ACGEGAADII   480
IGHLCIRHEM TPVNPGVGQC CTSSYANRRP CFSSLVVDET YVPPAFSDDK FIFHKDLCQA   540
QGVALQTMKQ EFLINLVKQK PQITEEQLEA VIADFSGLLE KCCQGQEQEV CFAEEGQKLI   600
SKTRAALGV
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Seq ID NO: 386 DNA sequence
Nucleic Acid Accession #: NM_002205.1
Coding sequence: 1..3149

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1          11         21         31         41         51
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ATGGGGAGCC GGACGCCAGA GTCCCCTCTC CACGCCGTGC AGCTGCGCTG GGGCCCCCGG    60
CGCCGACCCC CGCTSSTGCC GCTGCTGTTG CTGCTSSTGC CGCCGCCACC CAGGGTCGGG   120
GGCTTCAACT TAGACGCGGA GGCCCCAGCA GTACTCTCGG GGCCCCCGGG CTCCTTCTTC   180
GGATTCTCAG TGGAGTTTTA CCGGCCGGGA ACAGACGGGG TCAGTGTGCT GGTGGGAGCA   240
CCCAAGGCTA ATACCAGCCA GCCAGGAGTG CTGCAGGGTG GTGCTGTCTA CCTCTGTCCT   300
TGGGGTGCCA GCCCCACACA GTGCACCCCC ATTGAATTTG ACAGCAAAGG CTCTCGGCTC   360
CTGGAGTCCT CACTGTCCAG CTCAGAGGGA GAGGAGCCTG TGGAGTACAA GTCCTTGCAG   420
TGGTTCGGGG CAACAGTTCG AGCCCATGGC TCCTCCATCT TGGCATGCGC TCCACTGTAC   480
AGCTGGCGCA CAGAGAAGGA GCCACTGAGC GACCCCGTGG GCACCTGCTA CCTCTCCACA   540
GATAACTTCA CCCGAATTCT GGAGTATGCA CCCTGCCGCT CAGATTTCAG CTGGGCAGCA   600
GGACAGGGTT ACTGCCAAGG AGGCTTCAGT GCCGAGTTCA CCAAGACTGG CCGTGTGGTT   660
TTAGGTGGAC CAGGAAGCTA TTTCTGGCAA GGCCAGATCC TGTCTGCCAC TCAGGAGCAG   720
ATTGCAGAAT CTTATTACCC CGAGTACCTG ATCAACCTGG TTCAGGGGCA GCTGCAGACT   780
CGCCAGGCCA GTTCCATCTA TGATGACAGC TACCTAGGAT ACTCTGTGGC TGTTGGTGAA   840
TTCAGTGGTG ATGACACAGA AGACTTTGTT GCTGGTGTGC CCAAAGGGAA CCTCACTTAC   900
GGCTATGTCA CCATCCTTAA TGGCTCAGAC ATTCGATCCC TCTACAACTT CTCAGGGGAA   960
CAGATGGCCT CCTACTTTGG CTATGCAGTG GCCGCCACAG ACGTCAATGG GGACGGGCTG  1020
GATGACTTGC TGGTGGGGGC ACCCCTGCTC ATGGATCGGA CCCCTGACGG GCGGCCTCAG  1080
GAGGTGGGCA GGGTCTACGT CTACCTGCAG CACCCAGCCG GCATAGAGCC CACGCCCACC  1140
CTTACCCTCA CTGGCCATGA TGAGTTTGGC CGATTTGGCA GCTCCTTGAC CCCCCTGGGG  1200
GACCTGGACC AGGATGGCTA CAATGATGTG GCCATCGGGG CTCCCTTTGG TGGGGAGACC  1260
CAGCAGGGAG TAGTGTTTGT ATTTCCTGGG GGCCCAGGAG GGCTGGGCTC TAAGCCTTCC  1320
CAGGTTCTGC AGCCCCTGTG GGCAGCCAGC CACACCCCAG ACTTCTTTGG CTCTGCCCTT  1380
CGAGGAGGCC GAGACCTGGA TGGCAATGGA TATCCTGATC TGATTGTGGG GTCCTTTGGT  1440
GTGGACAAGG CTGTGGTATA CAGGGGCCGC CCCATCGTGT CCGCTAGTGC CTCCCTCACC  1500
ATCTTCCCCG CCATGTTCAA CCCAGAGGAG CGGAGCTGCA GCTTAGAGGG GAACCCTGTG  1560
GCCTGCATCA ACCTTAGCTT CTGCCTCAAT GCTTCTGGAA AACACGTTGC TGACTCCATT  1620
GGTTTCACAG TGGAACTTCA GCTGGACTGG CAGAAGCAGA AGGGAGGGGT ACGGCGGGCA  1680
CTGTTCCTGG CCTCCAGGCA GGCAACCCTG ACCCAGACCC TGCTCATCCA GAATGGGGCT  1740
CGAGAGGATT GCAGAGAGAT GAAGATCTAC CTCAGGAACG AGTCAGAATT TCGAGACAAA  1800
CTCTCGCCGA TTCACATCGC TCTCAACTTC TCCTTGGACC CCCAAGCCCC AGTGGACAGC  1860
CACGGCCTCA GGCCAGCCCT ACATTATCAG AGCAAGAGCC GGATAGAGGA CAAGGCTCAG  1920
ATCTTGCTGG ACTGTGGAGA AGACAACATC TGTGTGCCTG ACCTGCAGCT GGAAGTGTTT  1980
GGGGAGCAGA ACCATGTGTA CCTGGGTGAC AAGAATGCCC TGAACCTCAC TTTCCATGCC  2040
CAGAATGTGG GTGAGGGTGG CGCCTATGAG GCTGAGCTTC GGGTCACCGC CCCTCCAGAG  2100
GCTGAGTACT CAGGACTCGT CAGACACCCA GGGAACTTCT CCAGCCTGAG CTGTGACTAC  2160
TTTGCCGTGA ACCAGAGCCG CCTGCTGGTG TGTGACCTGG GCAACCCCAT GAAGGCAGGA  2220
GCCAGTCTGT GGGGTGGCCT TCGGTTTACA GTCCCTCATC TCCGGGACAC TAAGAAAACC  2280
ATCCAGTTTG ACTTCCAGAT CCTCAGCAAG AATCTCAACA ACTCGCAAAG CGACGTGGTT  2340
TCCTTTCGGC TCTCCGTGGA GGCTCAGGCC CAGGTCACCC TGAACGGTGT CTCCAAGCCT  2400
GAGGCAGTGC TATTCCCAGT AAGCGACTGG CATCCCCGAG ACCAGCCTCA GAAGGAGGAG  2460
GACCTGGGAC CTGCTGTCCA CCATGTCTAT GAGCTCATCA ACCAAGGCCC CAGCTCCATT  2520
AGCCAGGGTG TGCTGGAACT CAGCTGTCCC CAGGCTCTGG AAGGTCAGCA GCTCCTATAT  2580
GTGACCAGAG TTACGGGACT CAACTGCACC ACCAATCACC CCATTAACCC AAAGGGCCTG  2640
GAGTTGGATC CCGAGGGTTC CCTGCACCAC CAGCAAAAAC GGGAAGCTCC AAGCCGCAGC  2700
TCTGCTTCCT CGGGACCTCA GATCCTGAAA TGCCCGGAGG CTGAGTGTTT CAGGCTGCGC  2760
TGTGAGCTCG GGCCCCTGCA CCAACAAGAG AGCCAAAGTC TGCAGTTGCA TTTCCGAGTC  2820
TGGGCCAAGA CTTTCTTGCA GCGGGAGCAC CAGCCATTTA GCCTGCAGTG TGAGGCTGTG  2880
TACAAAGCCC TGAAGATGCC CTACCGAATC CTGCCTCGGC AGCTGCCCCA AAAAGAGCGT  2940
CAGGTGGCCA CAGCTGTGCA ATGGACCAAG GCAGAAGGCA GCTATGGCGT CCCACTGTGG  3000
ATCATCATCC TAGCCATCCT GTTTGGCCTC CTGCTCCTAG GTCTACTCAT CTACATCCTC  3060
TACAAGCTTG GATTCTTCAA ACGCTCCCTC CCATATGGCA CCGCCATGGA AAAAGCTCAG  3120
CTCAAGCCTC CAGCCACCTC TGATGCCTGA
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Seq ID NO: 387 Protein sequence
Protein Accession #: NP_002196.1

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1          11         21         31         41         51
|          |          |          |          |          |
MGSRTPESPL HAVQLRWGPR RRPPLLPLLL LLLPPPPRVG GFNLDAEAPA VLSGPPGSFF    60
GFSVEFYRPG TDGVSVLVGA PKANTSQPGV LQGGAVYLCP WGASPTQCTP IEFDSKGSRL   120
LESSLSSSEG EEPVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DPVGTCYLST   180
DNFTRILEYA PCRSDFSWAA GQGYCQGGPS AEFTKTGRVV LGGPGSYFWQ GQILSATQEQ   240
IAESYYPEYL INLVQGQLQT RQASSIYDDS YLGYSVAVGE FSGDDTEDFV AGVPKGNLTY   300
GYVTILNGSD IRSLYNFSGE QMASYFGYAV AATDVNGDGL DDLLVGAPLL MDRTPDGRPQ   360
EVGRVYVYLQ HPAGIEPTPT LTLTGHDEFG RFGSSLTPLG DLDQDGYNDV AIGAPFGGET   420
QQGVVFVFPG GPGGLGSKPS QVLQPLWAAS HTPDFFGSAL RGGRDLDGNG YPDLIVGSFG   480
VDKAVVYRGR PIVSASASLT IFPAMFNPEE RSCSLEGNPV ACINLSFCLN ASGKHVADSI   540
GFTVELQLDW QKQKGGVRRA LFLASRQATL TQTLLIQNGA REDCREMKIY LRNESEFRDK   600
LSPIHIALNF SLDPQAPVDS HGLRPALHYQ SKSRIEDKAQ ILLDCGEDNI CVPDLQLEVF   660
GEQNHVYLGD KNALNLTFHA QNVGEGGAYE AELRVTAPPE AEYSGLVRHP GNFSSLSCDY   720
FAVNQSRLLV CDLGNPMKAG ASLWGGLRFT VPHLRDTKKT IQFDFQILSK NLNNSQSDVV   780
SFRLSVEAQA QVTLNGVSKP EAVLFPVSDW HPRDQPQKEE DLGPAVHHVY ELINQGPSSI   840
SQGVLELSCP QALEGQQLLY VTRVTGLNCT TNHPINPKGL ELDPEGSLHH QQKREAPSRS   900
SASSGPQILK CPEAECFRLR CELGPLHQQE SQSLQLHFRV WAKTFLQREH QPFSLQCEAV   960
YKALKMPYRI LPRQLPQKER QVATAVQWTK AEGSYGVPLW IIILAILFGL LLLGLLIYIL  1020
YKLGFFKRSL PYGTAMEKAQ LKPPATSDA
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Seq ID NO: 388 DNA sequence
Nucleic Acid Accession #: NM_002425
Coding sequence: 26..1453

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1          11         21         31         41         51
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AAAGAAGGTA AGGGCAGTGA GAATGATGCA TCTTGCATTC CTTGTGCTGT TGTGTCTGCC    60
AGTCTGCTCT GCCTATCCTC TGAGTGGGGC AGCAAAAGAG GAGGACTCCA ACAAGGATCT   120
TGCCCAGCAA TACCTAGAAA AGTACTACAA CCTCGAAAAG GATGTGAAAC AGTTTAGAAG   180
AAAGGACAGT AATCTCATTG TTAAAAAAAT CCAAGGAATG CAGAAGTTCC TTGGGTTGGA   240
GGTGACAGGG AAGCTAGACA CTGACACTCT GGAGGTGATG CGCAAGCCCA GGTGTGGAGT   300
TCCTGACGTT GGTCACTTCA GCTCCTTTCC TGGCATGCCG AAGTGGAGGA AAACCCACCT   360
TACATACAGG ATTGTGAATT ATACACCAGA TTTGCCAAGA GATGCTGTTG ATTCTGCCAT   420
TGAGAAAGCT CTGAAAGTCT GGGAAGAGGT GACTCCACTC ACATTCTCCA GGCTGTATGA   480
AGGAGAGGCT GATATAATGA TCTCTTTCGC AGTTAAAGAA CATGGAGACT TTTACTCTTT   540
TGATGGCCCA GGACACAGTT TGGCTCATGC CTACCCACCT GGACCTGGGC TTTATGGAGA   600
TATTCACTTT GATGATGATG AAAAATGGAC AGAAGATGCA TCAGGCACCA ATTTATTCCT   660
CGTTGCTGCT CATGAACTTG GCCACTCCCT GGGGCTCTTT CACTCAGCCA ACACTGAAGC   720
TTTGATGTAC CCACTCTACA ACTCATTCAC AGAGCTCGCC CAGTTCCGCC TTTCGCAAGA   780
TGATGTGAAT GGCATTCAGT CTCTCTACGG ACCTCCCCCT GCCTCTACTG AGGAACCCCT   840
GGTGCCCACA AAATCTGTTC CTTCGGGATC TGAGATGCCA GCCAAGTGTG ATCCTGCTTT   900
GTCCTTCGAT GCCATCAGCA CTCTGAGGGG AGAATATCTG TTCTTTAAAG ACAGATATTT   960
TTGGCGAAGA TCCCACTGGA ACCCTGAACC TGAATTTCAT TTGATTTCTG CATTTTGGCC  1020
CTCTCTTCCA TCATATTTGG ATGCTGCATA TGAAGTTAAC AGCAGGGACA CCGTTTTTAT  1080
TTTTAAAGGA AATGAGTTCT GGGCCATCAG AGGAAATGAG GTACAAGCAG GTTATCCAAG  1140
AGGCATCCAT ACCCTGGGTT TTCCTCCAAC CATAAGGAAA ATTGATGCAG CTGTTTCTGA  1200
CAAGGAAAAG AAGAAAACAT ACTTCTTTGC AGCGGACAAA TACTGGAGAT TTGATGAAAA  1260
TAGCCAGTCC ATGGAGCAAG GCTTCCCTAG ACTAATAGCT GATGACTTTC CAGGAGTTGA  1320
GCCTAAGGTT GATGCTGTAT TACAGGCATT TGGATTTTTC TACTTCTTCA GTGGATCATC  1380
ACAGTTTGAG TTTGACCCCA ATGCCAGGAT GGTGACACAC ATATTAAAGA GTAACAGCTG  1440
GTTACATTGC TAGGCGAGAT AGGGGGAAGA CAGATATGGG TGTTTTTAAT AAATCTAATA  1500
ATTATTCATC TAATGTATTA TGAGCCAAAA TGGTTAATTT TTCCTGCATG TTCTGTGACT  1560
GAAGAAGATG AGCCTTGCAG ATATCTGCAT GTGTCATGAA GAATGTTTCT GGAATTCTTC  1620
ACTTGCTTTT GAATTGCACT GAACAGAATT AAGAAATACT CATGTGCAAT AGGTGAGAGA  1680
ATGTATTTTC ATAGATGTGT TATTACTTCC TCAATAAAAA GTTTTATTTT GGGCCTGTTC  1740
CTT
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Seq ID NO: 389 Protein sequence
Protein Accession #: NP_002416

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1          11         21         31         41         51
|          |          |          |          |          |
MHLAFLVLLC LPVCSAYPLS GAAKEEDSNK DLAQQYLEKY YNLEKDVKQF RRKDSNLIVK    60
KIQGMQKFLG LEVTGKLDTD TLEVMRKPRC GVPDVGHFSS FPGMPKWRKT HLTYRIVNYT   120
PDLPRDAVDS AIEKALKVWE EVTPLTFSRL YEGEADIMIS FAVKEHGDFY SFDGPGHSLA   180
HAYPPGPGLY GDIHFDDDEK WTEDASGTNL FLVAAHELGH SLGLFHSANT EALMYPLYNS   240
FTELAQFRLS QDDVNGIQSL YGPPPASTEE PLVPTKSVPS GSEMPAKCDP ALSFDAISTL   300
RGEYLFFKDR YFWRRSHWNP EPEFHLISAF WPSLPSYLDA AYEVNSRDTV FIFKGNEFWA   360
IRGNEVQAGY PRGIHTLGFP PTIRKIDAAV SDKEKKKTYF FAADKYWRFD ENSQSMEQGF   420
PRLIADDFPG VEPKVDAVLQ AFGFFYFFSG SSQFEFDPNA RMVTHILKSN SWLHC
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Seq ID NO: 390 DNA sequence
Nucleic Acid Accession #: NM_002421.2
Coding sequence: 1..1409

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1          11         21         31         41         51
|          |          |          |          |          |
ATGCACAGCT TTCCTCCACT GCTGCTGCTG CTGTTCTGGG GTGTGGTGTC ACACAGCTTC    60
CCAGCGACTC TAGAAACACA AGAGCAAGAT GTGGACTTAG TCCAGAAATA CCTGGAAAAA   120
TACTACAACC TGAAGAATGA TGGGAGGCAA GTTGAAAAGC GGAGAAATAG TGGCCCAGTG   180
GTTGAAAAAT TGAAGCAAAT GCAGGAATTC TTTGGGCTGA AAGTGACTGG GAAACCAGAT   240
GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCCTGATGT GGCTCAGTTT   300
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GTCCTCACTG AGGGGAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAT   360
TACACGCCAG ATTTGCCAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCAACTC   420
TGGAGTAATG TCACACCTCT GACATTCACC AAGGTCTCTG AGGGTCAAGC AGACATCATG   480
ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGACC TGGAGGAAAT   540
CTTGCTCATG CTTTTCAACC AGGCCCAGGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT   600
GAAAGGTGGA CCAACAATTT CAGAGAGTAC AACTTACATC GTGTTGCGGC TCATGAACTC   660
GGCCATTCTC TTGGACTCTC CCATTCTACT GATATCGGGG CTTTGATGTA CCCTAGCTAC   720
ACCTTCAGTG GTGATGTTCA GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT   780
GGACGTTCCC AAAATCCTGT CCAGCCCATC GGCCCACAAA CCCCAAAAGC ATGTGACAGT   840
AAGCTAACCT TTGATGCTAT AACTACGATT CGGGGAGAAG TGATGTTCTT TAAAGACAGA   900
TTCTACATGC GCACAAATCC CTTCTACCCG GAAGTTGAGC TCAATTTCAT TTCTGTTTTC   960
TGGCCACAAC TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCCGACAG AGATGAAGTC  1020
CGGTTTTTCA AAGGGAATAA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC  1080
CCCAAGGACA TCTACAGCTC CTTTGGCTTC CCTAGAACTG TGAAGCATAT CGATGCTGCT  1140
CTTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTTG CTAACAAATA CTGGAGGTAT  1200
GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTCCT  1260
GGAATTGGCC ACAAAGTTGA TGCAGTTTTC ATGAAAGATG GATTTTTCTA TTTCTTTCAT  1320
GGAACAAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT  1380
AATAGCTGGT TCAACTGCAG GAAAAATTAG
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Seq ID NO: 391 Protein sequence
Protein Accession #: NP_002412.1

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1          11         21         31         41         51
|          |          |          |          |          |
MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV    60
VEKLKQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN   120
YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGQADIM ISFVRGDHRD NSPFDGPGGN   180
LAHAFQPGPG IGGDAHFDED ERWTNNFREY NLHRVAAHEL GHSLGLSHST DIGALMYPSY   240
TFSGDVQLAQ DDIDGIQAIY GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMFFKDR   300
FYMRTNPFYP EVELNFISVF WPQLPNGLEA AYEFADRDEV RFFKGNKYWA VQGQNVLHGY   360
PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFVANKYWRY DEYKRSMDPG YPKMIAHDFP   420
GIGHKVDAVF MKDGFFYFFH GTRQYKFDPK TKRILTLQKA NSWFNCRKN
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Seq ID NO: 392 DNA sequence
Nucleic Acid Accession #: NM_002421.2
Coding sequence: 1..1409

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CCAGCGACTC TAGAAACACA AGAGCAAGAT GTGGACTTAG TCCAGAAATA CCTGGAAAAA   120
TACTACAACC TGAAGAATGA TGGGAGGCAA GTTGAAAAGC GGAGAAATAG TGGCCCAGTG   180
GTTGAAAAAT TGAAGCAAAT GCAGGAATTC TTTGGGCTGA AAGTGACTGG GAAACCAGAT   240
GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCCTGATGT GGCTCAGTTT   300
GTCCTCACTG AGGGGAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAT   360
TACACGCCAG ATTTGCCAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCAACTC   420
TGGAGTAATG TCACACCTCT GACATTCACC AAGGTCTCTG AGGGTCAAGC AGACATCATG   480
ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGACC TGGAGGAAAT   540
CTTGCTCATG CTTTTCAACC AGGCCCAGGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT   600
GAAAGGTGGA CCAACAATTT CAGAGAGTAC AACTTACATC GTGTTGCGGC TCATGCCCTC   660
GGCCATTCTC TTGGACTCTC CCATTCTACT GATATCGGGG CTTTGATGTA CCCTAGCTAC   720
ACCTTCAGTG GTGATGTTCA GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT   780
GGACGTTCCC AAAATCCTGT CCAGCCCATC GGCCCACAAA CCCCAAAAGC ATGTGACAGT   840
AAGCTAACCT TTGATGCTAT AACTACGATT CGGGGAGAAG TGATGTTCTT TAAAGACAGA   900
TTCTACATGC GCACAAATCC CTTCTACCCG GAAGTTGAGC TCAATTTCAT TTCTGTTTTC   960
TGGCCACAAC TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCCGACAG AGATGAAGTC  1020
CGGTTTTTCA AAGGGAATAA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC  1080
CCCAAGGACA TCTACAGCTC CTTTGGCTTC CCTAGAACTG TGAAGCATAT CGATGCTGCT  1140
CTTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTTG CTAACAAATA CTGGAGGTAT  1200
GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTCCT  1260
GGAATTGGCC ACAAAGTTGA TGCAGTTTTC ATGAAAGATG GATTTTTCTA TTTCTTTCAT  1320
GGAACAAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT  1380
AATAGCTGGT TCAACTGCAG GAAAAATTAG
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Seq ID NO: 393 Protein sequence
Protein Accession #: NP_002412.1

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1          11         21         31         41         51
|          |          |          |          |          |
MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV    60
VEKLKQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN   120
YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGQADIM ISFVRGDHRD NSPFDGPGGN   180
LAHAFQPGPG IGGDAHFDED ERWTNNFREY NLHRVAAHAL GHSLGLSHST DIGALMYPSY   240
TFSGDVQLAQ DDIDGIQAIY GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMFFKDR   300
FYMRTNPFYP EVELNFISVF WPQLPNGLEA AYEFADRDEV RFFKGNKYWA VQGQNVLHGY   360
PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFVANKYWRY DEYKRSMDPG YPKMIAHDFP   420
GIGHKVDAVF MKDGFFYFFH GTRQYKFDPK TKRILTLQKA NSWFNCRKN
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Seq ID NO: 394 DNA sequence
Nucleic Acid Accession #: NM_014331.2
Coding sequence: 1..1506

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1          11         21         31         41         51
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ATGGTCAGAA AGCCTGTTGT GTCCACCATC TCCAAAGGAG GTTACCTGCA GGGAAATGTT    60
AACGGGAGGC TGCCTTCCCT GGGCAACAAG GAGCCACCTG GGCAGGAGAA AGTGCAGCTG   120
AAGAGGAAAG TCACTTTACT GAGGGGAGTC TCCATTATCA TTGGCACCAT CATTGGAGCA   180
GGAATCTTCA TCTCTCCTAA GGGCGTGCTC CAGAACACGG GCAGCGTGGG CATGTCTCTG   240
ACCATCTGGA CGGTGTGTGG GGTCCTGTCA CTATTTGGAG CTTTGTCTTA TGCTGAATTG   300
GGAACAACTA TAAAGAAATC TGGAGGTCAT TACACATATA TTTTGGAAGT CTTTGGTCCA   360
TTACCAGCTT TTGTACGAGT CTGGGTGGAA CTCCTCATAA TACGCCCTGC AGCTACTGCT   420
GTGATATCCC TGGCATTTGG ACGCTACATT CTGGAACCAT TTTTTATTCA ATGTGAAATC   480
CCTGAACTTG CGATCAAGCT CATTACAGCT GTGGGCATAA CTGTAGTGAT GGTCCTAAAT   540
AGCATGAGTG TCAGCTGGAG CGCCCGGATC CAGATTTTCT TAACCTTTTG CAAGCTCACA   600
GCAATTCTGA TAATTATAGT CCCTGGAGTT ATGCAGCTAA TTAAAGGTCA AACGCAGAAC   660
TTTAAAGACG CGTTTTCAGG AAGAGATTCA AGTATTACGC GGTTGCCACT GGCTTTTTAT   720
TATGGAATGT ATGCATATGC TGGCTGGTTT TACCTCAACT TTGTTACTGA AGAAGTAGAA   780
AACCCTGAAA AAACCATTCC CCTTGCAATA TGTATATCCA TGGCCATTGT CACCATTGGC   840
TATGTGCTGA CAAATGTGGC CTACTTTACG ACCATTAATG CTGAGGAGCT GCTGCTTTCA   900
AATGCAGTGG CAGTGACCTT TTCTGAGCGG CTACTGGGAA ATTTCTCATT AGCAGTTCCG   960
ATCTTTGTTG CCCTCTCCTG CTTTGGCTCC ATGAACGGTG GTGTGTTTGC TGTCTCCAGG  1020
TTATTCTATG TTGCGTCTCG AGAGGGTCAC CTTCCAGAAA TCCTCTCCAT GATTCATGTC  1080
CGCAAGCACA CTCCTCTACC AGCTGTTATT GTTTTGCACC CTTTGACAAT GATAATGCTC  1140
TTCTCTGGAG ACCTCGACAG TCTTTTGAAT TTCCTCAGTT TTGCCAGGTG GCTTTTTATT  1200
GGGCTGGCAG TTGCTGGGCT GATTTATCTT CGATACAAAT GCCCAGATAT GCATCGTCCT  1260
TTCAAGGTGC CACTGTTCAT CCCAGCTTTG TTTTCCTTCA CATGCCTCTT CATGGTTGCC  1320
CTTTCCCTCT ATTCGGACCC ATTTAGTACA GGGATTGGCT TCGTCATCAC TCTGACTGGA  1380
GTCCCTGCGT ATTATCTCTT TATTATATGG GACAAGAAAC CCAGGTGGTT TAGAATAATG  1440
TCAGAGAAAA TAACCAGAAC ATTACAAATA ATACTGGAAG TTGTACCAGA AGAAGATAAG  1500
TTATGAACTA ATGGACTTGA GATCTTGGCA ATCTGCCCAA GGGGAGACAC AAAATAGGGA  1560
TTTTTACTTC ATTTTCTGAA AGTCTAGAGA ATTACAACTT TGGTGATAAA CAAAAGGAGT  1620
CAGTTATTTT TATTCATATA TTTTAGCATA TTCGAACTAA TTTCTAAGAA ATTTAGTTAT  1680
AACTCTATGT AGTTATAGAA AGTGAATATG CAGTTATTCT ATGAGTCGCA CAATTCTTGA  1740
GTCTCTGATA CCTACCTATT GGGGTTAGGA GAAAAGACTA GACAATTACT ATGTGGTCAT  1800
TCTCTACAAC ATATGTTAGC ACGGCAAAGA ACCTTCAAAT TGAAGACTGA GATTTTTCTG  1860
TATATATGGG TTTTGTAAAG ATGGTTTTAC ACACTACAGA TGTCTATACT GTGAAAAGTG  1920
TTTTCAATTC TGAAAAAAAG CATACATCAT GATTATGGCA AAGAGGAGAG AAAGAAATTT  1980
ATTTTACATT GACATTGCAT TGCTTCCCCT TAGATACCAA TTTAGATAAC AAACACTCAT  2040
GCTTTAATGG ATTATACCCA GAGCACTTTG AACAAAGGTC AGTGGGGATT GTTGAATACA  2100
TTAAAGAAGA GTTTCTAGGG GCTACTGTTT ATGAGACACA TCCAGGAGTT ATGTTTAAGT  2160
AAAAATCCTT GAGAATTTAT TATGTCAGAT GTTTTTTCAT TCATTATCAG GAAGTTTTAG  2220
TTATCTGTCA TTTTTTTTTT TCACATCAGT TTGATCAGGA AAGTGTATAA CACATCTTAG  2280
AGCAAGAGTT AGTTTGGTAT TAAATCCTCA TTAGAACAAC CACCTGTTTC ACTAATAACT  2340
TACCCCTGAT GAGTCTATCT AAACATATGC ATTTTAAGCC TTCAAATTAC ATTATCAACA  2400
TGAGAGAAAT AACCAACAAA GAAGATGTTC AAAATAATAG TCCCATATCT GTAATCATAT  2460
CTACATGCAA TGTTAGTAAT TCTGAAGTTT TTTAAATTTA TGGCTATTTT TACACGATGA  2520
TGAATTTTGA CAGTTTGTGC ATTTTCTTTA TACATTTTAT ATTCTTCTGT TAAAATATCT  2580
CTTCAGATGA AACTGTCCAG ATTAATTAGG AAAAGGCATA TATTAACATA AAAATTGCAA  2640
AAGAAATGTC GCTGTAAATA AGATTTACAA CTGATGTTTC TAGAAAATTT CCACTTCTAT  2700
ATCTAGGCTT TGTCAGTAAT TTCCACACCT TAATTATCAT TCAACTTGCA AAAGAGACAA  2760
CTGATAAGAA GAAAATTGAA ATGAGAATCT GTGGATAAGT GTTTGTGTTC AGAAGATGTT  2820
GTTTTGCCAG TATTAGAAAA TACTGTGAGC CGGGCATGGT GGCTTACATC TGTAATCCCA  2880
GCACTTTGGG AGGCTGAGGG GGTGGATCAC CTGAGGTCGG GAGTTCTAGA CCAGCCTGAC  2940
CAACATGGAG AAACCCCATC TCTACTAAAA ATACAAAATT AGCTGGGCAT GGTGGCACAT  3000
GCTGGTAATC TCAGCTATTG AGGAGGCTGA GGCAGGAGAA TTGCTTGAAC CCGGGAGGCG  3060
GAGGTTGCAG TGAGCCAAGA TTGCACCACT GTACTCCAGC CTGGGTGACA AAGTCAGACT  3120
CCATCTCCAA AAAAAAAAAA AAAA
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Seq ID NO: 395 Protein sequence
Protein Accession #: NP_055146.1

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1          11         21         31         41         51
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MVRKPVVSTI SKGGYLQGNV NGRLPSLGNK EPPGQEKVQL KRKVTLLRGV SIIIGTIIGA    60
GIFISPKGVL QNTGSVGMSL TIWTVCGVLS LFGALSYAEL GTTIKKSGGH YTYILEVFGP   120
LPAFVRVWVE LLIIRPAATA VISLAFGRYI LEPFFIQCEI PELAIKLITA VGITVVMVLN   180
SMSVSWSARI QIFLTFCKLT AILIIIVPGV MQLIKGQTQN FKDAFSGRDS SITRLPLAFY   240
YGMYAYAGWP YLNFVTEEVE NPEKTIPLAI CISMAITIGV YVLTNVAYFT TINAEELLLS   300
NAVAVTFSER LLGNFSLAVP IFVALSCFGS MNGGVFAVSR LFYVASREGH LPEILSMIHV   360
RKHTPLPAVI VLHPLTMIML PSGDLDSLLN FLSFARWLFI GLAVAGLIYL RYKCPDMHRP   420
FKVPLFIPAL FSFTCLFMVA LSLYSDPFST GIGFVITLTG VPAYYLFIIW DKKPRWFRIM   480
SEKITRTLQI ILEVVPEEDK L
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Seq ID NO: 396 DNA sequence
Nucleic Acid Accession #: NM_006528
Coding sequence: 57..764

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1          11         21         31         41         51
|          |          |          |          |          |
GCCGCCAGCG GCTTTCTCGG ACGCCTTGCC CAGCGGGCCG CCCGACCCCC TGCACCATGG    60
ACCCCGCTCG CCCCCTGGGG CTGTCGATTC TGCTGCTTTT CCTGACGGAG GCTGCACTGG   120
GCGATGCTGC TCAGGAGCCA ACAGGAAATA ACGCGGAGAT CTGTCTCCTG CCCCTAGACT   180
ACGGACCCTG CCGGGCCCTA CTTCTCCGTT ACTACTACGA CAGGTACACG CAGAGCTGCC   240
GCCAGTTCCT GTACGGGGGC TGCGAGGGCA ACGCCAACAA TTTCTACACC TGGGAGGCTT   300
GCGACGATGC TTGCTGGAGG ATAGAAAAAG TTCCCAAAGT TTGCCGGCTG CAAGTGAGTG   360
TGGACGACCA GTGTGAGGGG TCCACAGAAA AGTATTTCTT TAATCTAAGT TCCATGACAT   420
GTGAAAAATT CTTTTCCGGT GGGTGTCACC GGAACCGGAT TGAGAACAGG TTTCCAGATG   480
AAGCTACTTG TATGGGCTTC TGCGCACCAA AGAAAATTCC ATCATTTTGC TACAGTCCAA   540
AAGATGAGGG ACTGTGCTCT GCCAATGTGA CTCGCTATTA TTTTAATCCA AGATACAGAA   600
CCTGTGATGC TTTCACCTAT ACTGGCTGTG GAGGGAATGA CAATAACTTT GTTAGCAGGG   660
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AGGATTGCAA ACGTGCATGT GCAAAAGCTT TGAAAAAGAA AAAGAAGATG CCAAAGCTTC   720
GCTTTGCCAG TAGAATCCGG AAAATTCGGA AGAAGCAATT TTAAACATTC TTAATATGTC   780
ATCTTGTTTG TCTTTATGGC TTATTTGCCT TTATGGTTGT ATCTGAAGAA TAATATGACA   840
GCATGAGGAA ACAAATCATT GGTGATTTAT TCACCAGTTT TTATTAATAC AAGTCACTTT   900
TTCAAAAATT TGGATTTTTT TATATATAAC TAGCTGCTAT TCAAATGTGA GTCTACCATT   960
TTTAATTTAT GGTTCAACTG TTTGTGAGAC GAATTCTTGC AATGCATAAG ATATAAAAGC  1020
AAATATGACT CACTCATTTC TTGGGGTCGT ATTCCTGATT TCAGAAGAGG ATCATAACTG  1080
AAACAACATA AGACAATATA ATCATGTGCT TTTAACATAT TTGAGAATAA AAAGGACTAG  1140
CC
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Seq ID NO: 397 Protein sequence
Protein Accession #: NP_006519

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1          11         21         31         41         51
|          |          |          |          |          |
MDPARPLGLS ILLLFLTEAA LGDAAQEPTG NNAEICLLPL DYGPCRALLL RYYYDRYTQS    60
CRQFLYGGCE GNANNFYTWE ACDDACWRIE KVPKVCRLQV SVDDQCEGST EKYFFNLSSM   120
TCEKFFSGGC HRNRIENRFP DEATCMGFCA PKKIPSFCYS PKDEGLCSAN VTRYYFNPRY   180
RTCDAFTYTG CGGNDNNFVS REDCKRACAK ALKKKKKMPK LRFASRIRKI RKKQF
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Seq ID NO: 398 DNA sequence
Nucleic Acid Accession #: NM_001508.1
Coding sequence: 1..1361

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1          11         21         31         41         51
|          |          |          |          |          |
ATGGCTTCAC CCAGCCTCCC GGGCAGTGAC TGCTCCCAAA TCATTGATCA CAGTCATGTC    60
CCCGAGTTTG AGGTGGCCAC CTGGATCAAA ATCACCCTTA TTCTGGTGTA CCTGATCATC   120
TTCGTGATGG GCCTTCTGGG GAACAGCGTC ACCATTCGGG TCACCCAGGT GCTGCAGAAG   180
AAAGGATACT TGCAGAAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTCGGACATC   240
TTGGTGTTCC TCATCGGCAT GCCCATGGAG TTCTACAGCA TCATCTGGAA TCCCCTGACC   300
ACGTCCAGCT ACACCCTGTC CTGCAAGCTG CACACTTTCC TCTTCGAGGC CTGCAGCTAC   360
GCTACGCTGC TGCACGTGCT GACGCTCAGC TTTGAGCGCT ACATCGCCAT CTGTCACCCC   420
TTCAGGTACA AGGCTGTGTC GGGACCTTGC CAGGTGAAGC TGCTGATTGG CTTCGTCTGG   480
GTCACCTCCG CCCTGGTGGC ACTGCCCTTG CTGTTTGCCA TGGGTACTGA GTACCCCCTG   540
GTGAACGTGC CCAGCCACCG GGGTCTCACT TGCAACCGCT CCAGCACCCG CCACCACGAG   600
CAGCCCGAGA CCTCCAATAT GTCCATCTGT ACCAACCTCT CCAGCCGCTG GACCGTGTTC   660
CAGTCCAGCA TCTTCGGCGC CTTCGTGGTC TACCTCGTGG TCCTGCTCTC CGTAGCCTTC   720
ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGGCTCGCT GGCCGGGGGC   780
ACGCGGCCTC CGCAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCGC CAGGAGGCAG   840
ACCATCATCT TCCTGAGGCT GATTGTTGTG ACATTGGCCG TATGCTGGAT GCCCAACCAG   900
ATTCGGAGGA TCATGGCTGC GGCCAAACCC AAGCACGACT GGACGAGGTC CTACTTCCGG   960
GCGTACATGA TCCTCCTCCC CTTCTCGGAG ACGTTTTTCT ACCTCAGCTC GGTCATCAAC  1020
CCGCTCCTGT ACACGGTGTC CTCGCAGCAG TTTCGGCGGG TGTTCGTGCA GGTGCTGTGC  1080
TGCCGCCTGT CGCTGCAGCA CGCCAACCAC GAGAAGCGCC TGCGCGTACA TGCGCACTCC  1140
ACCACCGACA GCGCCCGCTT TGTGCAGCGC CCGTTGCTCT TCGCGTCCCG GCGCCAGTCC  1200
TCTGCAAGGA GAACTGAGAA GATTTTCTTA AGCACTTTTC AGAGCGAGGC CGAGCCCCAG  1260
TCTAAGTCCC AGTCATTGAG TCTCGAGTCA CTAGAGCCCA ACTCAGGCGC GAAACCAGCC  1320
AATTCTGCTG CAGAGAATGG TTTTCAGGAG CATGAAGTTT GA
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Seq ID NO: 399 Protein sequence
Protein Accession #: NP_001499.1

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1          11         21         31         41         51
|          |          |          |          |          |
MASPSLPGSD CSQIIDHSHV PEFEVATWIK ITLILVYLII FVMGLLGNSV TIRVTQVLQK    60
KGYLQKEVTD HMVSLACSDI LVFLIGMPME FYSIIWNPLT TSSYTLSCKL HTFLFEACSY   120
ATLLHVLTLS FERYIAICHP FRYKAVSGPC QVKLLIGFVW VTSALVALPL LFAMGTEYPL   180
VNVPSHRGLT CNRSSTRHHE QPETSNMSIC TNLSSRWTVF QSSIFGAFVV YLVVLLSVAF   240
MCWNMMQVLM KSQKGSLAGG TRPPQLRKSE SEESRTARRQ TIIFLRLIVV TLAVCWMPNQ   300
IRRIMAAAKP KHDWTRSYFR AYMILLPFSE TFFYLSSVIN PLLYTVSSQQ FRRVFVQVLC   360
CRLSLQHANH EKRLRVHAHS TTDSARFVQR PLLFASRRQS SARRTEKIFL STFQSEAEPQ   420
SKSQSLSLES LEPNSGAKPA NSAAENGFQE HEV
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Seq ID NO: 400 DNA sequence
Nucleic Acid Accession #: NM_006475.1
Coding sequence: 28..2538

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1          11         21         31         41         51
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TTGCTGCTTA TTGTTAACCC TATAAACGCC AACAATCATT ATGACAAGAT CTTGGCTCAT   120
AGTCGTATCA GGGGTCGGGA CCAAGGCCCA AATGTCTGTG CCCTTCAACA GATTTTGGGC   180
ACCAAAAAGA AATACTTCAG CACTTGTAAG AACTGGTATA AAAAGTCCAT CTGTGGACAG   240
AAAACGACTG TTTTATATGA ATGTTGCCCT GGTTATATGA GAATGGAAGG AATGAAAGGC   300
TGCCCAGCAG TTTTGCCCAT TGACCATGTT TATGGCACTC TGGGCATCGT GGGAGCCACC   360
ACAACGCAGC GCTATTCTGA CGCCTCAAAA CTGAGGGAGG AGATCGAGGG AAAGGGATCC   420
TTCACTTACT TTGCACCGAG TAATGAGGCT TGGGACAACT TGGATTCTGA TATCCGTAGA   480
GGTTTGGAGA GCAACGTGAA TGTTGAATTA CTGAATGCTT TACATAGTCA CATGATTAAT   540
AAGAGAATGT TGACCAAGGA CTTAAAAAAT GGCATGATTA TTCCTTCAAT GTATAACAAT   600
TTGGGGCTTT TCATTAACCA TTATCCTAAT GGGGTTGTCA CTGTTAATTG TGCTCGAATC   660
ATCCATGGGA ACCAGATTGC AACAAATGGT GTTGTCCATG TCATTGACCG TGTGCTTACA   720
CAAATTGGTA CCTCAATTCA AGACTTCATT GAAGCAGAAG ATGACCTTTC ATCTTTTAGA   780
GCAGCTGCCA TCACATCGGA CATATTGGAG GCCCTTGGAA GAGACGGTCA CTTCACACTC   840
TTTGCTCCCA CCAATGAGGC TTTTGAGAAA CTTCCACGAG GTGTCCTAGA AAGGTTCATG   900
GGAGACAAAG TGGCTTCCGA AGCTCTTATG AAGTACCACA TCTTAAATAC TCTCCAGTGT   960
TCTGAGTCTA TTATGGGAGG AGCAGTCTTT GAGACGCTGG AAGGAAATAC AATTGAGATA  1020
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GGATGTGACG GTGACAGTAT AACAGTAAAT GGAATCAAAA TGGTGAACAA AAAGGATATT  1080
GTGACAAATA ATGGTGTGAT CCATTTGATT GATCAGGTCC TAATTCCTGA TTCTGCCAAA  1140
CAAGTTATTG AGCTGGCTGG AAAACAGCAA ACCACCTTCA CGGATCTTGT GGCCCAATTA  1200
GGCTTGGCAT CTGCTCTGAG GCCAGATGGA GAATACACTT TGCTGGCACC TGTGAATAAT  1260
GCATTTTCTG ATGATACTCT CAGCATGGTT CAGCGCCTCC TTAAATTAAT TCTGCAGAAT  1320
CACATATTGA AAGTAAAAGT TGGCCTTAAT GAGCTTTACA ACGGGCAAAT ACTGGAAACC  1380
ATCGGAGGCA AACAGCTCAG AGTCTTCGTA TATCGTACAG CTGTCTGCAT TGAAAATTCA  1440
TGCATGGAGA AAGGGAGTAA GCAAGGGAGA AACGGTGCGA TTCACATATT CCGCGAGATC  1500
ATCAAGCCAG CAGAGAAATC CCTCCATGAA AAGTTAAAAC AAGATAAGCG CTTTAGCACC  1560
TTCCTCAGCC TACTTGAAGC TGCAGACTTG AAAGAGCTCC TGACACAACC TGGAGACTGG  1620
ACATTATTTG TGCCAACCAA TGATGCTTTT AAGGGAATGA CTAGTGAAGA AAAAGAAATT  1680
CTGATACGGG ACAAAAATGC TCTTCAAAAC ATCATTCTTT ATCACCTGAC ACCAGGAGTT  1740
TTCATTGGAA AAGGATTTGA ACCTGGTGTT ACTAACATTT TAAAGACCAC ACAAGGAAGC  1800
AAAATCTTTC TGAAAGAAGT AAATGATACA CTTCTGGTGA ATGAATTGAA ATCAAAAGAA  1860
TCTGACATCA TGACAACAAA TGGTGTAATT CATGTTGTAG ATAAACTCCT CTATCCAGCA  1920
GACACACCTG TTGGAAATGA TCAACTGCTG GAAATACTTA ATAAATTAAT CAAATACATC  1980
CAAATTAAGT TTGTTCGTGG TAGCACCTTC AAAGAAATCC CCGTGACTGT CTATACAACT  2040
AAAATTATAA CCAAAGTTGT GGAACCAAAA ATTAAAGTGA TTGAAGGCAG TCTTCAGCCT  2100
ATTATCAAAA CTGAAGGACC CACACTAACA AAAGTCAAAA TTGAAGGTGA ACCTGAATTC  2160
AGACTGATTA AAGAAGGTGA AACAATAACT GAAGTGATCC ATGGAGAGCC AATTATTAAA  2220
AAATACACCA AAATCATTGA TGGAGTGCCT GTGGAAATAA CTGAAAAAGA GACACGAGAA  2280
GAACGAATCA TTACAGGTCC TGAAATAAAA TACACTAGGA TTTCTACTGG AGGTGGAGAA  2340
ACAGAAGAAA CTCTGAAGAA ATTGTTACAA GAAGAGGTCA CCAAGGTCAC CAAATTCATT  2400
GAAGGTGGTG ATGGTCATTT ATTTGAAGAT GAAGAAATTA AAAGACTGCT TCAGGGAGAC  2460
ACACCCGTGA GGAAGTTGCA AGCCAACAAA AAAGTTCAAG GTTCTAGAAG ACGATTAAGG  2520
GAAGGTCGTT CTCAGTGAAA ATCCAAAAAC CAGAAAAAAA TGTTTATACA ACCCTAAGTC  2580
AATAACCTGA CCTTAGAAAA TTGTGAGAGC CAAGTTGACT TCAGGAACTG AAACATCAGC  2640
ACAAAGAAGC AATCATCAAA TAATTCTGAA CACAAATTTA ATATTTTTTT TTCTGAATGA  2700
GAAACATGAG GGAAATTGTG GAGTTAGCCT CCTGTGGTAA AGGAATTGAA GAAAATATAA  2760
CACCTTACAC CCTTTTTCAT CTTGACATTA AAAGTTCTGG CTAACTTTGG AATCCATTAG  2820
AGAAAAATCC TTGTCACCAG ATTCATTACA ATTCAAATCG AAGAGTTGTG AACTGTTATC  2880
CCATTGAAAA GACCGAGCCT TGTATGTATG TTATGGATAC ATAAAATGCA CGCAAGCCAT  2940
TATCTCTCCA TGGGAAGCTA AGTTATAAAA ATAGGTGCTT GGTGTACAAA ACTTTTTATA  3000
TCAAAAGGCT TTGCACATTT CTATATGAGT GGGTTTACTG GTAAATTATG TTATTTTTTA  3060
CAACTAATTT TGTACTCTCA GAATGTTTGT CATATGCTTC TTGCAATGCA TATTTTTTAA  3120
TCTCAAACGT TTCAATAAAA CCATTTTTCA GATATAAAGA GAATTACTTC AAATTGAGTA  3180
ATTCAGAAAA ACTCAAGATT TAAGTTAAAA AGTGGTTTGG ACTTGGGAA
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Seq ID NO: 401 Protein sequence
Protein Accession #: NP_006466.1

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1          11         21         31         41         51
|          |          |          |          |          |
MIPFLPMFSL LLLLIVNPIN ANNHYDKILA HSRIRGRDQG PNVCALQQIL GTKKKYFSTC    60
KNWYKKSICG QKTTVLYECC PGYMRMEGMK GCPAVLPIDH VYGTLGIVGA TTTQRYSDAS   120
KLREEIEGKG SFTYFAPSNE AWDNLDSDIR RGLESNVNVE LLNALHSHMI NKRMLTKDLK   180
NGMIIPSMYN NLGLFINHYP NGVVTVNCAR IIHGNQIATN GVVHVIDRVL TQIGTSIQDF   240
IEAEDDLSSF RAAAITSDIL EALGRDGHFT LFAPTNEAFE KLPRGVLERF MGDKVASEAL   300
MKYHILNTLQ CSESIMGGAV FETLEGNTIE IGCDGDSITV NGIKMVNKKD IVTNNGVIHL   360
IDQVLIPDSA KQVIELAGKQ QTTFTDLVAQ LGLASALRPD GEYTLLAPVN NAFSDDTLSM   420
VQRLLKLILQ NHILKVKVGL NELYNGQILE TIGGKQLRVF VYRTAVCIEN SCMEKGSKQG   480
RNGAIHIFRE IIKPAEKSLH EKLKQDKRFS TFLSLLEAAD LKELLTQPGD WTLFVPTNDA   540
FKGMTSEEKE ILIRDKNALQ NIILYHLTPG VFIGKGFEPG VTNILKTTQG SKIFLKEVND   600
TLLVNELKSK ESDIMTTNGV IHVVDKLLYP ADTPVGNDQL LEILNKLIKY IQIKFVRGST   660
FKEIPVTVYT TKIITKVVEP KIKVIEGSLQ PIIKTEGPTL TKVKIEGEPE FRLIKEGETI   720
TEVIHGEPII KKYTKIIDGV PVEITEKETR EERIITGPEI KYTRISTGGG ETEETLKKLL   780
QEEVTKVTKF IEGGDGHLFE DEEIKRLLQG DTPVRKLQAN KKVQGSRRRL REGRSQ
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Seq ID NO: 402 DNA sequence
Nucleic Acid Accession #: NM_002416
Coding sequence: 40..417

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1          11         21         31         41         51
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ATCCAATACA GGAGTGACTT GGAACTCCAT TCTATCACTA TGAAGAAAAG TGGTGTTCTT    60
TTCCTCTTGG GCATCATCTT GCTGGTTCTG ATTGGAGTGC AAGGAACCCC AGTAGTGAGA   120
AAGGGTCGCT GTTCCTGCAT CAGCACCAAC CAAGGGACTA TCCACCTACA ATCCTTGAAA   180
GACCTTAAAC AATTTGCCCC AAGCCCTTCC TGCGAGAAAA TTGAAATCAT TGCTACACTG   240
AAGAATGGAG TTCAAACATG TCTAAACCCA GATTCAGCAG ATGTGAAGGA ACTGATTAAA   300
AAGTGGGAGA AACAGGTCAG CCAAAAGAAA AAGCAAAAGA ATGGGAAAAA ACATCAAAAA   360
AAGAAAGTTC TGAAAGTTCG AAAATCTCAA CGTTCTCGTC AAAAGAAGAC TACATAAGAG   420
ACCACTTCAC CAATAAGTAT TCTGTGTTAA AAATGTTCTA TTTTAATTAT ACCGCTATCA   480
TTCCAAAGGA GGATGGCATA TAATACAAAG GCTTATTAAT TTGACTAGAA AATTTAAAAC   540
ATTACTCTGA AATTGTAACT AAAGTTAGAA AGTTGATTTT AAGAATCCAA ACGTTAAGAA   600
TTGTTAAAGG CTATGATTGT CTTTGTTCTT CTACCACCCA CCAGTTGAAT TTCATCATGC   660
TTAAGGCCAT GATTTTAGCA ATACCCATGT CTACACAGAT GTTCACCCAA CCACATCCCA   720
CTCACAACAG CTGCCTGGAA GAGCAGCCCT AGGCTTCCAC GTACTGCAGC CTCCAGAGAG   780
TATCTGAGGC ACATGTCAGC AAGTCCTAAG CCTGTTAGCA TGCTGGTGAG CCAAGCAGTT   840
TGAAATTGAG CTGGACCTCA CCAAGCTGCT GTGGCCATCA ACCTCTGTAT TTGAATCAGC   900
CTACAGGCCT CACACACAAT GTGTCTGAGA GATTCATGCT GATTGTTATT GGGTATCACC   960
ACTGGAGATC ACCAGTGTGT GGCTTTCAGA GCCTCCTTTC TGGCTTTGGA AGCCATGTGA  1020
TTCCATCTTG CCCGCTCAGG CTGACCACTT TATTTCTTTT TGTTCCCCTT TGCTTCATTC  1080
AAGTCAGCTC TTCTCCATCC TACCACAATG CAGTGCCTTT CTTCTCTCCA GTGCACCTGT  1140
CATATGCTCT GATTTATCTG AGTCAACTCC TTTCTCATCT TGTCCCCAAC ACCCCACAGA  1200
AGTGCTTTCT TCTCCCAATT CATCCTCACT CAGTCCAGCT TAGTTCAAGT CCTGCCTCTT  1260
AAATAAACCT TTTTGGACAC ACAAATTATC TTAAAACTCC TGTTTCACTT GGTTCAGTAC  1320
CACATGGGTG AACACTCAAT GGTTAACTAA TTCTTGGGTG TTTATCCTAT CTCTCCAACC  1380
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AGATTGTCAG CTCCTTGAGG GCAAGAGCCA CAGTATATTT CCCTGTTTCT TCCACAGTGC 1440
CTAATAATAC TGTGGAACTA GGTTTTAATA ATTTTTTAAT TGATGTTGTT ATGGGCAGGA 1500
TGGCAACCAG ACCATTGTCT CAGAGCAGGT GCTGGCTCTT TCCTGGCTAC TCCATGTTGG 1560
CTAGCCTCTG GTAACCTCTT ACTTATTATC TTCAGGACAC TCACTACAGG GACCAGGGAT 1620
GATGCAACAT CCTTGTCTTT TTATGACAGG ATGTTTGCTC AGCTTCTCCA ACAATAAGAA 1680
GCACGTGGTA AAACACTTGC GGATATTCTG GACTGTTTTT AAAAAATATA CAGTTTACCG 1740
AAAATCATAT AATCTTACAA TGAAAAGGAC TTTATAGATC AGCCAGTGAC CAACCTTTTC 1800
CCAACCATAC AAAAATTCCT TTTCCCGAAG GAAAAGGGCT TTCTCAATAA GCCTCAGCTT 1860
TCTAAGATCT AACAAGATAG CCACCGAGAT CCTTATCGAA ACTCATTTTA GGCAAATATG 1920
AGTTTTATTG TCCGTTTACT TGTTTCAGAG TTTGTATTGT GATTATCAAT TACCACACCA 1980
TCTCCCATGA AGAAAGGGAA CGGTGAAGTA CTAAGCGCTA GAGGAAGCAG CCAAGTCGGT 2040
TAGTGGAAGC ATGATTGGTG CCCAGTTAGC CTCTGCAGGA TGTGGAAACC TCCTTCCAGG 2100
GGAGGTTCAG TGAATTGTGT AGGAGAGGTT GTCTGTGGCC AGAATTTAAA CCTATACTCA 2160
CTTTCCCAAA TTGAATCACT GCTCACACTG CTGATGATTT AGAGTGCTGT CCGGTGGAGA 2220
TCCCACCCGA ACGTCTTATC TAATCATGAA ACTCCCTAGT TCCTTCATGT AACTTCCCTG 2280
AAAAATCTAA GTGTTTCATA AATTTGAGAG TCTGTGACCC ACTTACCTTG CATCTCACAG 2340
GTAGACAGTA TATAACTAAC AACCAAAGAC TACATATTGT CACTGACACA CACGTTATAA 2400
TCATTTATCA TATATATACA TACATGCATA CACTCTCAAA GCAAATAATT TTTCACTTCA 2460
AAACAGTATT GACTTGTATA CCTTGTAATT TGAAATATTT TCTTTGTTAA AATAGAATGG 2520
TATCAATAAA TAGACCATTA ATCAG
```

Seq ID NO: 403 Protein sequence
Protein Accession #: NP_002407

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1          11         21         31         41         51
|          |          |          |          |          |
MKKSGVLFLL GIILLVLIGV QGTPVVRKGR CSCISTNQGT IHLQSLKDLK QFAPSPSCEK   60
IEIIATLKNG VQTCLNPDSA DVKELIKKWE KQVSQKKKQK NGKKHQKKKV LKVRKSQRSR  120
QKKTT
```

Seq ID NO: 404 DNA sequence
Nucleic Acid Accession #: NM_006670
Coding sequence: 85..1347

```
1          11         21         31         41         51
|          |          |          |          |          |
CCGGCTCGCG CCCTCCGGGC CCAGCCTCCC GAGCCTTCGG AGCGGGCGCC GTCCCAGCCC   60
AGCTCCGGGG AAACGCGAGC CGCGATGCCT GGGGGGTGCT CCCGGGGCCC CGCCGCCGGG  120
GACGGGCGTC TGCGGCTGGC GCGACTAGCG CTGGTACTCC TGGGCTGGGT CTCCTCGTCT  180
TCTCCCACCT CCTCGGCATC CTCCTTCTCC TCCTCGGCGC CGTTCCTGGC TTCCGCCGTG  240
TCCGCCCAGC CCCCGCTGCC GGACCAGTGC CCCGCGCTGT GCGAGTGCTC CGAGGCAGCG  300
CGCACAGTCA AGTGCGTTAA CCGCAATCTG ACCGAGGTGC CCACGGACCT GCCCGCCTAC  360
GTGCGCAACC TCTTCCTTAC CGGCAACCAG CTGGCCGTGC TCCCTGCCGG CGCCTTCGCC  420
CGCCGGCCGC CGCTGGCGGA GCTGGCCGCG CTCAACCTCA GCGGCAGCCG CCTGGACGAG  480
GTGCGCGCGG GCGCCTTCGA GCATCTGCCC AGCCTGCGCC AGCTCGACCT CAGCCACAAC  540
CCACTGGCCG ACCTCAGTCC CTTCGCTTTC TCGGGCAGCA ATGCCAGCGT CTCGGCCCCC  600
AGTCCCCTTG TGGAACTGAT CCTGAACCAC ATCGTGCCCC CTGAAGATGA GCGGCAGAAC  660
CGGAGCTTCG AGGGCATGGT GGTGGCGGCC CTGCTGGCGG GCCGTGCACT GCAGGGGCTC  720
CGCCGCTTGG AGCTGGCCAG CAACCACTTC CTTTACCTGC CGCGGGATGT GCTGGCCCAA  780
CTGCCCAGCC TCAGGCACCT GGACTTAAGT AATAATTCGC TGGTGAGCCT GACCTACGTG  840
TCCTTCCGCA ACCTGACACA TCTAGAAAGC CTCCACCTGG AGGACAATGC CCTCAAGGTC  900
CTTCACAATG GCACCCTGGC TGAGTTGCAA GGTCTACCCC ACATTAGGGT TTTCCTGGAC  960
AACAATCCCT GGGTCTGCGA CTGCCACATG GCAGACATGG TGACCTGGCT CAAGGAAACA 1020
GAGGTAGTGC AGGGCAAAGA CCGGCTCACC TGTGCATATC CGGAAAAAAT GAGGAATCGG 1080
GTCCTCTTGG AACTCAACAG TGCTGACCTG GACTGTGACC CGATTCTTCC CCCATCCCTG 1140
CAAACCTCTT ATGTCTTCCT GGGTATTGTT TTAGCCCTGA TAGGCGCTAT TTTCCTCCTG 1200
GTTTTGTATT TGAACCGCAA GGGGATAAAA AAGTGGATGC ATAACATCAG AGATGCCTGC 1260
AGGGATCACA TGGAAGGGTA TCATTACAGA TATGAAATCA ATGCGGACCC CAGATTAACA 1320
AACCTCAGTT CTAACTCGGA TGTCTGAGAA ATATTAGAGG ACAGACCAAG GACAACTCTG 1380
CATGAGATGT AGACTTAAGC TTTATCCCTA CTAGGCTTGC TCCACTTTCA TCCTCCACTA 1440
TAGATACAAC GGACTTTGAC TAAAAGCAGT GAAGGGGATT TGCTTCCTTG TTATGTAAAG 1500
TTTCTCGGTG TGTTCTGTTA ATGTAAGACG ATGAACAGTT GTGTATAGTG TTTTACCCTC 1560
TTCTTTTTCT TGGAACTCCT CAACACGTAT GGAGGGATTT TTCAGGTTTC AGCATGAACA 1620
TGGGCTTCTT GCTGTCTGTC TCTCTCTCAG TACAGTTCAA GGTGTAGCAA GTGTACCCAC 1680
ACAGATAGCA TTCAACAAAA GCTGCCTCAA CTTTTTCGAG AAAAATACTT TATTCATAAA 1740
TATCAGTTTT ATTCTCATGT ACCTAAGTTG TGGAGAAAAT AATTGCATCC TATAAACTGC 1800
CTGCAGACGT TAGCAGGCTC TTCAAAATAA CTCCATGGTG CACAGGAGCA CCTGCATCCA 1860
AGAGCATGCT TACATTTTAC TGTTCTGCAT ATTACAAAAA ATAACTTGCA ACTTCATAAC 1920
TTCTTTGACA AAGTAAATTA CTTTTTTGAT TGCAGTTTAT ATGAAAATGT ACTGATTTTT 1980
TTTTAATAAA CTGCATCGAG ATCCAACCGA CTGAATTGTT AAAAAAAAAA AAAAATAAAG 2040
ATTCTTAAAA GAA
```

Seq ID NO: 405 Protein sequence
Protein Accession #: NP_006661

```
1          11         21         31         41         51
|          |          |          |          |          |
MPGGCSRGPA AGDGRLRLAR LALVLLGWVS SSSPTSSASS FSSSAPFLAS AVSAQPPLPD   60
QCPALCECSE AARTVKCVNR NLTEVPTDLP AYVRNLFLTG NQLAVLPAGA FARRPPLAEL  120
AALNLSGSRL DEVRAGAFEH LPSLRQLDLS HNPLADLSPF AFSGSNASVS APSPLVELIL  180
NHIVPPEDER QNRSFEGMVV AALLAGRALQ GLRRLELASN HFLYLPRDVL AQLPSLRHLD  240
LSNNSLVSLT YVSFRNLTHL ESLHLEDNAL KVLHNGTLAE LQGLPHIRVF LDNNPWVCDC  300
HMADMVTWLK ETEVVQGKDR LTCAYPEKMR NRVLLELNSA DLDCDPILPP SLQTSYVFLG  360
IVLALIGAIF LLVLYLNRKG IKKWMHNIRD ACRDHMEGYH YRYEINADPR LTNLSSNSDV
```

Seq ID NO: 406 DNA sequence
Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..927

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGCCTGGGG GGTGCTCCCG GGGCCCCGCC GCCGGGGACG GGCGTCTGCG GCTGGCGCGA     60
CTAGCGCTGG TACTCCTGGG CTGGGTCTCC TCGTCTTCTC CCACCTCCTC GGCATCCTCC    120
TTCTCCTCCT CGGCGCCGTT CCTGGCTTCC GCCGTGTCCG CCCAGCCCCC GCTGCCGGAC    180
CAGTGCCCCG CGCTGTGCGA GTGCTCCGAG GCAGCGCGCA CAGTCAAGTG CGTTAACCGC    240
AATCTGACCG AGGTGCCCAC GGACCTGCCC GCCTACGTGC GCAACCTCTT CCTTACCGGC    300
AACCAGCTGG CCAGCAACCA CTTCCTTTAC CTGCCGCGGG ATGTGCTGGC CCAACTGCCC    360
AGCCTCAGGC ACCTGGACTT AAGTAATAAT TCGCTGGTGA GCCTGACCTA CGTGTCCTTC    420
CGCAACCTGA CACATCTAGA AAGCCTCCAC CTGGAGGACA ATGCCCTCAA GGTCCTTCAC    480
AATGGCACCC TGGCTGAGTT GCAAGGTCTA CCCCACATTA GGGTTTTCCT GGACAACAAT    540
CCCTGGGTCT GCGACTGCCA CATGGCAGAC ATGGTGACCT GGCTCAAGGA AACAGAGGTA    600
GTGCAGGGCA AAGACCGGCT CACCTGTGCA TATCCGGAAA AAATGAGGAA TCGGGTCCTC    660
TTGGAACTCA ACAGTGCTGA CCTGGACTGT GACCCGATTC TTCCCCCATC CCTGCAAACC    720
TCTTATGTCT TCCTGGGTAT TGTTTTAGCC CTGATAGGCG CTATTTTCCT CCTGGTTTTG    780
TATTTGAACC GCAAGGGGAT AAAAAAGTGG ATGCATAACA TCAGAGATGC CTGCAGGGAT    840
CACATGGAAG GGTATCATTA CAGATATGAA ATCAATGCGG ACCCCAGATT AACAAACCTC    900
AGTTCTAACT CGGATGTCCT CGAGTGA
```

Seq ID NO: 407 Protein sequence
Protein Accession #: Eos sequence

```
1          11         21         31         41         51
|          |          |          |          |          |
MPGGCSRGPA AGDGRLRLAR LALVLLGWVS SSSPTSSASS FSSSAPFLAS AVSAQPPLPD     60
QCPALCECSE AARTVKCVNR NLTEVPTDLP AYVRNLFLTG NQLASNHFLY LPRDVLAQLP    120
SLRHLDLSNN SLVSLTYVSF RNLTHLESLH LEDNALKVLH NGTLAELQGL PHIRVFLDNN    180
PWVCDCHMAD MVTWLKETEV VQGKDRLTCA YPEKMRNRVL LELNSADLDC DPILPPSLQT    240
SYVFLGIVLA LIGAIFLLVL YLNRKGIKKW MHNIRDACRD HMEGYHYRYE INADPRLTNL    300
SSNSDVLE
```

Seq ID NO: 408 DNA sequence
Nucleic Acid Accession #: NM_000095.1
Coding sequence: 26..2299

```
1          11         21         31         41         51
|          |          |          |          |          |
CAGCACCCAG CTCCCCGCCA CCGCCATGGT CCCCGACACC GCCTGCGTTC TTCTGCTCAC     60
CCTGGCTGCC CTCGGCGCGT CCGGACAGGG CCAGAGCCCG TTGGGCTCAG ACCTGGGCCC    120
GCAGATGCTT CGGGAACTGC AGGAAACCAA CGCGGCGCTG CAGGACGTGC GGGACTGGCT    180
GCGGCAGCAG GTCAGGGAGA TCACGTTCCT GAAAAACACG GTGATGGAGT GTGACGCGTG    240
CGGGATGCAG CAGTCAGTAC GCACCGGCCT ACCCAGCGTG CGGCCCCTGC TCCACTGCGC    300
GCCCGGCTTC TGCTTCCCCG GCGTGGCCTG CATCCAGACG GAGAGCGGCG GCCGCTGCGG    360
CCCCTGCCCC GCGGGCTTCA CGGGCAACGG CTCGCACTGC ACCGACGTCA ACGAGTGCAA    420
CGCCCACCCC TGCTTCCCCC GAGTCCGCTG TATCAACACC AGCCCGGGGT TCCGCTGCGA    480
GGCTTGCCCG CCGGGGTACA GCGGCCCCAC CCACCAGGGC GTGGGGCTGG CTTTCGCCAA    540
GGCCAACAAG CAGGTTTGCA CGGACATCAA CGAGTGTGAG ACCGGGCAAC ATAACTGCGT    600
CCCCAACTCC GTGTGCATCA ACACCCGGGG CTCCTTCCAG TGCGGCCCGT GCCAGCCCGG    660
CTTCGTGGGC GACCAGGCGT CCGGCTGCCA GCGCGGCGCA CAGCGCTTCT GCCCCGACGG    720
CTCGCCCAGC GAGTGCCACG AGCATGCAGA CTGCGTCCTA GAGCGCGATG GCTCGCGGTC    780
GTGCGTGTGT CGCGTTGGCT GGGCCGGCAA CGGGATCCTC TGTGGTCGCG ACACTGACCT    840
AGACGGCTTC CCGGACGAGA AGCTGCGCTG CCCGGAGCCG CAGTGCCGTA AGGACAACTG    900
CGTGACTGTG CCCAACTCAG GGCAGGAGGA TGTGGACCGC GATGGCATCG GAGACGCCTG    960
CGATCCGGAT GCCGACGGGG ACGGGGTCCC CAATGAAAAG GACAACTGCC CGCTGGTGCG   1020
GAACCCAGAC CAGCGCAACA CGGACGAGGA CAAGTGGGGC GATGCGTGCG ACAACTGCCG   1080
GTCCCAGAAG AACGACGACC AAAAGGACAC AGACCAGGAC GGCCGGGGCG ATGCGTGCGA   1140
CGACGACATC GACGGCGACC GGATCCGCAA CCAGGCCGAC AACTGCCCTA GGGTACCCAA   1200
CTCAGACCAG AAGGACAGTG ATGGCGATGG TATAGGGGAT GCCTGTGACA ACTGTCCCCA   1260
GAAGAGCAAC CCGGATCAGG CGGATGTGGA CCACGACTTT GTGGGAGATG CTTGTGACAG   1320
CGATCAAGAC CAGGATGGAG ACGGACATCA GGACTCTCGG GACAACTGTC CCACGGTGCC   1380
TAACAGTGCC CAGGAGGACT CAGACCACGA TGGCCAGGGT GATGCCTGCG ACGACGACGA   1440
CGACAATGAC GGAGTCCCTG ACAGTCGGGA CAACTGCCGC CTGGTGCCTA ACCCCGGCCA   1500
GGAGGACGCG GACAGGGACG GCGTGGGCGA CGTGTGCCAG GACGACTTTG ATGCAGACAA   1560
GGTGGTAGAC AAGATCGACG TGTGTCCGGA GAACGCTGAA GTCACGCTCA CCGACTTCAG   1620
GGCCTTCCAG ACAGTCGTGC TGGACCCGGA GGGTGACGCG CAGATTGACC CCAACTGGGT   1680
GGTGCTCAAC CAGGGAAGGG AGATCGTGCA GACAATGAAC AGCGACCCAG GCCTGGCTGT   1740
GGGTTACACT GCCTTCAATG GCGTGGACTT CGAGGGCACG TTCCATGTGA ACACGGTCAC   1800
GGATGACGAC TATGCGGGCT TCATCTTTGG CTACCAGGAC AGCTCCAGCT TCTACGTGGT   1860
CATGTGGAAG CAGATGGAGC AAACGTATTG GCAGGCGAAC CCCTTCCGTG CTGTGGCCGA   1920
GCCTGGCATC CAACTCAAGG CTGTGAAGTC TTCCACAGGC CCCGGGGAAC AGCTGCGGAA   1980
CGCTCTGTGG CATACAGGAG ACACAGAGTC CCAGGTGCGG CTGCTGTGGA AGGACCCGCG   2040
AAACGTGGGT TGGAAGGACA AGAAGTCCTA TCGTTGGTTC CTGCAGCACC GGCCCCAAGT   2100
GGGCTACATC AGGGTGCGAT TCTATGAGGG CCCTGAGCTG GTGGCCGACA GCAACGTGGT   2160
CTTGGACACA ACCATGCGGG GTGGCCGCCT GGGGGTCTTC TGCTTCTCCC AGGAGAACAT   2220
CATCTGGGCC AACCTGCGTT ACCGCTGCAA TGACACCATC CCAGAGGACT ATGAGACCCA   2280
TCAGCTGCGG CAAGCCTAGG GACCAGGGTG AGGACCCGCC GGATGACAGC CACCCTCACC   2340
GCGGCTGGAT GGGGGCTCTG CACCCAGCCC AAGGGGTGGC CGTCCTGAGG GGGAAGTGAG   2400
AAGGGCTCAG AGAGGACAAA ATAAAGTGTG TGTGCAGGG
```

Seq ID NO: 409 Protein sequence
Protein Accession #: NP_000086.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MVPDTACVLL LTLAALGASG QGQSPLGSDL GPQMLRELQE TNAALQDVRD WLRQQVREIT     60
```

```
FLKNTVMECD ACGMQQSVRT GLPSVRPLLH CAPGFCFPGV ACIQTESGGR CGPCPAGFTG   120
NGSHCTDVNE CNAHPCFPRV RCINTSPGFR CEACPPGYSG PTHQGVGLAF AKANKQVCTD   180
INECETGQHN CVPNSVCINT RGSFQCGPCQ PGFVGDQASG CQRGAQRFCP DGSPSECHEH   240
ADCVLERDGS RSCVCRVGWA GNGILCGRDT DLDGFPDEKL RCPEPQCRKD NCVTVPNSGQ   300
EDVDRDGIGD ACDPDADGDG VPNEKDNCPL VRNPDQRNTD EDKWGDACDN CRSQKNDDQK   360
DTDQDGRGDA CDDDIDGDRI RNQADNCPRV PNSDQKDSDG DGIGDACDNC PQKSNPDQAD   420
VDHDFVGDAC DSDQDQDGDG HQDSRDNCPT VPNSAQEDSD HDGQGDACDD DDDNDGVPDS   480
RDNCRLVPNP GQEDADRDGV GDVCQDDFDA DKVVDKIDVC PENAEVTLTD FRAFQTVVLD   540
PEGDAQIDPN WVVLNQGREI VQTMNSDPGL AVGYTAFNGV DFEGTFHVNT VTDDDYAGFI   600
FGYQDSSSFY VVMWKQMEQT YWQANPFRAV AEPGIQLKAV KSSTGPGEQL RNALWHTGDT   660
ESQVRLLWKD PRNVGWKDKK SYRWFLQHRP QVGYIRVRFY EGPELVADSN VVLDTTMRGG   720
RLGVFCFSQE NIIWANLRYR CNDTIPEDYE THQLRQA
```

Seq ID NO: 410 DNA sequence
Nucleic Acid Accession #: NM_001565.1
Coding sequence: 67..363

```
1          11         21         31         41         51
|          |          |          |          |          |
GAGACATTCC TCAATTGCTT AGACATATTC TGAGCCTACA GCAGAGGAAC CTCCAGTCTC    60
AGCACCATGA ATCAAACTGC GATTCTGATT TGCTGCCTTA TCTTTCTGAC TCTAAGTGGC   120
ATTCAAGGAG TACCTCTCTC TAGAACCGTA CGCTGTACCT GCATCAGCAT TAGTAATCAA   180
CCTGTTAATC CAAGGTCTTT AGAAAAACTT GAAATTATTC CTGCAAGCCA ATTTTGTCCA   240
CGTGTTGAGA TCATTGCTAC AATGAAAAAG AAGGGTGAGA AGAGATGTCT GAATCCAGAA   300
TCGAAGGCCA TCAAGAATTT ACTGAAAGCA GTTAGCAAGG AAATGTCTAA AAGATCTCCT   360
TAAAACCAGA GGGGAGCAAA ATCGATGCAG TGCTTCCAAG GATGGACCAC ACAGAGGCTG   420
CCTCTCCCAT CACTTCCCTA CATGGAGTAT ATGTCAAGCC ATAATTGTTC TTAGTTTGCA   480
GTTACACTAA AAGGTGACCA ATGATGGTCA CCAAATCAGC TGCTACTACT CCTGTAGGAA   540
GGTTAATGTT CATCATCCTA AGCTATTCAG TAATAACTCT ACCCTGGCAC TATAATGTAA   600
GCTCTACTGA GGTGCTATGT TCTTAGTGGA TGTTCTGACC CTGCTTCAAA TATTTCCCTC   660
ACCTTTCCCA TCTTCCAAGG GTACTAAGGA ATCTTTCTGC TTTGGGGTTT ATCAGAATTC   720
TCAGAATCTC AAATAACTAA AAGGTATGCA ATCAAATCTG CTTTTTAAAG AATGCTCTTT   780
ACTTCATGGA CTTCCACTGC CATCCTCCCA AGGGGCCCAA ATTCTTTCAG TGGCTACCTA   840
CATACAATTC CAAACACATA CAGGAAGGTA GAAATATCTG AAAATGTATG TGTAAGTATT   900
CTTATTTAAT GAAAGACTGT ACAAAGTATA AGTCTTAGAT GTATATATTT CCTATATTGT   960
TTTCAGTGTA CATGGAATAA CATGTAATTA AGTACTATGT ATCAATGAGT AACAGGAAAA  1020
TTTTAAAAAT ACAGATAGAT ATATGCTCTG CATGTTACAT AAGATAAATG TGCTGAATGG  1080
TTTTCAAATA AAAATGAGGT ACTCTCCTGG AAATATTAAG
```

Seq ID NO: 411 Protein sequence
Protein Accession #: NP_001556.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MNQTAILICC LIFLTLSGIQ GVPLSRTVRC TCISISNQPV NPRSLEKLEI IPASQFCPRV    60
EIIATMKKKG EKRCLNPESK AIKNLLKAVS KEMSKRSP
```

Seq ID NO: 412 DNA sequence
Nucleic Acid Accession #: XM_057014
Coding sequence: 143..874

```
1          11         21         31         41         51
|          |          |          |          |          |
GGGAGGGAGA GAGGCGCGCG GGTGAAAGGC GCATTGATGC AGCCTGCGGC GGCCTCGGAG    60
CGCGGCGGAG CCAGACGCTG ACCACGTTCC TCTCCTCGGT CTCCTCCGCC TCCAGCTCCG   120
CGCTGCCCGG CAGCCGGGAG CCATGCGACC CCAGGGCCCC GCCGCCTCCC CGCAGCGGCT   180
CCGCGGCCTC CTGCTGCTCC TGCTGCTGCA GCTGCCCGCG CCGTCGAGCG CCTCTGAGAT   240
CCCCAAGGGG AAGCAAAAGG CGCAGCTCCG GCAGAGGGAG GTGGTGGACC TGTATAATGG   300
AATGTGCTTA CAAGGGCCAG CAGGAGTGCC TGGTCGAGAC GGGAGCCCTG GGGCCAATGG   360
CATTCCGGGT ACACCTGGGA TCCCAGGTCG GGATGGATTC AAAGGAGAAA AGGGGGAATG   420
TCTGAGGGAA AGCTTTGAGG AGTCCTGGAC ACCCAACTAC AAGCAGTGTT CATGGAGTTC   480
ATTGAATTAT GGCATAGATC TTGGGAAAAT TGCGGAGTGT ACATTTACAA AGATGCGTTC   540
AAATAGTGCT CTAAGAGTTT TGTTCAGTGG CTCACTTCGG CTAAAATGCA GAAATGCATG   600
CTGTCAGCGT TGGTATTTCA CATTCAATGG AGCTGAATGT TCAGGACCTC TTCCCATTGA   660
AGCTATAATT TATTTGGACC AAGGAAGCCC TGAAATGAAT TCAACAATTA ATATTCATCG   720
CACTTCTTCT GTGGAAGGAC TTTGTGAAGG AATTGGTGCT GGATTAGTGG ATGTTGCTAT   780
CTGGGTTGGC ACTTGTTCAG ATTACCCAAA AGGAGATGCT TCTACTGGAT GGAATTCAGT   840
TTCTCGCATC ATTATTGAAG AACTACCAAA ATAAATGCTT TAATTTTCAT TTGCTACCTC   900
TTTTTTTATT ATGCCTTGGA ATGGTTCACT TAAATGACAT TTTAAATAAG TTTATGTATA   960
CATCTGAATG AAAAGCAAAG CTAAATATGT TTACAGACCA AAGTGTGATT TCACACTGTT  1020
TTTAAATCTA GCATTATTCA TTTTGCTTCA ATCAAAAGTG GTTTCAATAT TTTTTTTAGT  1080
TGGTTAGAAT ACTTTCTTCA TAGTCACATT CTCTCAACCT ATAATTTGGA ATATTGTTGT  1140
GGTCTTTTGT TTTTTCTCTT AGTATAGCAT TTTTAAAAAA ATATAAAAGC TACCAATCTT  1200
TGTACAATTT GTAAATGTTA AGAATTTTTT TTATATCTGT TAAATAAAAA TTATTTCCAA  1260
CAACCTTAAA AAAAAAAAAA AAAA
```

Seq ID NO: 413 Protein sequence
Protein Accession #: XP_057014

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1          11         21         31         41         51
|          |          |          |          |          |
MRPQGPAASP QRLRGLLLLL LLQLPAPSSA SEIPKGKQKA QLRQREVVDL YNGMCLQGPA    60
GVPGRDGSPG ANGIPGTPGI PGRDGFKGEK GECLRESFEE SWTPNYKQCS WSSLNYGIDL   120
GKIAECTFTK MRSNSALRVL FSGSLRLKCR NACCQRWYFT FNGAECSGPL PIEAIIYLDQ   180
GSPEMNSTIN IHRTSSVEGL CEGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRIIIEE   240
LPK
```

Seq ID NO: 414 DNA sequence
Nucleic Acid Accession #: XM_084007
Coding sequence: 138..2405

```
1          11         21         31         41         51
|          |          |          |          |          |
CTCGTGCCGA ATTCGGCACG AGACCGCGTG TTCGCGCCTG GTAGAGATTT CTCGAAGACA    60
CCAGTGGGCC CGTGTGGAAC CAAACCTGCG CGCGTGGCCG GGCCGTGGGA CAACGAGGCC   120
GCGGAGACGA AGGCGCAATG GCGAGGAAGT TATCTGTAAT CTTGATCCTG ACCTTTGCCC   180
TCTCTGTCAC AAATCCCCTT CATGAACTAA AAGCAGCTGC TTTCCCCCAG ACCACTGAGA   240
AAATTAGTCC GAATTGGGAA TCTGGCATTA ATGTTGACTT GGCAATTTCC ACACGGCAAT   300
ATCATCTACA ACAGCTTTTC TACCGCTATG GAGAAAATAA TTCTTTGTCA GTTGAAGGGT   360
TCAGAAAATT ACTTCAAAAT ATAGGCATAG ATAAGATTAA AAGAATCCAT ATACACCATG   420
ACCACGACCA TCACTCAGAC CACGAGCATC ACTCAGACCA TGAGCGTCAC TCAGACCATG   480
AGCATCACTC AGACCACGAG CATCACTCTG ACCATGATCA TCACTCCCAC CATAATCATG   540
CTGCTTCTGG TAAAAATAAG CGAAAAGCTC TTTGCCCAGA CCATGACTCA GATAGTTCAG   600
GTAAAGATCC TAGAAACAGC CAGGGGAAAG GAGCTCACCG ACCAGAACAT GCCAGTGGTA   660
GAAGGAATGT CAAGGACAGT GTTAGTGCTA GTGAAGTGAC CTCAACTGTG TACAACACTG   720
TCTCTGAAGG AACTCACTTT CTAGAGACAA TAGAGACTCC AAGACCTGGA AAACTCTTCC   780
CCAAAGATGT AAGCAGCTCC ACTCCACCCA GTGTCACATC AAAGAGCCGG GTGAGCCGGC   840
TGGCTGGTAG GAAAACAAAT GAATCTGTGA GTGAGCCCCG AAAAGGCTTT ATGTATTCCA   900
GAAACACAAA TGAAAATCCT CAGGAGTGTT TCAATGCATC AAAGCTACTG ACATCTCATG   960
GCATGGGCAT CCAGGTTCCG CTGAATGCAA CAGAGTTCAA CTATCTCTGT CCAGCCATCA  1020
TCAACCAAAT TGATGCTAGA TCTTGTCTGA TTCATACAAG TGAAAAGAAG GCTGAAATCC  1080
CTCCAAAGAC CTATTCATTA CAAATAGCCT GGGTTGGTGG TTTTATAGCC ATTTCCATCA  1140
TCAGTTTCCT GTCTCTGCTG GGGGTTATCT TAGTGCCTCT CATGAATCGG GTGTTTTTCA  1200
AATTTCTCCT GAGTTTCCTT GTGGCACTGG CCGTTGGGAC TTTGAGTGGT GATGCTTTTT  1260
TACACCTTCT TCCACATTCT CATGCAAGTC ACCACCATAG TCATAGCCAT GAAGAACCAG  1320
CAATGGAAAT GAAAAGAGGA CCACTTTTCA GTCATCTGTC TTCTCAAAAC ATAGAAGAAA  1380
GTGCCTATTT TGATTCCACG TGGAAGGGTC TAACAGCTCT AGGAGGCCTG TATTTCATGT  1440
TTCTTGTTGA ACATGTCCTC ACATTGATCA AACAATTTAA AGATAAGAAG AAAAAGAATC  1500
AGAAGAAACC TGAAAATGAT GATGATGTGG AGATTAAGAA GCAGTTGTCC AAGTATGAAT  1560
CTCAACTTTC AACAAATGAG GAGAAAGTAG ATACAGATGA TCGAACTGAA GGCTATTTAC  1620
GAGCAGACTC ACAAGAGCCC TCCCACTTTG ATTCTCAGCA GCCTGCAGTC TTGGAAGAAG  1680
AAGAGGTCAT GATAGCTCAT GCTCATCCAC AGGAAGTCTA CAATGAATAT GTACCCAGAG  1740
GGTGCAAGAA TAAATGCCAT TCACATTTCC ACGATACACT CGGCCAGTCA GACGATCTCA  1800
TTCACCACCA TCATGACTAC CATCATATTC TCCATCATCA CCACCACCAA AACCACCATC  1860
CTCACAGTCA CAGCCAGCGC TACTCTCGGG AGGAGCTGAA AGATGCCGGC GTCGCCACTT  1920
TGGCCTGGAT GGTGATAATG GGTGATGGCC TGCACAATTT CAGCGATGGC CTAGCAATTG  1980
GTGCTGCTTT TACTGAAGGC TTATCAAGTG GTTTAAGTAC TTCTGTTGCT GTGTTCTGTC  2040
ATGAGTTGCC TCATGAATTA GGTGACTTTG CTGTTCTACT AAAGGCTGGC ATGACCGTTA  2100
AGCAGGCTGT CCTTTATAAT GCATTGTCAG CCATGCTGGC GTATCTTGGA ATGGCAACAG  2160
GAATTTTCAT TGGTCATTAT GCTGAAAATG TTTCTATGTG GATATTTGCA CTTACTGCTG  2220
GCTTATTCAT GTATGTTGCT CTGGTTGATA TGGTACCTGA AATGCTGCAC AATGATGCTA  2280
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DGSLVNSFMQ SDDSGGRTKR YVVFNNGTLY FNEVGMREEG DYTCFAENQV GKDEMRVRVK  2340
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ASVFDRGTYV CRMETEYGPS VTSIPVIVIA YPPRITSEPT PVIYTRPGNT VKLNCMAMGI  2760
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Seq ID NO: 418 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..5001

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Seq ID NO: 419 Protein sequence
Protein Accession #: Eos sequence

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FQNTFFHTPR LSNHLEQSPS PILETLLLPW WMVCSLGNAI FSKSGPQTGE AWDLTPKPSL 240
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Seq ID NO: 420 DNA sequence
Nucleic Acid Accession #: NM_022743
Coding sequence: 128..1237

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Seq ID NO: 421 Protein sequence
Protein Accession #: NP_073580

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LDMLMTSEER RKQLRDQYCF ECDCFRCQTQ DKDADMLTGD EQVWKEVQES LKKIEELKAH   240
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Seq ID NO: 422 DNA sequence
Nucleic Acid Accession #: NM_003014.2
Coding sequence: 238..648

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Seq ID NO: 423 Protein sequence
Protein Accession #: NP_003005.1

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ESLACDELPV YDRGVCISPE AIVTDLPEDV KWIDITPDMM VQERPLDVDC KRLSPDRCKC   180
KKVKPTLATY LSKNYSYVIH AKIKAVQRSG CNEVTTVVDV KEIFKSSSPI PRTQVPLITN   240
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Seq ID NO: 424 DNA sequence
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Coding sequence: 248..1780

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GCTGCTACTG CTGGCATCAT TTACAGGCCG GTGCCCCGCG GGTGAGCTGG AGACCTCAGA   360
CGTGGTAACT GTGGTGCTGG GCCAGGACGC AAAACTGCCC TGCTTCTACC GAGGGGACTC   420
CGGCGAGCAA GTGGGGCAAG TGGCATGGGC TCGGGTGGAC GCGGGCGAAG GCGCCCAGGA   480
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GGAGCAGCCG CCGCCCCCAC GCAACCCCCT GGACGGCTCA GTGCTCCTGC GCAACGCAGT   600
GCAGGCGGAT GAGGGCGAGT ACGAGTGCCG GGTCAGCACC TTCCCCGCCG GCAGCTTCCA   660
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ACTAGAAGAG GGCCAGGGCC TGACCCTGGC AGCCTCCTGC ACAGCTGAGG GCAGCCCAGC   780
CCCCAGCGTG ACCTGGGACA CGGAGGTCAA AGGCACAACG TCCAGCCGTT CCTTCAAGCA   840
CTCCCGCTCT GCTGCCGTCA CCTCAGAGTT CCACTTGGTG CCTAGCCGCA GCATGAATGG   900
GCAGCCACTG ACTTGTGTGG TGTCCCATCC TGGCCTGCTC CAGGACCAAA GGATCACCCA   960
CATCCTCCAC GTGTCCTTCC TTGCTGAGGC CTCTGTGAGG GGCCTTGAAG ACCAAAATCT  1020
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CTCATACAAC TGGACACGGC TGGATGGGCC TCTGCCCAGT GGGGTACGAG TGGATGGGGA  1140
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ACTTTTAATT TTTTTCTTTT TTTTTTCTTG CCCTTTCCAT TAGTTGTATT TTTTATTTAT  2580
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Seq ID NO: 425 Protein sequence
Protein Accession #: AAH10423

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DEGEYECRVS TFPAGSFQAR LRLRVLVPPL PSLNPGPALE EGQGLTLAAS CTAEGSPAPS   180
VTWDTEVKGT TSSRSFKHSR SAAVTSEFHL VPSRSMNGQP LTCVVSHPGL LQDQRITHIL   240
HVSFLAEASV RGLEDQNLWH IGREGAMLKC LSEGQPPPSY NWTRLDGPLP SGVRVDGDTL   300
GFPPLTTEHS GIYVCHVSNE FSSRDSQVTV DVLDPQEDSG KQVDLVSASV VVVGVIAALL   360
FCLLVVVVVL MSRYHRRKAQ QMTQKYEEEL TLTRENSIRR LHSHHTDPRS QPEESVGLRA   420
EGHPDSLKDN SSCSVMSEEP EGRSYSTLTT VREIETQTEL LSPGSGRAEE EEDQDEGIKQ   480
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Seq ID NO: 426 DNA sequence
Nucleic Acid Accession #: NM_003474.2
Coding sequence: 37..3036

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CCGGAGCTGA CTCGCCGAGG CAGGAAATCC CTCCGGTCGC GACGCCCGGC CCCGCTCGGC   240
GCCCGCGTGG GATGGTGCAG CGCTCGCCGC CGGGCCCGAG AGCTGCTGCA CTGAAGGCCG   300
GCGACGATGG CAGCGCGCCC GCTGCCCGTG TCCCCCGCCC GCGCCCTCCT GCTCGCCCTG   360
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GCTGATGAAG TTGTCAGTGC CTCTGTTCGG AGTGGGGACC TCTGGATCCC AGTGAAGAGC   480
TTCGACTCCA AGAATCATCC AGAAGTGCTG AATATTCGAC TACAACGGGA AAGCAAAGAA   540
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CAGACATGGG CAAGAAGGCA TAAAAGAGAG ACCCTCAAGG CAACTAAGTA TGTGGAGCTG   960
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CAGCGATTAA TAGAGATTGC TAATCACGTT GACAAGTTTT ACAGACCACT GAACATTCGG  1080
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TCCCATGACA ATGCGCAGCT TGTCAGTGGG GTTTATTTCC AAGGGACCAC CATCGGCATG  1260
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GAGGCCCACT GGGCACCTCC CTTCTGTGAC AAGTTTGGCT TTGGAGGAAG CACAGACAGC  2400
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TGACCCTGAG CTGACCAGCC GTGAGCATGT TTGGAAGGGG TCTGTAGTGT CACTCAAGGC  3780
GGTGCTTGAT AGAAATGCCA AGCACTTCTT TTTCTCGCTG TCCTTTCTAG AGCACTGCCA  3840
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Seq ID NO: 427 Protein sequence
Protein Accession #: NP_003465

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YHGHVRGYSD SAVSLSTCSG LRGLIVFENE SYVLEPMKSA TNRYKLFPAK KLKSVRGSCG   180
SHHNTPNLAA KNVFPPPSQT WARRHKRETL KATKYVELVI VADNREFQRQ GKDLEKVKQR   240
LIEIANHVDK FYRPLNIRIV LVGVEVWNDM DKCSVSQDPF TSLHEFLDWR KMKLLPRKSH   300
DNAQLVSGVY FQGTTIGMAP IMSMCTADQS GGIVMDHSDN PLGAAVTLAH ELGHNFGMNH   360
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ACRDSSNSCD LPEFCTGASP HCPANVYLHD GHSCQDVDGY CYNGICQTHE QQCVTLWGPG   540
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IETNIPLQQG GRILCRGTHV YLGDDMPDPG LVLAGTKCAD GKICLNRQCQ NISVFGVHEC   660
AMQCHGRGVC NNRKNCHCEA HWAPPFCDKF GFGGSTDSGP IRQADNQGLT IGILVTILCL   720
LAAGFVVYLK RKTLIRLLFT NKKTTIEKLR CVRPSRPPRG FQPCQAHLGH LGKGLMRKPP   780
DSYPPKDNPR RLLQCQNVDI SRPLNGLNVP QPQSTQRVLP PLHRAPRAPS VPARPLPAKP   840
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Seq ID NO: 428 DNA sequence
Nucleic Acid Accession #: NM_003714
Coding sequence: 135..1043

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TGGCCACCTT TGACCCGGCG CGGGGGACCG ACGCCACCAA CCCACCCGAG GGTCCCCAAG   240
ACAGGAGCTC CCAGCAGAAA GGCCGCCTGT CCCTGCAGAA TACAGCGGAG ATCCAGCACT   300
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Seq ID NO: 429 Protein sequence
Protein Accession #: NP_003705

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CGEEVKEAIT HSVQVQCEQN WGSLCSILSF CTSAIQKPPT APPERQPQVD RTKLSRAHHG  240
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Seq ID NO: 430 DNA sequence
Nucleic Acid Accession #: NM_005940
Coding sequence: 23..1489

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AGCGACTGTC TCAGACTGGG CAGGGAGGCT TTGGCATGAC TTAAGAGGAA GGGCAGTCTT 1740
GGGACCCGCT ATGCAGGTCC TGGCAAACCT GGCTGCCCTG TCTCATCCCT GTCCCTCAGG 1800
GTAGCACCAT GGCAGGACTG GGGGAACTGG AGTGTCCTTG CTGTATCCCT GTTGTGAGGT 1860
TCCTTCCAGG GGCTGGCACT GAAGCAAGGG TGCTGGGGCC CCATGGCCTT CAGCCCTGGC 1920
TGAGCAACTG GGCTGTAGGG CAGGGCCACT TCCTGAGGTC AGGTCTTGGT AGGTGCCTGC 1980
ATCTGTCTGC CTTCTGGCTG ACAATCCTGG AAATCTGTTC TCCAGAATCC AGGCCAAAAA 2040
GTTCACAGTC AAATGGGGAG GGGTATTCTT CATGCAGGAG ACCCCAGGCC CTGGAGGCTG 2100
CAACATACCT CAATCCTGTC CCAGGCCGGA TCCTCCTGAA GCCCTTTTCG CAGCACTGCT 2160
ATCCTCCAAA GCCATTGTAA ATGTGTGTAC AGTGTGTATA AACCTTCTTC TTCTTTTTTT 2220
TTTTTAAACT GAGGATTGTC ATTAAACACA GTTGTTTTCT
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Seq ID NO: 431 Protein sequence
Protein Accession #: NP_005931

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1          11         21         31         41         51
|          |          |          |          |          |
MAPAAWLRSA AARALLPPML LLLLQPPPLL ARALPPDVHH LHAERRGPQP WHAALPSSPA   60
PAPATQEAPR PASSLRPPRC GVPDPSDGLS ARNRQKRFVL SGGRWEKTDL TYRILRFPWQ  120
LVQEQVRQTM AEALKVWSDV TPLTFTEVHE GRADIMIDFA RYWHGDDLPF DGPGGILAHA  180
FFPKTHREGD VHFDYDETWT IGDDQGTDLL QVAAHEFGHV LGLQHTTAAK ALMSAFYTFR  240
YPLSLSPDDC RGVQHLYGQP WPTVTSRTPA LGPQAGIDTN EIAPLEPDAP PDACEASFDA  300
VSTIRGELFF FKAGFVWRLR GGQLQPGYPA LASRHWQGLP SPVDAAFEDA QGHIWFFQGA  360
QYWVYDGEKP VLGPAPLTEL GLVRFPVHAA LVWGPEKNKI YFFRGRDYWR FHPSTRRVDS  420
PVPRRATDWR GVPSEIDAAF QDADGYAYFL RGRLYWKFDP VKVKALEGFP RLVGPDFFGC  480
AEPANTFL
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Seq ID NO: 432 DNA sequence
Nucleic Acid Accession #: NM_024022
Coding sequence: 202..1563

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1          11         21         31         41         51
|          |          |          |          |          |
ACCGGGCACC GGACGGCTCG GGTACTTTCG TTCTTAATTA GGTCATGCCC GTGTGAGCCA   60
GGAAAGGGCT GTGTTTATGG GAAGCCAGTA ACACTGTGGC CTACTATCTC TTCCGTGGTG  120
CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGGATGTC  180
AGAGGTCCTG AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTTGA AGCCCCCTTC  240
TCATTCCGAT CGCTTTTTGG CCTTGATGAT TTGAAAATAA GTCCTGTTGC ACCAGATGCA  300
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GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTCC AATCATCGTC   360
ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC   420
TCAGGGAAGT ACAGATGTCG CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC   480
GGAGTCTCGG ATTGCAAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG   540
AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGGAAGA CCATGTGCTC CGATGACTGG   600
AAGGGTCACT ACGCAAATGT TGCCTGTGCC CAACTGGGTT TCCCAAGCTA TGTGAGTTCA   660
GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCCGGG AGGAGTTTGT GTCCATCGAT   720
CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA   780
TGTGCCTCTG GCCACGTGGT TACCTTGCAG TGCACAGCCT GTGGTCATAG AAGGGGCTAC   840
AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTCGC AGTGGCCCTG GCAGGCCAGC   900
CTTCAGTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCACGCCCCT GTGGATCATC   960
ACTGCTGCAC ACTGTGTTTA TGACTTGTAC CTCCCCAAGT CATGGACCAT CCAGGTGGGT  1020
CTAGTTTCCC TGTTGGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCAC  1080
AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCCGGGCCA  1140
CTCACGTTCA ATGAAATGAT CCAGCCTGTG TGCCTGCCCA ACTCTGAAGA GAACTTCCCC  1200
GATGGAAAAG TGTGCTGGAC GTCAGGATGG GGGGCCACAG AGGATGGAGG TGACGCCTCC  1260
CCTGTCCTGA ACCACGCGGC CGTCCCTTTG ATTTCCAACA AGATCTGCAA CCACAGGGAC  1320
GTGTACGGTG GCATCATCTC CCCCTCCATG CTCTGCGCGG GCTACCTGAC GGGTGGCGTG  1380
GACAGCTGCC AGGGGGACAG CGGGGGGCCC CTGGTGTGTC AAGAGAGGAG GCTGTGGAAG  1440
TTAGTGGGAG CGACCAGCTT TGGCATCGGC TGCGCAGAGG TGAACAAGCC TGGGGTGTAC  1500
ACCCGTGTCA CCTCCTTCCT GGACTGGATC CACGAGCAGA TGGAGAGAGA CCTAAAAACC  1560
TGAAGAGGAA GGGGACAAGT AGCCACCTGA GTTCCTGAGG TGATGAAGAC AGCCCGATCC  1620
TCCCCTGGAC TCCCGTGTAG GAACCTGCAC ACGAGCAGAC ACCCTTGGAG CTCTGAGTTC  1680
CGGCACCAGT AGCAGGCCCG AAAGAGGCAC CCTTCCATCT GATTCCAGCA CAACCTTCAA  1740
GCTGCTTTTT GTTTTTTGTT TTTTTGAGGT GGAGTCTCGC TCTGTTGCCC AGGCTGGAGT  1800
GCAGTGGCGA AATCCCTGCT CACTGCAGCC TCCGCTTCCC TGGTTCAAGC GATTCTCTTG  1860
CCTCAGCTTC CCCAGTAGCT GGGACCACAG GTGCCCGCCA CCACACCCAA CTAATTTTTG  1920
TATTTTTAGT AGAGACAGGG TTTCACCATG TTGGCCAGGC TGCTCTCAAA CCCCTGACCT  1980
CAAATGATGT GCCTGCTTCA GCCTCCCACA GTGCTGGGAT TACAGGCATG GGCCACCACG  2040
CCTAGCCTCA CGCTCCTTTC TGATCTTCAC TAAGAACAAA AGAAGCAGCA ACTTGCAAGG  2100
GCGGCCTTTC CCACTGGTCC ATCTGGTTTT CTCTCCAGGG GTCTTGCAAA ATTCCTGACG  2160
AGATAAGCAG TTATGTGACC TCACGTGCAA AGCCACCAAC AGCCACTCAG AAAAGACGCA  2220
CCAGCCCAGA AGTGCAGAAC TGCAGTCACT GCACGTTTTC ATCTCTAGGG ACCAGAACCA  2280
AACCCACCCT TTCTACTTCC AAGACTTATT TTCACATGTG GGGAGGTTAA TCTAGGAATG  2340
ACTCGTTTAA GGCCTATTTT CATGATTTCT TTGTAGCATT TGGTGCTTGA CGTATTATTG  2400
TCCTTTGATT CCAAATAATA TGTTTCCTTC CCTCAAAAAA AAAAAAAAAA AAAAAAAAAA  2460
AAAAA
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Seq ID NO: 433 Protein sequence
Protein Accession #: NP_076927

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1          11         21         31         41         51
|          |          |          |          |          |
MGENDPPAVE APFSFRSLFG LDDLKISPVA PDADAVAAQI LSLLPLKFFP IIVIGIIALI    60
LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVLQVF   120
TAASWKTMCS DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK   180
VTALHHSVYV REGCASGHVV TLQCTACGHR RGYSSRIVGG NMSLLSQWPW QASLQFQGYH   240
LCGGSVITPL WIITAAHCVY DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR   300
LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFPDGKVCWT SGWGATEDGG DASPVLNHAA   360
VPLISNKICN HRDVYGGIIS PSMLCAGYLT GGVDSCQGDS GGPLVCQERR LWKLVGATSF   420
GIGCAEVNKP GVYTRVTSFL DWIHEQMERD LKT
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Seq ID NO: 434 DNA sequence
Nucleic Acid Accession #: NM_000493.2
Coding sequence: 97..2139

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1          11         21         31         41         51
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CCAGGAACTC CCAGCACGCA GAATCCATCT GAGAATATGC TGCCACAAAT ACCCTTTTTG   120
CTGCTAGTAT CCTTGAACTT GGTTCATGGA GTGTTTTACG CTGAACGATA CCAAATGCCC   180
ACAGGCATAA AAGGCCCACT ACCCAACACC AAGACACAGT TCTTCATTCC CTACACCATA   240
AAGAGTAAAG GTATAGCAGT AAGAGGAGAG CAAGGTACTC CTGGTCCACC AGGCCCTGCT   300
GGACCTCGAG GGCACCCAGG TCCTTCTGGA CCACCAGGAA AACCAGGCTA CGGAAGTCCT   360
GGACTCCAAG GAGAGCCAGG GTTGCCAGGA CCACCGGGAC CATCAGCTGT AGGGAAACCA   420
GGTGTGCCAG GACTCCCAGG AAAACCAGGA GAGAGAGGAC CATATGGACC AAAAGGAGAT   480
GTTGGACCAG CTGGCCTACC AGGACCCCGG GGCCCACCAG GACCACCTGG AATCCCTGGA   540
CCGGCTGGAA TTTCTGTGCC AGGAAAACCT GGACAACAGG GACCCACAGG AGCCCCAGGA   600
CCCAGGGGCT TTCCTGGAGA AAAGGGTGCA CCAGGAGTCC CTGGTATGAA TGGACAGAAA   660
GGGGAAATGG GATATGGTGC TCCTGGTCGT CCAGGTGAGA GGGGTCTTCC AGGCCCTCAG   720
GGTCCCACAG GACCATCTGG CCCTCCTGGA GTGGGAAAAA GAGGTGAAAA TGGGGTTCCA   780
GGACAGCCAG GCATCAAAGG TGATAGAGGT TTTCCGGGAG AAATGGGACC AATTGGCCCA   840
CCAGGTCCCC AAGGCCCTCC TGGGGAACGA GGGCCAGAAG GCATTGGAAA GCCAGGAGCT   900
GCTGGAGCCC CAGGCCAGCC AGGGATTCCA GGAACAAAAG GTCTCCCTGG GGCTCCAGGA   960
ATAGCTGGGC CCCCAGGGCC TCCTGGCTTT GGGAAACCAG GCTTGCCAGG CCTGAAGGGA  1020
GAAAGAGGAC CTGCTGGCCT TCCTGGGGGT CCAGGTGCCA AAGGGGAACA AGGGCCAGCA  1080
GGTCTTCCTG GGAAGCCAGG TCTGACTGGA CCCCCTGGGA ATATGGGACC CCAAGGACCA  1140
AAAGGCATCC CGGGTAGCCA TGGTCTCCCA GGCCCTAAAG GTGAGACAGG GCCAGCTGGG  1200
CCTGCAGGAT ACCCTGGGGC TAAGGGTGAA AGGGGTTCCC CTGGGTCAGA TGGAAAACCA  1260
GGGTACCCAG GAAAACCAGG TCTCGATGGT CCTAAGGGTA ACCCAGGGTT ACCAGGTCCA  1320
AAAGGTGATC CTGGAGTTGG AGGACCTCCT GGTCTCCCAG GCCCTGTGGG CCCAGCAGGA  1380
GCAAAGGGAA TGCCCGGACA CAATGGAGAG GCTGGCCCAA GAGGTGCCCC TGGAATACCA  1440
GGTACTAGAG GCCCTATTGG GCCACCAGGC ATTCCAGGAT TCCCTGGGTC TAAAGGGGAT  1500
CCAGGAAGTC CCGGTCCTCC TGGCCCAGCT GGCATAGCAA CTAAGGGCCT CAATGGACCC  1560
ACCGGGCCAC CAGGGCCTCC AGGTCCAAGA GGCCACTCTG GAGAGCCTGG TCTTCCAGGG  1620
CCCCCTGGGC CTCCAGGCCC ACCAGGTCAA GCAGTCATGC CTGAGGGTTT TATAAAGGCA  1680
GGCCAAAGGC CCAGTCTTTC TGGGACCCCT CTTGTTAGTG CCAACCAGGG GGTAACAGGA  1740
```

ATGCCTGTGT CTGCTTTTAC TGTTATTCTC TCCAAAGCTT ACCCAGCAAT AGGAACTCCC 1800
ATACCATTTG ATAAAATTTT GTATAACAGG CAACAGCATT ATGACCCAAG GACTGGAATC 1860
TTTACTTGTC AGATACCAGG AATATACTAT TTTTCATACC ACGTGCATGT GAAAGGGACT 1920
CATGTTTGGG TAGGCCTGTA TAAGAATGGC ACCCCTGTAA TGTACACCTA TGATGAATAC 1980
ACCAAAGGCT ACCTGGATCA GGCTTCAGGG AGTGCCATCA TCGATCTCAC AGAAAATGAC 2040
CAGGTGTGGC TCCAGCTTCC CAATGCCGAG TCAAATGGCC TATACTCCTC TGAGTATGTC 2100
CACTCCTCTT TCTCAGGATT CCTAGTGGCT CCAATGTGAG TACACCCCAC AGAGCTAATC 2160
TAAATCTTGT GCTAGAAAAA GCATTCTCTA ACTCTACCCC ACCCTACAAA ATGCATATGG 2220
AGGTAGGCTG AAAAGAATGT AATTTTTATT TTCTGAAATA CAGATTTGAG CTATCAGACC 2280
AACAAACCTT CCCCCTGAAA AGTGAGCAGC AACGTAAAAA CGTATGTGAA GCCTCTCTTG 2340
AATTTCTAGT TAGCAATCTT AAGGCTCTTT AAGGTTTTCT CCAATATTAA AAAATATCAC 2400
CAAAGAAGTC CTGCTATGTT AAAAACAAAC AACAAAAAAC AAAGCAACAA AAAAAAAAAT 2460
TAAAAAAAAA AACAGAAATA GAGCTCTAAG TTATGTGAAA TTTGATTTGA GAAACTCGGC 2520
ATTTCCTTTT TAAAAAAGCC TGTTTCTAAC TATGAATATG AGAACTTCTA GGAAACATCC 2580
AGGAGGTATC ATATAACTTT GTAGAACTTA AATACTTGAA TATTCAAATT TAAAAGACAC 2640
TGTATCCCCT AAAATATTTC TGATGGTGCA CTACTCTGAG GCCTGTATGG CCCCTTTCAT 2700
CAATATCTAT TCAAATATAC AGGTGCATAT ATACTTGTTA AAGCTCTTAT ATAAAAAAGC 2760
CCCAAAATAT TGAAGTTCAT CTGAAATGCA AGGTGCTTTC ATCAATGAAC CTTTTCAAAA 2820
CTTTTCTATG ATTGCAGAGA AGCTTTTTAT ATACCCAGCA TAACTTGGAA ACAGGTATCT 2880
GACCTATTCT TATTTAGTTA ACACAAGTGT GATTAATTTG ATTTCTTTAA TTCCTTATTG 2940
AATCTTATGT GATATGATTT TCTGGATTTA CAGAACATTA GCACATGTAC CTTGTGCCTC 3000
CCATTCAAGT GAAGTTATAA TTTACACTGA GGGTTTCAAA ATTCGACTAG AAGTGGAGAT 3060
ATATTATTTA TTTATGCACT GTACTGTATT TTTATATTGC TGTTTAAAAC TTTTAAGCTG 3120
TGCCTCACTT ATTAAAGCAC AAAATGTTTT ACCTACTCCT TATTTACGAC ACAATAAAAT 3180
AACATCAATA GATTTTTAGG CTGAATTAAT TTGAAAGCAG CAATTTGCTG TTCTCAACCA 3240
TTCTTTCAAG GCTTTTCATT CGACACAATA AAATAACATC AATAG

Seq ID NO: 435 Protein sequence
Protein Accession #: NP_000484.2

1 11 21 31 41 51
| | | | | |
MLPQIPFLLL VSLNLVHGVF YAERYQMPTG IKGPLPNTKT QFFIPYTIKS KGIAVRGEQG 60
TPGPPGPAGP RGHPGPSGPP GKPGYGSPGL QGEPGLPGPP GPSAVGKPGV PGLPGKPGER 120
GPYGPKGDVG PAGLPGPRGP PGPPGIPGPA GISVPGKPGQ QGPTGAPGPR GFPGEKGAPG 180
VPGMNGQKGE MGYGAPGRPG ERGLPGPQGP TGPSGPPGVG KRGENGVPGQ PGIKGDRGFP 240
GEMGPIGPPG PQGPPGERGP EGIGKPGAAG APGQPGIPGT KGLPGAPGIA GPPGPPGFGK 300
PGLPGLKGER GPAGLPGGPG AKGEQGPAGL PGKPGLTGPP GNMGPQGPKG IPGSHGLPGP 360
KGETGPAGPA GYPGAKGERG SPGSDGKPGY PGKPGLDGPK GNPGLPGPKG DPGVGGPPGL 420
PGPVGPAGAK GMPGHNGEAG PRGAPGIPGT RGPIGPPGIP GFPGSKGDPG SPGPPGPAGI 480
ATKGLNGPTG PPGPPGPRGH SGEPGLPGPP GPPGPPGQAV MPEGFIKAGQ RPSLSGTPLV 540
SANQGVTGMP VSAFTVILSK AYPAIGTPIP FDKILYNRQQ HYDPRTGIFT CQIPGIYYFS 600
YHVHVKGTHV WVGLYKNGTP VMYTYDEYTK GYLDQASGSA IIDLTENDQV WLQLPNAESN 660
GLYSSEYVHS SFSGFLVAPM

Seq ID NO: 436 DNA sequence
Nucleic Acid Accession #: XM_062811
Coding sequence: 1..888

1 11 21 31 41 51
| | | | | |
ATGTGGGGCG CTCGCCGCTC GTCCGTCTCC TCATCCTGGA ACGCCGCTTC GCTCCTGCAG 60
CTGCTGCTGG CTGCGCTGCT GGCGGCGGGG GCGAGGGCCA GCGGCGAGTA CTGCCACGGC 120
TGGCTGGACG CGCAGGGCGT CTGGCGCATC GGCTTCCAGT GTCCCGAGCG CTTCGACGGC 180
GGCGACGCCA CCATCTGCTG CGGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCCGAG 240
GCGCGCCTGG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGGCGCTGG CGAGCCTGGC 300
CGGGCGGACA AAGACGGCCC CGACGGCTCG GCAGTGCCCA TCTACGTGCC GTTCCTCATT 360
GTTGGCTCCG TGTTTGTCGC CTTTATCATC TTGGGGTCCC TGGTGGCAGC CTGTTGCTGC 420
AGATGTCTCC GGCCTAAGCA GGATCCCCAG CAGAGCCGAG CCCCAGGGGG TAACCGCTTG 480
ATGGAGACCA TCCCCATGAT CCCCAGTGCC AGCACCTCCC GGGGGTCGTC CTCACGCCAG 540
TCCAGCACAG CTGCCAGTTC CAGCTCCAGC GCCAACTCAG GGGCCCGGGC GCCCCCAACA 600
AGGTCACAGA CCAACTGTTG CTTGCCGGAA GGGACCATGA ACAACGTGTA TGTCAACATG 660
CCCACGAATT TCTCTGTGCT GAACTGTCAG CAGGCCACCC AGATTGTGCC ACATCAAGGG 720
CAGTATCTGC ATCCCCCATA CGTGGGGTAC ACGGTGCAGC ACGACTCTGT GCCCATGACA 780
GCTGTGCCAC CTTTCATGGA CGGCCTGCAG CCTGGCTACA GGCAGATTCA GTCCCCCTTC 840
CCTCACACCA ACAGTGAACA GAAGATGTAC CCAGCGGTGA CTGTATAA

Seq ID NO: 437 Protein sequence
Protein Accession #: XP_062811

1 11 21 31 41 51
| | | | | |
MWGARRSSVS SSWNAASLLQ LLLAALLAAG ARASGEYCHG WLDAQGVWRI GFQCPERFDG 60
GDATICCGSC ALRYCCSSAE ARLDQGGCDN DRQQGAGEPG RADKDGPDGS AVPIYVPFLI 120
VGSVFVAFII LGSLVAACCC RCLRPKQDPQ QSRAPGGNRL METIPMIPSA STSRGSSSRQ 180
SSTAASSSSS ANSGARAPPT RSQTNCCLPE GTMNNVYVNM PTNFSVLNCQ QATQIVPHQG 240
QYLHPPYVGY TVQHDSVPMT AVPPFMDGLQ PGYRQIQSPF PHTNSEQKMY PAVTV

Seq ID NO: 438 DNA sequence
Nucleic Acid Accession #: NM_004004.1
Coding sequence: 1..681

1 11 21 31 41 51
| | | | | |
ATGGATTGGG GCACGCTGCA GACGATCCTG GGGGGTGTGA ACAAACACTC CACCAGCATT 60
GGAAAGATCT GGCTCACCGT CCTCTTCATT TTTCGCATTA TGATCCTCGT TGTGGCTGCA 120
AAGGAGGTGT GGGGAGATGA GCAGGCCGAC TTTGTCTGCA ACACCCTGCA GCCAGGCTGC 180

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AAGAACGTGT GCTACGATCA CTACTTCCCC ATCTCCCACA TCCGGCTATG GGCCCTGCAG   240
CTGATCTTCG TGTCCAGCCC AGCGCTCCTA GTGGCCATGC ACGTGGCCTA CCGGAGACAT   300
GAGAAGAAGA GGAAGTTCAT CAAGGGGGAG ATAAAGAGTG AATTTAAGGA CATCGAGGAG   360
ATCAAAACCC AGAAGGTCCG CATCGAAGGC TCCCTGTGGT GGACCTACAC AAGCAGCATC   420
TTCTTCCGGG TCATCTTCGA AGCCGCCTTC ATGTACGTCT TCTATGTCAT GTACGACGGC   480
TTCTCCATGC AGCGGCTGGT GAAGTGCAAC GCCTGGCCTT GTCCCAACAC TGTGGACTGC   540
TTTGTGTCCC GGCCCACGGA GAAGACTGTC TTCACAGTGT TCATGATTGC AGTGTCTGGA   600
ATTTGCATCC TGCTGAATGT CACTGAATTG TGTTATTTGC TAATTAGATA TTGTTCTGGG   660
AAGTCAAAAA AGCCAGTTTA A
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Seq ID NO: 439 Protein sequence
Protein Accession #: NP_003995.1

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1          11         21         31         41         51
|          |          |          |          |          |
MDWGTLQTIL GGVNKHSTSI GKIWLTVLFI FRIMILVVAA KEVWGDEQAD FVCNTLQPGC    60
KNVCYDHYFP ISHIRLWALQ LIFVSSPALL VAMHVAYRRH EKKRKFIKGE IKSEFKDIEE   120
IKTQKVRIEG SLWWTYTSSI FFRVIFEAAF MYVFYVMYDG FSMQRLVKCN AWPCPNTVDC   180
FVSRPTEKTV FTVFMIAVSG ICILLNVTEL CYLLIRYCSG KSKKPV
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Seq ID NO: 440 DNA sequence
Nucleic Acid Accession #: XM_061091.1
Coding sequence: 1..2481

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1          11         21         31         41         51
|          |          |          |          |          |
ATGCCAAATA CTTCAGGAAC AACCAGGATT GAAATTTGGC TTCTCCAAGA GCCGCCCGGG    60
CACCGAGCGC TGGTCGCCGC TCTCCTTCCG GTGAGTCCCA GCCCCGAGTT GGCTCTGGCG   120
CCCGGGTACC CGCCAGTGCC GGCTGCCGAT GACCGATTCA CGCTCCCGAT GATTGGAGGT   180
CAGATGCATG GTGAGAAGGT AGATCTCTGG AGCCTTGGTG TTCTTTGCTA TGAATTTTTA   240
GTTGGGAAGC CTCCTTTTGA GGCAAACGAA GTCCATGTAA GCAAAGAAAC CATCGGGAAG   300
ATTTCAGCTG CCAGCAAAAT GATGTGGTGC TCGGCTGCAG TGGACATCAT GTTTCTGTTA   360
GATGGGTCTA ACAGCGTCGG GAAAGGGAGC TTTGAAAGGT CCAAGCACTT TGCCATCACA   420
GTCTGTGACG GTCTGGACAT CAGCCCCGAG AGGGTCAGAG TGGGAGCATT CCAGTTCAGT   480
TCCACTCCTC ATCTGGAATT CCCCTTGGAT TCATTTTCAA CCCAACAGGA AGTGAAGGCA   540
AGAATCAAGA GGATGGTTTT CAAAGGAGGG CGCACGGAGA CGGAACTTGC TCTGAAATAC   600
CTTCTGCACA GAGGGTTGCC TGGAGGCAGA AATGCTTCTG TGCCCCAGAT CCTCATCATC   660
GTCACTGATG GGAAGTCCCA GGGGGATGTG GCACTGCCAT CCAAGCAGCT GAAGGAAAGG   720
GGTGTCACTG TGTTTGCTGT GGGGGTCAGG TTTCCCAGGT GGGAGGAGCT GCATGCACTG   780
GCCAGCGAGC CTAGAGGGCA GCACGTGCTG TTGGCTGAGC AGGTGGAGGA TGCCACCAAC   840
GGCCTCTTCA GCACCCTCAG CAGCTCGGCC ATCTGCTCCA GCGCCACGCC AGCTGGGAGC   900
CCCGAGCTTG TCTTCATGGA GCGGTTAATG GGCATCTCTC TGATAGGCCC CTGTGACTCG   960
CAGCCCTGCC AGAATGGAGG CACATGTGTT CCAGAAGGAC TGGACGGCTA CCAGTGCCTC  1020
TGCCCGCTGG CCTTTGGAGG GGAGGCTAAC TGTGCCCTGA AGCTGAGCCT GGAATGCAGG  1080
GTCGACCTCC TCTTCCTGCT GGACAGCTCT GCGGGCACCA CTCTGGACGG CTTCCTGCGG  1140
GCCAAAGTCT TCGTGAAGCG GTTTGTGCGG GCCGTGCTGA GCGAGGACTC TCGGGCCCGA  1200
GTGGGTGTGG CCACATACAG CAGGGAGCTG CTGGTGGCGG TGCCTGTGGG GGAGTACCAG  1260
GATGTGCCTG ACCTGGTCTG GAGCCTCGAT GGCATTCCCT TCCGTGGTGG CCCCACCCTG  1320
ACGGGCAGTG CCTTGCGGCA GGCGGCAGAG CGTGGCTTCG GGAGCGCCAC CAGGACAGGC  1380
CAGGACCGGC CACGTAGAGT GGTGGTTTTG CTCACTGAGT CACACTCCGA GGATGAGGTT  1440
GCGGGCCCAG CGCGTCACGC AAGGGCGCGA GAGCTGCTCC TGCTGGGTGT AGGCAGTGAG  1500
GCCGTGCGGG CAGAGCTGGA GGAGATCACA GGCAGCCCAA AGCATGTGAT GGTCTACTCG  1560
GATCCTCAGG ATCTGTTCAA CCAAATCCCT GAGCTGCAGG GGAAGCTGTG CAGCCGGCAG  1620
CGGCCAGGGT GCCGGACACA AGCCCTGGAC CTCGTCTTCA TGTTGGACAC CTCTGCCTCA  1680
GTAGGGCCCG AGAATTTTGC TCAGATGCAG AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT  1740
GAGGTGAACC CTGACGTGAC ACAGGTCGGC CTGGTGGTGT ATGGCAGCCA GGTGCAGACT  1800
GCCTTCGGGC TGGACACCAA ACCCACCCGG GCTGCGATGC TGCGGGCCAT TAGCCAGGCC  1860
CCCTACCTAG GTGGGGTGGG CTCAGCCGGC ACCGCCCTGC TGCACATCTA TGACAAAGTG  1920
ATGACCGTCC AGAGGGGTGC CCGGCCTGGT GTCCCCAAAG CTGTGGTGGT GCTCACAGGC  1980
GGGAGAGGCG CAGAGGATGC AGCCGTTCCT GCCCAGAAGC TGAGGAACAA TGGCATCTCT  2040
GTCTTGGTCG TGGGCGTGGG GCCTGTCCTA AGTGAGGGTC TGCGGAGGCT TGCAGGTCCC  2100
CGGGATTCCC TGATCCACGT GGCAGCTTAC GCCGACCTGC GGTACCACCA GGACGTGCTC  2160
ATTGAGTGGC TGTGTGGAGA AGCCAAGCAG CCAGTCAACC TCTGCAAACC CAGCCCGTGC  2220
ATGAATGAGG GCAGCTGCGT CCTGCAGAAT GGGAGCTACC GCTGCAAGTG TCGGGATGGC  2280
TGGGAGGGCC CCCACTGCGA GAACCGTGAG TGGAGCTCTT GCTCTGTATG TGTGAGCCAG  2340
GGATGGATTC TTGAGACGCC CCTGAGGCAC ATGGCTCCCG TGCAGGAGGG CAGCAGCCGT  2400
ACCCCTCCCA GCAACTACAG AGAAGGCCTG GGCACTGAAA TGGTGCCTAC CTTCTGGAAT  2460
GTCTGTGCCC CAGGTCCTTA G
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Seq ID NO: 441 Protein sequence
Protein Accession #: XP_061091.1

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1          11         21         31         41         51
|          |          |          |          |          |
MPNTSGTTRI EIWLLQEPPG HRALVAALLP VSPSPELALA PGYPPVPAAD DRFTLPMIGG    60
QMHGEKVDLW SLGVLCYEFL VGKPPFEANE VHVSKETIGK ISAASKMMWC SAAVDIMFLL   120
DGSNSVGKGS FERSKHFAIT VCDGLDISPE RVRVGAFQFS STPHLEFPLD SFSTQQEVKA   180
RIKRMVFKGG RTETELALKY LLHRGLPGGR NASVPQILII VTDGKSQGDV ALPSKQLKER   240
GVTVFAVGVR FPRWEELHAL ASEPRGQHVL LAEQVEDATN GLFSTLSSSA ICSSATPAGS   300
PELVFMERLM GISLIGPCDS QPCQNGGTCV PEGLDGYQCL CPLAFGGEAN CALKLSLECR   360
VDLLFLLDSS AGTTLDGFLR AKVFVKRFVR AVLSEDSRAR VGVATYSREL LVAVPVGEYQ   420
DVPDLVWSLD GIPFRGGPTL TGSALRQAAE RGFGSATRTG QDRPRRVVVL LTESHSEDEV   480
AGPARHARAR ELLLLGVGSE AVRAELEEIT GSPKHVMVYS DPQDLFNQIP ELQGKLCSRQ   540
RPGCRTQALD LVFMLDTSAS VGPENFAQMQ SFVRSCALQF EVNPDVTQVG LVVYGSQVQT   600
AFGLDTKPTR AAMLRAISQA PYLGGVGSAG TALLHIYDKV MTVQRGARPG VPKAVVVLTG   660
GRGAEDAAVP AQKLRNNGIS VLVVGVGPVL SEGLRRLAGP RDSLIHVAAY ADLRYHQDVL   720
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IEWLCGEAKQ PVNLCKPSPC MNEGSCVLQN GSYRCKCRDG WEGPHCENRE WSSCSVCVSQ   780
GWILETPLRH MAPVQEGSSR TPPSNYREGL GTEMVPTFWN VCAPGP
```

Seq ID NO: 442 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..2424

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1          11         21         31         41         51
|          |          |          |          |          |
ATGCCCCCTT TCCTGTTGCT GGAGGCCGTC TGTGTTTTCC TGTTTTCCAG AGTGCCCCCA     60
TCTCTCCCTC TCCAGGAAGT CCATGTAAGC AAAGAAACCA TCGGGAAGAT TTCAGCTGCC    120
AGCAAAATGA TGTGGTGCTC GGCTGCAGTG GACATCATGT TTCTGTTAGA TGGGTCTAAC    180
AGCGTCGGGA AAGGGAGCTT TGAAAGGTCC AAGCACTTTG CCATCACAGT CTGTGACGGT    240
CTGGACATCA GCCCCGAGAG GGTCAGAGTG GGAGCATTCC AGTTCAGTTC CACTCCTCAT    300
CTGGAATTCC CCTTGGATTC ATTTTCAACC CAACAGGAAG TGAAGGCAAG AATCAAGAGG    360
ATGGTTTTCA AAGGAGGGCG CACGGAGACG GAACTTGCTC TGAAATACCT TCTGCACAGA    420
GGGTTGCCTG GAGGCAGAAA TGCTTCTGTG CCCCAGATCC TCATCATCGT CACTGATGGG    480
AAGTCCCAGG GGGATGTGGC ACTGCCATCC AAGCAGCTGA AGGAAAGGGG TGTCACTGTG    540
TTTGCTGTGG GGGTCAGGTT TCCCAGGTGG GAGGAGCTGC ATGCACTGGC CAGCGAGCCT    600
AGAGGGCAGC ACGTGCTGTT GGCTGAGCAG GTGGAGGATG CCACCAACGG CCTCTTCAGC    660
ACCCTCAGCA GCTCGGCCAT CTGCTCCAGC GCCACGCCAG ACTGCAGGGT CGAGGCTCAC    720
CCCTGTGAGC ACAGGACGCT GGAGATGGTC CGGGAGTTCG CTGGCAATGC CCCATGCTGG    780
AGAGGATCGC GGCGGACCCT TGCGGTGCTG GCTGCACACT GTCCCTTCTA CAGCTGGAAG    840
AGAGTGTTCC TAACCCACCC TGCCACCTGC TACAGGACCA CCTGCCCAGG CCCCTGTGAC    900
TCGCAGCCCT GCCAGAATGG AGGCACATGT GTTCCAGAAG GACTGGACGG CTACCAGTGC    960
CTCTGCCCGC TGGCCTTTGG AGGGGAGGCT AACTGTGCCC TGAAGCTGAG CCTGGAATGC   1020
AGGGTCGACC TCCTCTTCCT GCTGGACAGC TCTGCGGGCA CCACTCTGGA CGGCTTCCTG   1080
CGGGCCAAAG TCTTCGTGAA GCGGTTTGTG CGGGCCGTGC TGAGCGAGGA CTCTCGGGCC   1140
CGAGTGGGTG TGGCCACATA CAGCAGGGAG CTGCTGGTGG CGGTGCCTGT GGGGGAGTAC   1200
CAGGATGTGC CTGACCTGGT CTGGAGCCTC GATGGCATTC CCTTCCGTGG TGGCCCCACC   1260
CTGACGGGCA GTGCCTTGCG GCAGGCGGCA GAGCGTGGCT TCGGGAGCGC CACCAGGACA   1320
GGCCAGGACC GGCCACGTAG AGTGGTGGTT TTGCTCACTG AGTCACACTC CGAGGATGAG   1380
GTTGCGGGCC CAGCGCGTCA CGCAAGGGCG CGAGAGCTGC TCCTGCTGGG TGTAGGCAGT   1440
GAGGCCGTGC GGGCAGAGCT GGAGGAGATC ACAGGCAGCC CAAAGCATGT GATGGTCTAC   1500
TCGGATCCTC AGGATCTGTT CAACCAAATC CCTGAGCTGC AGGGGAAGCT GTGCAGCCGG   1560
CAGCGGCCAG GGTGCCGGAC ACAAGCCCTG GACCTCGTCT TCATGTTGGA CACCTCTGCC   1620
TCAGTAGGGC CCGAGAATTT TGCTCAGATG CAGAGCTTTG TGAGAAGCTG TGCCCTCCAG   1680
TTTGAGGTGA ACCCTGACGT GACACAGGTC GGCCTGGTGG TGTATGGCAG CCAGGTGCAG   1740
ACTGCCTTCG GGCTGGACAC CAAACCCACC CGGGCTGCGA TGCTGCGGGC CATTAGCCAG   1800
GCCCCCTACC TAGGTGGGGT GGGCTCAGCC GGCACCGCCC TGCTGCACAT CTATGACAAA   1860
GTGATGACCG TCCAGAGGGG TGCCCGGCCT GGTGTCCCCA AAGCTGTGGT GGTGCTCACA   1920
GGCGGGAGAG GCGCAGAGGA TGCAGCCGTT CCTGCCCAGA AGCTGAGGAA CAATGGCATC   1980
TCTGTCTTGG TCGTGGGCGT GGGGCCTGTC CTAAGTGAGG GTCTGCGGAG GCTTGCAGGT   2040
CCCCGGGATT CCCTGATCCA CGTGGCAGCT TACGCCGACC TGCGGTACCA CCAGGACGTG   2100
CTCATTGAGT GGCTGTGTGG AGAAGCCAAG CAGCCAGTCA ACCTCTGCAA ACCCAGCCCG   2160
TGCATGAATG AGGGCAGCTG CGTCCTGCAG AATGGGAGCT ACCGCTGCAA GTGTCGGGAT   2220
GGCTGGGAGG GCCCCCACTG CGAGAACCGT GAGTGGAGCT CTTGCTCTGT ATGTGTGAGC   2280
CAGGGATGGA TTCTTGAGAC GCCCCTGAGG CACATGGCTC CCGTGCAGGA GGGCAGCAGC   2340
CGTACCCCTC CCAGCAACTA CAGAGAAGGC CTGGGCACTG AAATGGTGCC TACCTTCTGG   2400
AATGTCTGTG CCCCAGGTCC TTAG
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Seq ID NO: 443 Protein sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MPPFLLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN     60
SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR    120
MVFKGGRTET ELALKYLLHR GLPGGRNASV PQILIIVTDG KSQGDVALPS KQLKERGVTV    180
FAVGVRFPRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH    240
PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPFYSWK RVFLTHPATC YRTTCPGPCD    300
SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLLDS SAGTTLDGFL    360
RAKVFVKRFV RAVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPFRGGPT    420
LTGSALRQAA ERGFGSATRT GQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVGS    480
EAVRAELEEI TGSPKHVMVY SDPQDLFNQI PELQGKLCSR QRPGCRTQAL DLVFMLDTSA    540
SVGPENFAQM QSFVRSCALQ FEVNPDVTQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ    600
APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVVLT GGRGAEDAAV PAQKLRNNGI    660
SVLVVGVGPV LSEGLRRLAG PRDSLIHVAA YADLRYHQDV LIEWLCGEAK QPVNLCKPSP    720
CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS    780
RTPPSNYREG LGTEMVPTFW NVCAPGP
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Seq ID NO: 444 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 89..2356

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1          11         21         31         41         51
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GTCGCCGCTC TCCTTCCGTT ATATCAACAT GCCCCCTTTC CTGTTGCTGG AAGCCGTCTG    120
TGTTTTCCTG TTTTCCAGAG TGCCCCCATC TCTCCCTCTC CAGGAAGTCC ATGTAAGCAA    180
AGAAACCATC GGGAAGATTT CAGCTGCCAG CAAAATGATG TGGTGCTCGG CTGCAGTGGA    240
CATCATGTTT CTGTTAGATG GGTCTAACAG CGTCGGGAAA GGGAGCTTTG AAAGGTCCAA    300
GCACTTTGCC ATCACAGTCT GTGACGGTCT GGACATCAGC CCCGAGAGGG TCAGAGTGGG    360
AGCATTCCAG TTCAGTTCCA CTCCTCATCT GGAATTCCCC TTGGATTCAT TTTCAACCCA    420
ACAGGAAGTG AAGGCAAGAA TCAAGAGGAT GGTTTTCAAA GGAGGGCGCA CGGAGACGGA    480
ACTTGCTCTG AAATACCTTC TGCACAGAGG GTTGCCTGGA GGCAGAAATG CTTCTGTGCC    540
CCAGATCCTC ATCATCGTCA CTGATGGGAA GTCCCAGGGG GATGTGGCAC TGCCATCCAA    600
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GCAGCTGAAG GAAAGGGGTG TCACTGTGTT TGCTGTGGGG GTCAGGTTTC CCAGGTGGGA   660
GGAGCTGCAT GCACTGGCCA GCGAGCCTAG AGGGCAGCAC GTGCTGTTGG CTGAGCAGGT   720
GGAGGATGCC ACCAACGGCC TCTTCAGCAC CCTCAGCAGC TCGGCCATCT GCTCCAGCGC   780
CACGCCAGAC TGCAGGGTCG AGGCTCACCC CTGTGAGCAC AGGACGCTGG AGATGGTCCG   840
GGAGTTCGCT GGCAATGCCC CATGCTGGAG AGGATCGCGG CGGACCCTTG CGGTGCTGGC   900
TGCACACTGT CCCTTCTACA GCTGGAAGAG AGTGTTCCTA ACCCACCCTG CCACCTGCTA   960
CAGGACCACC TGCCCAGGCC CCTGTGACTC GCAGCCCTGC CAGAATGGAG GCACATGTGT  1020
TCCAGAAGGA CTGGACGGCT ACCAGTGCCT CTGCCCGCTG GCCTTTGGAG GGGAGGCTAA  1080
CTGTGCCCTG AAGCTGAGCC TGGAATGCAG GGTCGACCTC CTCTTCCTGC TGGACAGCTC  1140
TGCGGGCACC ACTCTGGACG GCTTCCTGCG GGCCAAAGTC TTCGTGAAGC GGTTTGTGCG  1200
GGCCGTGCTG AGCGAGGACT CTCGGGCCCG AGTGGGTGTG GCCACATACA GCAGGGAGCT  1260
GCTGGTGGCG GTGCCTGTGG GGGAGTACCA GGATGTGCCT GACCTGGTCT GGAGCCTCGA  1320
TGGCATTCCC TTCCGTGGTG GCCCCACCCT GACGGGCAGT GCCTTGCGGC AGGCGGCAGA  1380
GCGTGGCTTC GGGAGCGCCA CCAGGACAGG CCAGGACCGG CCACGTAGAG TGGTGGTTTT  1440
GCTCACTGAG TCACACTCCG AGGATGAGGT TGCGGGCCCA GCGCGTCACG CAAGGGCGCG  1500
AGAGCTGCTC CTGCTGGGTG TAGGCAGTGA GGCCGTGCGG GCAGAGCTGG AGGAGATCAC  1560
AGGCAGCCCA AAGCATGTGA TGGTCTACTC GGATCCTCAG GATCTGTTCA ACCAAATCCC  1620
TGAGCTGCAG GGGAAGCTGT GCAGCCGGCA GCGGCCAGGG TGCCGGACAC AAGCCCTGGA  1680
CCTCGTCTTC ATGTTGGACA CCTCTGCCTC AGTAGGGCCC GAGAATTTTG CTCAGATGCA  1740
GAGCTTTGTG AGAAGCTGTG CCCTCCAGTT TGAGGTGAAC CCTGACGTGA CACAGGTCGG  1800
CCTGGTGGTG TATGGCAGCC AGGTGCAGAC TGCCTTCGGG CTGGACACCA AACCCACCCG  1860
GGCTGCGATG CTGCGGGCCA TTAGCCAGGC CCCCTACCTA GGTGGGGTGG GCTCAGCCGG  1920
CACCGCCCTG CTGCACATCT ATGACAAAGT GATGACCGTC CAGAGGGGTG CCCGGCCTGG  1980
TGTCCCCAAA GCTGTGGTGG TGCTCACAGG CGGGAGAGGC GCAGAGGATG CAGCCGTTCC  2040
TGCCCAGAAG CTGAGGAACA ATGGCATCTC TGTCTTGGTC GTGGGCGTGG GGCCTGTCCT  2100
AAGTGAGGGT CTGCGGAGGC TTGCAGGTCC CCGGGATTCC CTGATCCACG TGGCAGCTTA  2160
CGCCGACCTG CGGTACCACC AGGACGTGCT CATTGAGTGG CTGTGTGGAG AAGCCAAGCA  2220
GCCAGTCAAC CTCTGCAAAC CCAGCCCGTG CATGAATGAG GGCAGCTGCG TCCTGCAGAA  2280
TGGGAGCTAC CGCTGCAAGT GTCGGGATGG CTGGGAGGGC CCCCACTGCG AGAACCGATT  2340
CTTGAGACGC CCCTGAGGCA CATGGCTCCC GTGCAGGAGG GCAGCAGCCG TACCCCTCCC  2400
AGCAACTACA GAGAAGGCCT GGGCACTGAA ATGGTGCCTA CCTTCTGGAA TGTCTGTGCC  2460
CCAGGTCCTT AGAATGTCTG CTTCCCGCCG TGGCCAGGAC CACTATTCTC ACTGAGGGAG  2520
GAGGATGTCC CAACTGCAGC CATGCTGCTT AGAGACAAGA AAGCAGCTGA TGTCACCCAC  2580
AAACGATGTT GTTGAAAAGT TTTGATGTGT AAGTAAATAC CCACTTTCTG TACCTGCTGT  2640
GCCTTGTTGA GGCTATGTCA TCTGCCACCT TTCCCTTGAG GATAAACAAG GGGTCCTGAA  2700
GACTTAAATT TAGCGGCCTG ACGTTCCTTT GCACACAATC AATGCTCGCC AGAATGTTGT  2760
TGACACAGTA ATGCCCAGCA GAGGCCTTTA CTAGAGCATC CTTTGGACGG
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Seq ID NO: 445 Protein sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MPPFLLLEAV CVFLPSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN    60
SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR   120
MVFKGGRTET ELALKYLLHR GLPGGRNASV PQILIIVTDG KSQGDVALPS KQLKERGVTV   180
FAVGVRFPRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH   240
PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPFYSWK RVFLTHPATC YRTTCPGPCD   300
SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLLDS SAGTTLDGFL   360
RAKVFVKRFV RAVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPFRGGPT   420
LTGSALRQAA ERGFGSATRT GQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVGS   480
EAVRAELEEI TGSPKHVMVY SDPQDLFNQI PELQGKLCSR QRPGCRTQAL DLVFMLDTSA   540
SVGPENFAQM QSFVRSCALQ FEVNPDVTQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ   600
APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVVLT GGRGAEDAAV PAQKLRNNGI   660
SVLVVGVGPV LSEGLRRLAG PRDSLIHVAA YADLRYHQDV LIEWLCGEAK QPVNLCKPSP   720
CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR FLRRP
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Seq ID NO: 446 DNA sequence
Nucleic Acid Accession #: NM_031942.1
Coding sequence: 145..1260

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1          11         21         31         41         51
|          |          |          |          |          |
CCCGAGCCCC GCCCCTCCGG GCCCGGGTCG GCGCGCCCAG CCTGCCAGCC GCGCTGCTGC    60
TGCTCCTCCT GCTGTGGGAC CGCTGACCGC GCGGCTGCTC CGCTCTCCCC GCTCCAAGCG   120
CCGATCTGGG CACCCGCCAC CAGCATGGAC GCTCGCCGCG TGCCGCAGAA AGATCTCAGA   180
GTAAAGAAGA ACTTAAAGAA ATTCAGATAT GTGAAGTTGA TTTCCATGGA AACCTCGTCA   240
TCCTCTGATG ACAGTTGTGA CAGCTTTGCT TCTGATAATT TTGCAAACAC GAGGCTGCAG   300
TCAGTTCGGG AAGGCTGTAG GACCCGCAGC CAGTGCAGGC ACTCTGGACC TCTCAGGGTG   360
GCGATGAAGT TTCCAGCGCG GAGTACCAGG GGAGCAACCA ACAAAAAAGC AGAGTCCCGC   420
CAGCCCTCAG AGAATTCTGT GACTGATTCC AACTCCGATT CAGAAGATGA AAGTGGAATG   480
AATTTTTTGG AGAAAAGGGC TTTAAATATA AAGCAAAACA AAGCAATGCT TGCAAAACTC   540
ATGTCTGAAT TAGAAAGCTT CCCTGGCTCG TTCCGTGGAA GACATCCCCT CCCAGGCTCC   600
GACTCACAAT CAAGGAGACC GCGAAGGCGT ACATTCCCGG GTGTTGCTTC CAGGAGAAAC   660
CCTGAACGGA GAGCTCGTCC TCTTACCAGG TCAAGGTCCC GGATCCTCGG GTCCCTTGAC   720
GCTCTACCCA TGGAGGAGGA GGAGGAAGAG GATAAGTACA TGTTGGTGAG AAAGAGGAAG   780
ACCGTGGATG GCTACATGAA TGAAGATGAC CTGCCCAGAA GCCGTCGCTC CAGATCATCC   840
GTGACCCTTC CGCATATAAT TCGCCCAGTG GAAGAAATTA CAGAGGAGGA GTTGGAGAAC   900
GTCTGCAGCA ATTCTCGAGA GAAGATATAT AACCGTTCAC TGGGCTCTAC TTGTCATCAA   960
TGCCGTCAGA AGACTATTGA TACCAAAACA AACTGCAGAA ACCCAGACTG CTGGGGCGTT  1020
CGAGGCCAGT TCTGTGGCCC CTGCCTTCGA AACCGTTATG GTGAAGAGGT CAGGGATGCT  1080
CTGCTGGATC CGAACTGGCA TTGCCCGCCT TGTCGAGGAA TCTGCAACTG CAGTTTCTGC  1140
CGGCAGCGAG ATGGACGGTG TGCGACTGGG GTCCTTGTGT ATTTAGCCAA ATATCATGGC  1200
TTTGGGAATG TGCATGCCTA CTTGAAAAGC CTGAAACAGG AATTTGAAAT GCAAGCATAA  1260
TATCTGGAAA ATTTGCTGCC TGCCTTCTAC TTCTCAAATC TTTCTTGTAA AAGTTTCCAA  1320
TTTTTTCACT GAAACCTGAG TTAAAAATCT TGATGATCAG CCTGTTTCAT AAGAAACTCC  1380
AATCAAGTTA ATCTTAGCAG ACATGTGTTT CTGGAGCATC ACAGAAGGTA TATTGCTAGT  1440
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TACACTTTGC CCTCCTGCAG TTTCTTCTCT GCTCCCAACC CCCATCTCAT AGCATCCCCC  1500
TCTATTTCCA ATGCTCCTCT CCAACCGCTT AGTTTCTGAA TTTCTTTTAA ATTACAGTTT  1560
TATGAAAGCA TATTTTATTT ACTTGGTGTT GAAATAGCCC TCATAAAACC TAAGCACTTG  1620
GAAACACAAT AATAGTATTA ACTAACTAGA TCTATTGAAT TTCAGAGAAG AGCCTTCTAA  1680
CTTGTTTACA CAAAAACGAG TATGATTTAG CACTCATACT AGTTGAAATT TTTAATAGAA  1740
TCAAGGCACA AAAGTCTTAA AACCATGTGG AAAAATTAGG TAATTATTGC AGATTGATGT  1800
CTCTCAATCC CATGTATTGC GCTTATGTTA CAAGTTGTTG TCACAGTTGA GACTTAATTT  1860
CTCCTAATTT CTTCTGCCCG AAGGGTAAGT GGTGCGTCCA GCTTACACGA TCATAATTCA  1920
AAGGTTGGTG GGCAATGTAA TACTTAATTA AAATAATGAT GGAAGAGCTA TCTGGAGATT  1980
ATGAGTAAGC TGATTTGAAT TTTCAGTATA AAACTTTAGT ATAATTGTAG TTTGCAAAGT  2040
TTATTTCAGT TCACATGTAA GGTATTGCAA ATAAATTCTT GGACAATTTT GTATGGAAAC  2100
TTGATATTAA AAACTAGTCT GTGGTTCTTT GCAGTTTCTT GTAAATTTAT AAACCAGGCA  2160
CAAGGTTCAA GTTTAGATTT TAAGCACTTT TATAACAATG ATAAGTGCCT TTTTGGAGAT  2220
GTAACTTTTA GCAGTTTGTT AACCTGACAT CTCTGCCAGT CTAGTTTCTG GGCAGGTTTC  2280
CTGTGTCAGT ATTCCCCCTC CTCTTTGCAT TAATCAAGGT ATTTGGTAGA GGTGGAATCT  2340
AAGTGTTTGT ATGTCCAATT TACTTGCATA TGTAAACCAT TGCTGTGCCA TTCAATGTTT  2400
GATGCATAAT TGGACCTTGA ATCGATAAGT GTAAATACAG CTTTTGATCT GTAATGCTTT  2460
TATACAAAAG TTTATTTTAA TAATAAAATG TTTGTTCTAA AAAAAAAAAA
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Seq ID NO: 447 Protein sequence
Protein Accession #: NP_114148.1

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1          11         21         31         41         51
|          |          |          |          |          |
MDARRVPQKD LRVKKNLKKP RYVKLISMET SSSSDDSCDS FASDNFANTR LQSVREGCRT    60
RSQCRHSGPL RVAMKFPARS TRGATNKKAE SRQPSENSVT DSNSDSEDES GMNFLEKRAL   120
NIKQNKAMLA KLMSELESFP GSFRGRHPLP GSDSQSRRPR RRTFPGVASR RNPERRARPL   180
TRSRSRILGS LDALPMEEEE EEDKYMLVRK RKTVDGYMNE DDLPRSRRSR SSVTLPHIIR   240
PVEEITEEEL ENVCSNSREK IYNRSLGSTC HQCRQKTIDT KTNCRNPDCW GVRGQFCGPC   300
LRNRYGEEVR DALLDPNWHC PPCRGICNCS FCRQRDGRCA TGVLVYLAKY HGFGNVHAYL   360
KSLKQEFEMQ A
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Seq ID NO: 448 DNA sequence
Nucleic Acid Accession #: NM_019894
Coding sequence: 1..1314

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1          11         21         31         41         51
|          |          |          |          |          |
ATGTTACAGG ATCCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCCTGCGC    60
AAACCCCGTA TCCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCCATCAT CATAGCACTA   120
CTGAGCCTGG CGAGTATCAT CATTGTGGTT GTCCTCATCA AGGTGATTCT GGATAAATAC   180
TACTTCCTCT GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG   240
CTGGACTGTC CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT   300
GCAGTGGCAG TCCGCCTCTC CAAGGACCGA TCCACACTGC AGGTGCTGGA CTCGGCCACA   360
GGGAACTGGT TCTCTGCCTG TTTCGACAAC TTCACAGAAG CTCTCGCTGA GACAGCCTGT   420
AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG   480
GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTCGCATGCG GAACTCAAGT   540
GGGCCCTGTC TCTCAGGCTC CCTGGTCTCC CTGCACTGTC TTGCCTGTGG GAAGAGCCTG   600
AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC   660
AGCATCCAGT ACGACAAACA GCACGTCTGT GGAGGGAGCA TCCTGGACCC CCACTGGGTC   720
CTCACGGCAG CCCACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA   780
GGCTCAGACA AACTGGGCAG CTTCCCATCC CTGGCTGTGG CCAAGATCAT CATCATTGAA   840
TTCAACCCCA TGTACCCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC   900
ACTTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA   960
GCCACCCCAC TCTGGATCAT TGGATGGGGC TTTACGAAGC AGAATGGAGG GAAGATGTCT  1020
GACATACTGC TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT  1080
GCGTACCAGG GGGAAGTCAC CGAGAAGATG ATGTGTGCAG GCATCCCGGA AGGGGGTGTG  1140
GACACCTGCC AGGGTGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG  1200
GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCCAGG AGTATACACC  1260
AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA
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Seq ID NO: 449 Protein sequence
Protein Accession #: NP_063947.1

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1          11         21         31         41         51
|          |          |          |          |          |
MLQDPDSDQP LNSLDVKPLR KPRIPMETFR KVGIPIIIAL LSLASIIIVV VLIKVILDKY    60
YFLCGQPLHF IPRKQLCDGE LDCPLGEDEE HCVKSFPEGP AVAVRLSKDR STLQVLDSAT   120
GNWFSACFDN FTEALAETAC RQMGYSSKPT FRAVEIGPDQ DLDVVEITEN SQELRMRNSS   180
GPCLSGSLVS LHCLACGKSL KTPRVVGGEE ASVDSWPWQV SIQYDKQHVC GGSILDPHWV   240
LTAAHCFRKH TDVFNWKVRA GSDKLGSFPS LAVAKIIIIE FNPMYPKDND IALMKLQFPL   300
TFSGTVRPIC LPFFDEELTP ATPLWIIGWG FTKQNGGKMS DILLQASVQV IDSTRCNADD   360
AYQGEVTEKM MCAGIPEGGV DTCQGDSGGP LMYQSDQWHV VGIVSWGYGC GGPSTPGVYT   420
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Seq ID NO: 450 DNA sequence
Nucleic Acid Accession #: XM_051860.2
Coding sequence: 52..3042

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1          11         21         31         41         51
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GCTCACCCAG GAAAAATATG CAATCGTCCC ATTGATATAC AGGCCACTAC AATGGATGGA    60
GTTAACCTCA GCACCGAGGT TGTCTACAAA AAAGGCCAGG ATTATAGGTT TGCTTGCTAC   120
GACCGGGGCA GAGCCTGCCG GAGCTACCGT GTACGGTTCC TCTGTGGGAA GCCTGTGAGG   180
CCCAAACTCA CAGTCACCAT TGACACCAAT GTGAACAGCA CCATTCTGAA CTTGGAGGAT   240
AATGTACAGT CATGGAAACC TGGAGATACC CTGGTCATTG CCAGTACTGA TTACTCCATG   300
TACCAGGCAG AAGAGTTCCA GGTGCTTCCC TGCAGATCCT GCGCCCCCAA CCAGGTCAAA   360
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GTGGCAGGGA AACCAATGTA CCTGCACATC GGGGAGGAGA TAGACGGCGT GGACATGCGG   420
GCGGAGGTTG GGCTTCTGAG CCGGAACATC ATAGTGATGG GGGAGATGGA GGACAAATGC   480
TACCCCTACA GAAACCACAT CTGCAATTTC TTTGACTTCG ATACCTTTGG GGGCCACATC   540
AAGTTTGCTC TGGGATTTAA GGCAGCACAC TTGGAGGGCA CGGAGCTGAA GCATATGGGA   600
CAGCAGCTGG TGGGTCAGTA CCCGATTCAC TTCCACCTGG CCGGTGATGT AGACGAAAGG   660
GGAGGTTATG ACCCACCCAC ATACATCAGG GACCTCTCCA TCCATCATAC ATTCTCTCGC   720
TGCGTCACAG TCCATGGCTC CAATGGCTTG TTGATCAAGG ACGTTGTGGG CTATAACTCT   780
TTGGGCCACT GCTTCTTCAC GGAAGATGGG CCGGAGGAAC GCAACACTTT TGACCACTGT   840
CTTGGCCTCC TTGTCAAGTC TGGAACCCTC CTCCCCTCGG ACCGTGACAG CAAGATGTGC   900
AAGATGATCA CAGGAGACTC CTACCCAGGG TACATCCCCA AGCCCAGGCA AGACTGCAAT   960
GCTGTGTCCA CCTTCTGGAT GGCCAATCCC AACAACAACC TCATCAACTG TGCCGCTGCA  1020
GGATCTGAGG AAACTGGATT TTGGTTTATT TTTCACCACG TACCAACGGG CCCCTCCGTG  1080
GGAATGTACT CCCCAGGTTA TTCAGAGCAC ATTCCACTGG GAAAATTCTA TAACAACCGA  1140
GCACATTCCA ACTACCGGGC TGGCATGATC ATAGACAACG GAGTCAAAAC CACCGAGGCC  1200
TCTGCCAAGG ACAAGCGGCC GTTCCTCTCA ATCATCTCTG CCAGATACAG CCCTCACCAG  1260
GACGCCGACC CGCTGAAGCC CCGGGAGCCG GCCATCATCA GACACTTCAT TGCCTACAAG  1320
AACCAGGACC ACGGGGCCTG GCTGCGCGGC GGGGATGTGT GGCTGGACAG CTGCCGGTTT  1380
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TCCAAGCAAG AGATAAAGAA CAGCTTGTTT GTTGGCGAGA GTGGCAACGT GGGGACGGAA  1500
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Seq ID NO: 451 Protein sequence
Protein Accession #: XP_051860.2

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Seq ID NO: 452 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 261..2861

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Seq ID NO: 453 Protein sequence
Protein Accession #: Eos sequence

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CACGCAGAAA TGGCCTCAAG GGGACTCTGC TCCACGTGGG GCCAGGCGTG TGACTGACGC  3180
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Seq ID NO: 455 Protein sequence
Protein Accession #: NP_037414.2

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PADEDMWDET ELGLYKVNEY VDARDTNMGA WFEAQVVRVT RKAPSRDEPC SSTSRPALEE   180
DVIYHVKYDD YPENGVVQMN SRDVRARART IIKWQDLEVG QVVMLNYNPD NPKERGFWYD   240
AEISRKRETR TARELYANVV LGDDSLNDCR IIFVDEVFKI ERPGEGSPMV DNPMRRKSGP   300
SCKHCKDDVN RLCRVCACHL CGGRQDPDKQ LMCDECDMAF HIYCLDPPLS SVPSEDEWYC   360
PECRNDASEV VLAGERLRES KKKAKMASAT SSSQRDWGKG MACVGRTKEC TIVPSNHYGP   420
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SGGRDLSGNK RTAEQSCDQK LTNTNRALAL NCFAPINDQE GAEAKDWRSG KPVRVVRNVK   540
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LGLTMQYPEG YLEALANRER EKENSKREEE EQQEGGFASP RTGKGKWKRK SAGGGPSRAG   660
SPRRTSKKTK VEPYSLTAQQ SSLIREDKSN AKLWNEVLAS LKDRPASGSP FQLFLSKVEE   720
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Seq ID NO: 456 DNA sequence
Nucleic Acid Accession #: NM_001200.1
Coding sequence: 325..1514

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Seq ID NO: 457 Protein sequence
Protein Accession #: NP_001191.1

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FGLKQRPTPS RDAVVPPYML DLYRRHSGQP GSPAPDHRLE RAASRANTVR SFHHEESLEE   120
LPETSGKTTR RFFFNLSSIP TEEFITSAEL QVFREQMQDA LGNNSSFHHR INIYEIIKPA   180
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Seq ID NO: 458 DNA sequence
Nucleic Acid Accession #: NM_001999.2
Coding sequence: 1..8736

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CAGCCGCCGC CGCAACAGGT TCGGTCCGCT ACAGCAGGCT CTGAAGGCGG GTTTCTAGCG   180
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CTGTGCTGAC CAAAGATTAG TAACCAGTTA TACCCAGTAT TTTGAGGTTT TATTGTTTTT 10140
TTAATAACTA AAAAAAAACT CGTGCC
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Seq ID NO: 459 Protein sequence
Protein Accession #: NP_001990.1

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PEYREEGAAV ASRVRRRGQQ DVLRGPNVCG SRFHSYCCPG WKTLPGGNQC IVPICRNSCG   120
DGFCSRPNMC TCSSGQISST CGSKSIQQCS VRCMNGGTCA DDHCQCQKGY IGTYCGQPVC   180
ENGCQNGGRC IAQPCACVYG FTGPQCERDY RTGPCFTQVN NQMCQGQLTG IVCTKTLCCA   240
TTGRAWGHPC EMCPAQPQPC RRGFIPNIRT GACQDVDECQ AIPGICQGGN CINTVGSFEC   300
RCPAGHKQSE TTQKCEDIDE CSIIPGICET GECSNTVGSY FCVCPRGYVT STDGSRCIDQ   360
RTGMCFSGLV NGRCAQELPG RMTKMQCCCE PGRCWGIGTI PEACPVRGSE EYRRLCMDGL   420
PMGGIPGSAG SRPGGTGGNG FAPSGNGNGY GPGGTGFIPI PGGNGFSPGV GGAGVGAGGQ   480
GPIITGLTIL NQTIDICKHH ANLCLNGRCI PTVSSYRCEC NMGYKQDANG DCIDVDECTS   540
NPCTNGDCVN TPGSYYCKCH AGFQRTPTKQ ACIDIDECIQ NGVLCKNGRC VNSDGSFQCI   600
CNAGFELTTD GKNCVDHDEC TTTNMCLNGM CINEDGSFKC ICKPGFVLAP NGRYCTDVDE   660
CQTPGICMNG HCINSEGSFR CDCPPGLAVG MDGRVCVDTH MRSTCYGGIK KGVCVRPFPG   720
AVTKSECCCA NPDYGFGEPC QPCPAKNSAE FHGLCSSGVG ITVDGRDINE CALDPDICAN   780
GICENLRGSY RCNCNSGYEP DASGRNCIDI DECLVNRLLC DNGLCRNTPG SYSCTCPPGY   840
VFRTETETCE DINECESNPC VNGACRNNLG SFNCECSPGS KLSSTGLICI DSLKGTCWLN   900
IQDSRCEVNI NGATLKSECC ATLGAAWGSP CERCELDTAC PRGLARIKGV TCEDVNECEV   960
FPGVCPNGRC VNSKGSFHCE CPEGLTLDGT GRVCLDIRME QCYLKWDEDE CIHPVPGKFR  1020
MDACCCAVGA AWGTECEECP KPGTKEYETL CPRGAGFANR GDVLTGRPFY KDINECKAFP  1080
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GQVCRNGRCF NEIGSFKCLC NEGYELTPDG KNCIDTNECV ALPGSCSPGT CQNLEGSFRC  2040
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SFCFTNFENG KCSVPKAFNT TKAKCCCSKM PGEGWGDPCE LCPKDDEVAF QDLCPYGHGT  2160
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GYALREDQKM CKDLDECAEG LHDCESRGMM CKNLIGTFMC ICPPGMARRP DGEGCVDENE  2340
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GYIQHYQWNQ CVDENECSNP NACGSASCYN TLGSYKCACP SGFSFDQFSS ACHDVNECSS  2700
SKNPCNYGCS NTEGGYLCGC PPGYYRVGQG HCVSGMGFNK GQYLSLDTEV DEENALSPEA  2760
CYECKINGYP KKDSRQKRSI HEPDPTAVEQ ISLESVDMDS PVNMKFNLSH LGSKEHILEL  2820
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Seq ID NO: 460 DNA sequence
Nucleic Acid Accession #: NM_013372.1
Coding sequence: 63..617

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AGCACAATGA CTCAGAGCAG ACTCAGTCGC CCCAGCAGCC TGGCTCCAGG AACCGGGGGC   240
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CCCTGCATGT GACGGAGCGC AAATACCTGA AGCGAGACTG GTGCAAAACC CAGCCGCTTA   360
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CCTGCTCCTT CTGCAAGCCC AAGAAATTCA CTACCATGAT GGTCACACTC AACTGCCCTG   540
AACTACAGCC ACCTACCAAG AAGAAGAGAG TCACACGTGT GAAGCAGTGT CGTTGCATAT   600
CCATCGATTT GGATTAAGCC AAATCCAGGT GCACCCAGCA TGTCCTAGGA ATGCAGCCCC   660
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AACCCCCAGC TGCCTCCTGG CAGGAGCCTG CTTGTGCGTA GTTCGTGTGC ATGAGTGTGG   780
ATGGGTGCCT GTGGGTGTTT TTAGACACCA GAGAAAACAC AGTCTCTGCT AGAGAGCACT   840
CCCTATTTTG TAAACATATC TGCTTTAATG GGATGTACCC AGAAACCCAC CTCACCCCGG   900
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CTTTCCTCCT CCTCCTCACA ATCCATCTCT TCTTAAGTTG ATAGTGACTA TGTCAGTCTA   1140
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Seq ID NO: 461 Protein sequence
Protein Accession #: NP_037504.1

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Seq ID NO: 462 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..2733

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GAGAAAAGAG ATTTGAGAAA TTTTCTGAAG CTCTTGAAGC CTCCATTATT ATGGTCACAT    240
GGGCTAATTA GAATTATCAG AGCAAAGGCT ACCACAGACT GCAACAGCCT GAATGGAGTC    300
CTGCAGTGTA CCTGTGAAGA CAGCTACACC TGGTTTCCTC CCTCATGCCT TGATCCCCAG    360
AACTGCTACC TTCACACGGC TGGAGCACTC CCAAGCTGTG AATGTCATCT CAACAACCTC    420
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Seq ID NO: 463 Protein sequence
Protein Accession #: Eos sequence

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LFPLEDGSFR VFGKAQCNDI VFGFGSKDDE YTLPCSSGYR GNITAKCESS GWQVIRETCV   300
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ASHFRVSNST MEDVISIADN ILNSASVTNW TVLLREEKYA SSRLLETLEN ISTLVPPTAL   420
PLNFSRKFID WKGIPVNKSQ LKRGYSYQIK MCPQNTSIPI RGRVLIGSDQ FQRSLPETII   480
SMASLTLGNI LPVSKNGNAQ VNGPVISTVI QNYSINEVFL FFSKIESNLS QPHCVFWDFS   540
HLQWNDAGCH LVNETQDIVT CQCTHLTSFS ILMSPFVPST IFPVVKWITY VGLGISIGSL   600
ILCLIIEALF WKQIKKSQTS HTRRICMVNI ALSLLIADVW FIVGATVDTT VNPSGVCTAA   660
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TQPSNTYKRK DVCWLNWSNG SKPLLAFVVP ALAIVAVNFV VVLLVLTKLW RPTVGERLSR   780
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Seq ID NO: 464 DNA sequence
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Coding sequence: 9845..10219

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TTGGTTTGAA AGCATACAGT AAATATGATG TCTGTCCCTG GCAGTGTTGG CAGAGTAGGA   240
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Seq ID NO: 465 Protein sequence
Protein Accession #: BAB21525.1

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DAIKKFYQTS VESTDFANAP EESRKKINSW VESQTNEKIK NLFPDGTIGN DTTLVLVNAI   180
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Coding sequence: 50..1240

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Protein Accession #: NP_001901.1

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FDGILGLGYP SLAVGGVTPV FDNMMAQNLV DLPMFSVYMS SNPEGGAGSE LIFGGYDHSH    240
FSGSLNWVPV TKQAYWQIAL DNIQVGGTVM FCSEGCQAIV DTGTSLITGP SDKIKQLQNA    300
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CCCAAGCCCA TCCATGCACA TTACTTAGCT AACAATTAGG GAGACTCGTA AGGCCAGGCC 1800
CTGTGCTGGG CACATAGCTG TGATCACAGC AGACAGGGTC GCTGCCCTGA TGGCGCTTAC 1860
ATTCCAGTGG GTCTAATGAC CATATCTTAG GACACAGATG TGCCCAGGGA GGTGGTGTCA 1920
CTGCACAGGA AGTATGAGGA CTTTAGTGTC CTGAGTTCAA ATCCTGATTC AGGAACTCAC 1980
AAAGCTATGT GACCTTACAC CAGTCACTTA ACTTGTTAGC CATCCATTAT CGCATCTGCA 2040
AAATGGGGAT TAAGAATAGA ATCTTGGGGT TAGTGTGGAG ATTAGATTAA ATGTATGTAA 2100
GACACTTGGC ACAAAACCTG GCACATAGTA AAGGCTCAAT AAAAACAAGT GCCTCTCACT 2160
GGGCTTTGTC AACACGTG

Seq ID NO: 469 Protein sequence
Protein Accession #: NP_060528.1

1 11 21 31 41 51
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MDPEASDLSR GILALRDVAA EAGVSKYTGG RGVSVGPILS SSASDIFCDN ENGPNFLFHN 60
RGDGTFVDAA ASAGVDDPHQ HGRGVALADF NRDGKVDIVY GNWNGPHRLY LQMSTHGKVR 120
FRDIASPKFS MPSPVRTVIT ADFDNDQELE IFFNNIAYRS SSANRLFRVI RREHGDPLIE 180
ELNPGDALEP EGRGTGGVVT DFDGDGMLDL ILSHGESMAQ PLSVFRGNQG FNNNWLRVVP 240
RTRVGAFARG AKVVLYTKKS GAHLRIIDGG SGYLCEMEPV AHFGLGKDEA SSVEVTWPDG 300
KMVSRNVASG EMNSVLEILY PRDEDTLQDP APLETPMNAS SSHSCALETS PYVSTPMEAT 360
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Seq ID NO: 470 DNA sequence
Nucleic Acid Accession #: AJ279016
Coding sequence: 1..1962

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AGTAATCCCA CCCAGCTCAA CTATGGTGTG GCAGTTACTG ATGTGGACCA TGATGGGGAC 180
TTTGAGATCG TCGTGGCGGG GTACAATGGA CCCAACCTGG TTCTGAAGTA TGACCGGGCC 240
CAGAAGCGGC TGGTGAACAT CGCGGTCGAT GAGCGCAGCT CACCCTACTA CGCGCTGCGG 300
GACCGGCAGG GGAACGCCAT CGGGGTCACA GCCTGCGACA TCGACGGGGA CGGCCGGGAG 360
GAGATCTACT TCCTCAACAC CAATAATGCC TTCTCGGGGG TGGCCACGTA CACCGACAAG 420
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GGACGCTACT CTATCTACAT TGCCAATTAC GCCTACGGTA ATGTGGGCCC TGATGCCCTC 600
ATTGAAATGG ACCCTGAGGC CAGTGACCTC TCCCGGGGCA TTCTGGCGCT CAGAGATGTG 660
GCTGCTGAGG CTGGGGTCAG CAAATATACA GGGGGCCGAG GCGTCAGCGT GGGCCCCATC 720
CTCAGCAGCA GTGCCTCGGA TATCTTCTGC GACAATGAGA ATGGGCCTAA CTTCCTTTTC 780
CACAACCGGG GCGATGGCAC CTTTGTGGAC GCTGCGGCCA GTGCTGGTGT GGACGACCCC 840
CACCAGCATG GGCGAGGTGT CGCCCTGGCT GACTTCAACC GTGATGGCAA AGTGGACATC 900
GTCTATGGCA ACTGGAATGG CCCCCACCGC CTCTATCTGC AAATGAGCAC CCATGGGAAG 960
GTCCGCTTCC GGGACATCGC CTCACCCAAG TTCTCCATGC CCTCCCCTGT CCGCACGGTC 1020
ATCACCGCCG ACTTTGACAA TGACCAGGAG CTGGAGATCT TCTTCAACAA CATTGCCTAC 1080
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GCTGCTGCCG CTGCTGGAGC TGCCACTGCT GCACCGGTCC TCGTAGATGG AGATCTCAAT 1920
CTGGGGTCGG TGGTTAAGGA GAGCTGCGAG CCCAGCTGCT GAGCAGGGGT GGGACATGAA 1980
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GGACACAGAT GTGCCCAGGG AGGTGGTGTC ACTGCACAGG AAGTATGAGG ACTTTAGTGT 2280
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AACTTGTTAG CCATCCATTA TCGCATCTGC AAAATGGGGA TTAAGAATAG AATCTTGGGG 2400
TTAGTGTGGA GATTAGATTA AATGTATGTA AGACACTTGG CACAAAACCT GGCACATAGT 2460
AAAGGCTCAA TAAAAACAAG TGCCTCTCAC TGGGCTTTGT CAACACG

Seq ID NO: 471 Protein sequence
Protein Accession #: CAC08451

1 11 21 31 41 51
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FEIVVAGYNG PNLVLKYDRA QKRLVNIAVD ERSSPYYALR DRQGNAIGVT ACDIDGDGRE 120
EIYFLNTNNA FSGVATYTDK LFKFRNNRWE DILSDEVNVA RGVASLFAGR SVACVDRKGS 180

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GRYSIYIANY AYGNVGPDAL IEMDPEASDL SRGILALRDV AAEAGVSKYT GGRGVSVGPI   240
LSSSASDIFC DNENGPNFLF HNRGDGTFVD AAASAGVDDP HQHGRGVALA DFNRDGKVDI   300
VYGNWNGPHR LYLQMSTHGK VRFRDIASPK FSMPSPVRTV ITADFDNDQE LEIFFNNIAY   360
RSSSANRLFR VIRREHGDPL IEELNPGDAL EPEGRGTGGV VTDFDGDGML DLILSHGESM   420
AQPLSVFRGN QGFNNNWLRV VPRTRFGAFA RGAKVVLYTK KSGAHLRIID GGSGYLCEME   480
PVAHFGLGKD EASSVEVTWP DGKMVSRNVA SGEMNSVLEI LYPRDEDTLQ DPAPLECGQG   540
FSQQENGHCM DTNECIQFPP VCPRDKPVCV NTYGSYRCRT NKKCSRGYEP NEDGTACVGT   600
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Seq ID NO: 472 DNA sequence
Nucleic Acid Accession #: FGENESHH
Coding sequence: 1..4794

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TCACCCTACT ACGCGCTGCG GGACCGGCAG GGGAACGCCA TCGGGGTCAC AGCCTGCGAC    240
ATCGACGGGG ACGGCCGGGA GGAGATCTAC TTCCTCAACA CCAATAATGC CTTCTCGGGC    300
CACAGCAGCT CAGCGCAGGT CCCTTCTGGG CTCCACAGAA ACAGGCCTGT GCTGAAGCCT    360
CCACCTACAA CCCCTGCAGG CCTCCTGGGT CTGCCTCCAC TCAGCGGAAG GGACTTTTCC    420
TCCTCCCTGG GTCAGGCTTC TCCGGACAGC AGGCAGGGAG AGAGGGTGCC GGTTCCCTGC    480
TGTCGGGGTG GACTGAGACC TACCCATGAA CCAGAACCAT TTCTTCTGAG ACCCAAATCA    540
GGGGTGGCCA CGTACACCGA CAAGTTGTTC AAGTTCCGCA ATAACCGGTG GGAAGACATC    600
CTGAGCGATG AGGTCAACGT GGCCCGTGGT GTGGCCAGCC TCTTTGCCGG ACGCTCTGTG    660
GCCTGTGTGG ACAGAAAGGG CTCTGGACGC TACTCTATCT ACATTGCCAA TTACGCCTAC    720
GGTAATGTGG GCCCTGATGC CCTCATTGAA ATGGACCCTG AGGCCAGTGA CCTCTCCCGG    780
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TTCTCCCACA CTGCCTCTCC AAGCATTGGT GAGATATCTG GCAGAACCGA GGAGCGGGAA    900
GGAGGAGACC CAGAGGAGGC AGATGAGGAG CACAGTGGGG ATGGAAGCAC CAGCCAACTG    960
TGCCGGCTGG GCTGGAAGGA CGGGCAGTTC AAGGAAGAAG CAGCAGCTTT GGTGGAGGAA   1020
CAGAGGGAGG CTGGGGCAGC TGGCGTGCCC AGAGGACGTG TTCGAACAGC TCTGCAGACT   1080
TCCAAAAGCC ATTTGGCTGA CAAGAACCTA TTTGGCCCAC CATGTTACTA TTCTGTCTGC   1140
GCGCCTTCTC CAGCCCACCC TTTCCCTGCC CGCCAAGCCC CCCAACACTA CCCTGTAGCC   1200
CCCCTTGTCA CTCAGCTAAT GACACATGGA CGTCTGGCTG GAAAACTAGC CCGGAGTGTC   1260
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CTGAGAAGCT GGGAGGAAAG CAGGCAGAAG GGGCAGGCCA TGTCCAGATG TGCACTCAGG   1440
GAGCTGGGAG GTCCCTGGAG CCAAGCCACA CAGCACCTGC CTGCTAGAGA GCTGTATGAC   1500
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CTCTCCCATC CCCTGGTCCC CAACTTCCCC AGCTGCTTGA GGCCTCTTGA AGCCGGGACA   1740
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CTGGCGTGGA ACCAGATGGA AAAAGAGGAG GGGAAGATTC ATGGAGACCA TGAGCCCAGA   1860
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GCCTTCATCG TTCACCTCAA ATATCACCTC TGCAGAGATT TTCCTCACTC CCTGTGCCAC   2220
CTAGCAGAAA CTGGTCCTTC CTCCTCCTGC TGCCCGTGGC ATGCACGTCT TCTTCAGGCT   2280
CCACATTGCC ATCATGGTTT GTCTATGAGC TTTACAAGGA CCGGGTCACG GTTCTATTCA   2340
TTCTTGACGC AAGGCTTGGC CTCCAGTGCC CACCGGAGGA CACTCAGCCT CCAGGGTTCT   2400
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ACTGCCTATT ACATTGTCCT GTGGTCTGCC ATCCCAGAGA GCCTGATGAC CCACAGCTAT   2520
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GCCCTGGCTG ACTTCAACCG TGATGGCAAA GTGGACATCG TCTATGGCAA CTGGAATGGC   2640
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GACCAGGAGC TGGAGATCTT CTTCAACAAC ATTGCCTACC GCAGCTCCTC AGCCAACCGC   2820
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GGTCAGGGAG AAGGTTTAAG AATCAGAAGG GGAGGGTTCC CAGGGCCAGG GGGTCAGGCC   2940
AAGGTCAACA CAGGTCCCCT GATGAAGAAA CAGAAAGGAA GGAAGGACGA GGACTGGGCA   3000
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AAAGGGAAGG GAAATGTGGC CCAAAGTGTG CCCAGAACCC AAGCGCCACA AGATACAAAG   3120
CCACACTACC ACAAAAAGGG GCTACAGGGT CCAATCACTA CCAGGAAAAG GGGCTACGGG   3180
GTCCAATCAC TACCAGGAAA AGGGGCTACG GGGTCCAATC ACTACCAGGA AAAGGGGCTA   3240
CGGGGTCCAA TCACTACCAG GAAAAGGGGC TACGGGGTCC AATCACTACC AGGAAAAGGG   3300
GCTACGGGCT CCAATCACTA CCAGGAAAAG GGGCTACAGG GTCCAATCAC TACCAGGAAA   3360
AGGGGCTACG GGCTCCAATC ACTACCAGGA AAAGGGGCTA CAGGGTCCAA TCACTACCAC   3420
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CCAGGAAAAG GGGCTACAGG GTCCAATCAC TACCAGGAAA AGGGGCTACG GGGTCCAATC   3540
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CGGGGTCCAA TCACTACCAG GAAAAGGGGC TACGGGCTCC AATCACTACC AGGAAAAGAG   3780
GCTATGGGGT CCAATCACTA CCAGGAAAAG GGGCTACGGG CTCCAATCAC TACCAGGAAA   3840
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AGAGAGCACG GAGACCCCCT CATCGAGGAG CTCAATCCCG GCGACGCCTT GGAGCCTGAG   3960
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TTGTCCCATG GAGAGTCCAT GGCTCAGCCG CTGTCCGTCT TCCGGGGCAA TCAGGGCTTC   4080
AACAACAACT GGCTGCGAGT GGTGCCACGC ACCCGGTTTG GGGCCTTTGC CAGGGGAGCT   4140
AAGGTCGTGC TCTACACCAA GAAGAGTGGG GCCCACCTGA GGATCATCGA CGGGGGCTCA   4200
GGCTACCTGT GTGAGATGGA GCCCGTGGCA CACTTTGGCC TGGGGAAGGA TGAAGCCAGC   4260
AGTGTGGAGG TGACGTGGCC AGATGGCAAG ATGGTGAGCC GGAACGTGGC CAGCGGGGAG   4320
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ATGAACTCAG TGCTGGAGAT CCTCTACCCC CGGGATGAGG ACACACTTCA GGACCCAGCC  4380
CCACTGGAGT GTGGCCAAGG ATTCTCCCAG CAGGAAAATG GCCATTGCAT GGACACCAAT  4440
GAATGCATCC AGTTCCCATT CGTGTGCCCT CGAGACAAGC CCGTATGTGT CAACACCTAT  4500
GGAAGCTACA GGTGCCGGAC CAACAAGAAG TGCAGTCGGG GCTACGAGCC CAACGAGGAT  4560
GGCACAGCCT GCGTGGGTAC TGAGCTAGGC TCTAGGCATA CAATGACGTG GAAACCAAGG  4620
CCCAAAAAGG AGCTGCAACT TTCCCAAGGC ATCTGCACCC CCGTCTGGTC CTTTTTCCTG  4680
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Seq ID NO: 473 Protein sequence
Protein Accession #: FGENESH predicted

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SPYYALRDRQ GNAIGVTACD IDGDGREEIY FLNTNNAFSG HSSSAQVPSG LHRNRPVLKP   120
PPTTPAGLLG LPPLSGRDFS SSLGQASPDS RQGERVPVPC CRGGLRPTHE PEPFLLRPKS   180
GVATYTDKLF KFRNNRWEDI LSDEVNVARG VASLFAGRSV ACVDRKGSGR YSIYIANYAY   240
GNVGPDALIE MDPEASDLSR GILALRDVAA EAGVSKYTEG FSHTASPSIG EISGRTEERE   300
GGDPEEADEE HSGDGSTSQL CRLGWKDGQF KEEAAALVEE QREAGAAGVP RGRVRTALQT   360
SKSHLADKNL FGPPCYYSVC APSPAHPFPA RQAPQHYPVA PLVTQLMTHG RLAGKLARSV   420
PHPRAPGMDP KCKGRHAEPG LMAEALGAWP ALSTTVVPGG LRSWEESRQK GQAMSRCALR   480
ELGGPWSQAT QHLPARELYD LGEPPILQRT DGDPGRRRDS PKVTQECHLV ATMPALGGLE   540
GPGRVAKREI GRETGAVGRP LSHPLVPNFP SCLRPLEAGT VPGAALPGNP GNWVLDMAKA   600
LAWNQMEKEE GKIHGDHEPR FRLRKAREAE FPPGSSEEPL LQFPSGLRGS PVLQVGLGLA   660
SATHCGSMSF LGGRGVSVGP ILSSSASDIF CDNENGPNFL FHNRGDGTFV DAAASAERRL   720
AFIVHLKYHL CRDFPHSLCH LAETGPSSSC CPWHARLLQA PHCHHGLSMS FTRTGSRFYS   780
FLTQGLASSA HRRTLSLQGS QGAPPCLLAR APCVLGSLIP TAYYIVLWSA -IPESLMTHSY   840
LSSERVNVGV DDPHQHGRGV ALADFNRDGK VDIVYGNWNG PHRLYLQMST HGKVRFRDIA   900
SPKFSMPSPV RTVITADFDN DQELEIFFNN IAYRSSSANR LFRCSILARG SSSLTAGGRN   960
GQGEGLRIRR GGFPGPGGQA KVNTGPLMKK QKGRKDEDWA RGCGNAGQSL AKEPASAIAG  1020
KGKGNVAQSV PRTQAPQDTK PHYHKKGLQG PITTRKRGYG VQSLPGKGAT GSNHYQEKGL  1080
RGPITTRKRG YGVQSLPGKG ATGSNHYQEK GLQGPITTRK RGYGLQSLPG KGATGSNHYH  1140
RKGLRAPITT RKRGYGVQSL PGKGATGSNH YQEKGLRGPI TTRKRGYGLQ SLPGKGATGS  1200
NHYQEKGLQG PITTRKRGYR VQSLPQKGAT GSNHYQEKGL RGPITTRKRG YGLQSLPGKE  1260
AMGSNHYQEK GLRAPITTRK RGYGVQSLPQ KGATGSNVIR REHGDPLIEE LNPGDALEPE  1320
GRGTGGVVTD FDGDGMLDLI LSHGESMAQP LSVFRGNQGF NNNWLRVVPR TRFGAFARGA  1380
KVVLYTKKSG AHLRIIDGGS GYLCEMEPVA HFGLGKDEAS SVEVTWPDGK MVSRNVASGE  1440
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GSYRCRTNKK CSRGYEPNED GTACVGTELG SRHTMTWKPR PKKELQLSQG ICTPVWSFFL  1560
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Seq ID NO: 474 DNA sequence
Nucleic Acid Accession #: NM_003661.1
Coding sequence: 1..1152

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GCTGCTGGCA CCATGGACCC AGAGAGCAGT ATCTTTATTG AGGATGCCAT TAAGTATTTC   180
AAGGAAAAAG TGAGCACACA GAATCTGCTA CTCCTGCTGA CTGATAATGA GGCCTGGAAC   240
GGATTCGTGG CTGCTGCTGA ACTGCCCAGG AATGAGGCAG ATGAGCTCCG TAAAGCTCTG   300
GACAACCTTG CAAGACAAAT GATCATGAAA GACAAAAACT GGCACGATAA AGGCCAGCAG   360
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ACACGAGGCA TTGGGAAGGA CATCCGTGCC CTCAGACGAG CCAGAGCCAA TCTTCAGTCA   840
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Seq ID NO: 475 Protein sequence
Protein Accession #: NP_003652.1

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YRNWFLKEFP RLKSELEDNI RRLRALADGV QKVHKGTTIA NVVSGSLSIS SGILTLVGMG   180
LAPFTEGGSL VLLEPGMELG ITAALTGITS STMDYGKKWW TQAQAHDLVI KSLDKLKEVR   240
EFLGENISNF LSLAGNTYQL TRGIGKDIRA LRRARANLQS VPHASASRPR VTEPISAESG   300
EQVERVNEPS ILEMSRGVKL TDVAPVSFFL VLDVVYLVYE SKHLHEGAKS ETAEELKKVA   360
QELEEKLNIL NNNYKILQAD QEL
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Seq ID NO: 476 DNA sequence
Nucleic Acid Accession #: NM_014452.1
Coding sequence: 1..1968

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GCTCAGCCAG AACAGAAGGC CTCGAATCTC ATTGGCACAT ACCGCCATGT TGACCGTGCC   180
ACCGGCCAGG TGCTAACCTG TGACAAGTGT CCAGCAGGAA CCTATGTCTC TGAGCATTGT   240
ACCAACACAA GCCTGCGCGT CTGCAGCAGT TGCCCTGTGG GGACCTTTAC CAGGCATGAG   300
AATGGCATAG AGAAATGCCA TGACTGTAGT CAGCCATGCC CATGGCCAAT GATTGAGAAA   360
TTACCTTGTG CTGCCTTGAC TGACCGAGAA TGCACTTGCC CACCTGGCAT GTTCCAGTCT   420
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ACAGAGACTG AGGATGTGCG GTGTAAGCAG TGTGCTCGGG GTACCTTCTC AGATGTGCCT   540
TCTAGTGTGA TGAAATGCAA AGCATACACA GACTGTCTGA GTCAGAACCT GGTGGTGATC   600
AAGCCGGGGA CCAAGGAGAC AGACAACGTC TGTGGCACAC TCCCGTCCTT CTCCAGCTCC   660
ACCTCACCTT CCCCTGGCAC AGCCATCTTT CCACGCCCTG AGCACATGGA AACCCATGAA   720
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TCTGTTAGAC CAAAGGTACT GAGTAGCATC CAGGAAGGGA CAGTCCCTGA CAACACAAGC   840
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CAGCAAGGCC CCCACCACAG ACACATCCTG AAGCTGCTGC CGTCCATGGA GGCCACTGGG   960
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CACAAGCATT TTGACATCAA TGAGCATTTG CCCTGGATGA TTGTGCTTTT CCTGCTGCTG  1080
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CCCCGGCAGG ATCCCAGTGC CATTGTGGAA AAGGCAGGGC TGAAGAAATC CATGACTCCA  1200
ACCCAGAACC GGGAGAAATG GATCTACTAC TGCAATGGCC ATGGTATCGA TATCCTGAAG  1260
CTTGTAGCAG CCCAAGTGGG AAGCCAGTGG AAAGATATCT ATCAGTTTCT TTGCAATGCC  1320
AGTGAGAGGG AGGTTGCTGC TTTCTCCAAT GGGTACACAG CCGACCACGA GCGGGCCTAC  1380
GCAGCTCTGC AGCACTGGAC CATCCGGGGC CCCGAGGCCA GCCTCGCCCA GCTAATTAGC  1440
GCCCTGCGCC AGCACCGGAG AAACGATGTT GTGGAGAAGA TTCGTGGGCT GATGGAAGAC  1500
ACCACCCAGC TGGAAACTGA CAAACTAGCT CTCCCGATGA GCCCCAGCCC GCTTAGCCCG  1560
AGCCCCATCC CCAGCCCCAA CGCGAAACTT GAGAATTCCG CTCTCCTGAC GGTGGAGCCT  1620
TCCCCACAGG ACAAGAACAA GGGCTTCTTC GTGGATGAGT CGGAGCCCCT TCTCCGCTGT  1680
GACTCTACAT CCAGCGGCTC CTCCGCGCTG AGCAGGAACG GTTCCTTTAT TACCAAAGAA  1740
AAGAAGGACA CAGTGTTGCG GCAGGTACGC CTGGACCCCT GTGACTTGCA GCCTATCTTT  1800
GATGACATGC TCCACTTTCT AAATCCTGAG GAGCTGCGGG TGATTGAAGA GATTCCCCAG  1860
GCTGAGGACA AACTAGACCG GCTATTCGAA ATTATTGGAG TCAAGAGCCA GGAAGCCAGC  1920
CAGACCCTCC TGGACTCTGT TTATAGCCAT CTTCCTGACC TGCTGTAG
```

Seq ID NO: 477 Protein sequence
Protein Accession #: NP_055267.1

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1          11         21         31         41         51
|          |          |          |          |          |
MGTSPSSSTA LASCSRIARR ATATMIAGSL LLLGFLSTTT AQPEQKASNL IGTYRHVDRA    60
TGQVLTCDKC PAGTYVSEHC TNTSLRVCSS CPVGTFTRHE NGIEKCHDCS QPCPWPMIEK   120
LPCAALTDRE CTCPPGMFQS NATCAPHTVC PVGWGVRKKG TETEDVRCKQ CARGTFSDVP   180
SSVMKCKAYT DCLSQNLVVI KPGTKETDNV CGTLPSFSSS TSPSPGTAIF PRPEHMETHE   240
VPSSTYVPKG MNSTESNSSA SVRPKVLSSI QEGTVPDNTS SARGKEDVNK TLPNLQVVNH   300
QQGPHHRHIL KLLPSMEATG GEKSSTPIKG PKRGHPRQNL HKHFDINEHL PWMIVLFLLL   360
VLVVIVVCSI RKSSRTLKKG PRQDPSAIVE KAGLKKSMTP TQNREKWIYY CNGHGIDILK   420
LVAAQVGSQW KDIYQFLCNA SEREVAAFSN GYTADHERAY AALQHWTIRG PEASLAQLIS   480
ALRQHRRNDV VEKIRGLMED TTQLETDKLA LPMSPSPLSP SPIPSPNAKL ENSALLTVEP   540
SPQDKNKGFF VDESEPLLRC DSTSSGSSAL SRNGSFITKE KKDTVLRQVR LDPCDLQPIF   600
DDMLHFLNPE ELRVIEEIPQ AEDKLDRLFE IIGVKSQEAS QTLLDSVYSH LPDLL
```

Seq ID NO: 478 DNA sequence
Nucleic Acid Accession #: XM_044533
Coding sequence: 238..2751

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1          11         21         31         41         51
|          |          |          |          |          |
GCTCTGCCCA AGCCGAGGCT GCGGGGCCGG CGCCGGCGGG AGGACTGCGG TGCCCCGCGG    60
AGGGGCTGAG TTTGCCAGGG CCCACTTGAC CCTGTTTCCC ACCTCCCGCC CCCCAGGTCC   120
GGAGGCGGGG GCCCCCGGGG CGACTCGGGG GCGGACCGCG GGGCGGAGCT GCCGCCCGTG   180
AGTCCGGCCG AGCCACCTGA GCCCGAGCCG CGGGACACCG TCGCTCCTGC TCTCCGAATG   240
CTGCGCACCG CGATGGGCCT GAGGAGCTGG CTCGCCGCCC CATGGGGCGC GCTGCCGCCT   300
CGGCCACCGC TGCTGCTGCT CCTGCTGCTG CTGCTCCTGC TGCAGCCGCC GCCTCCGACC   360
TGGGCGCTCA GCCCCCGGAT CAGCCTGCCT CTGGGCTCTG AAGAGCGGCC ATTCCTCAGA   420
TTCGAAGCTG AACACATCTC CAACTACACA GCCCTTCTGC TGAGCAGGGA TGGCAGGACC   480
CTGTACGTGG GTGCTCGAGA GGCCCTCTTT GCACTCAGTA GCAACCTCAG CTTCCTGCCA   540
GGCGGGGAGT ACCAGGAGCT GCTTTGGGGT GCAGACGCAG AGAAGAAACA GCAGTGCAGC   600
TTCAAGGGCA AGGACCCACA GCGCGACTGT CAAAACTACA TCAAGATCCT CCTGCCGCTC   660
AGCGGCAGTC ACCTGTTCAC CTGTGGCACA GCAGCCTTCA GCCCCATGTG TACCTACATC   720
AACATGGAGA ACTTCACCCT GGCAAGGGAC GAGAAGGGGA ATGTCCTCCT GGAAGATGGC   780
AAGGGCCGTT GTCCCTTCGA CCCGAATTTC AAGTCCACTG CCCTGGTGGT TGATGGCGAG   840
CTCTACACTG GAACAGTCAG CAGCTTCCAA GGGAATGACC CGGCCATCTC GCGGAGCCAA   900
AGCCTTCGCC CCACCAAGAC CGAGAGCTCC CTCAACTGGC TGCAAGACCC AGCTTTTGTG   960
GCCTCAGCCT ACATTCCTGA GAGCCTGGGC AGCTTGCAAG GCGATGATGA CAAGATCTAC  1020
TTTTTCTTCA GCGAGACTGG CCAGGAATTT GAGTTCTTTG AGAACACCAT TGTGTCCCGC  1080
ATTGCCCGCA TCTGCAAGGG CGATGAGGGT GGAGAGCGGG TGCTACAGCA GCGCTGGACC  1140
TCCTTCCTCA AGGCCCAGCT GCTGTGCTCA CGGCCCGACG ATGGCTTCCC CTTCAACGTG  1200
CTGCAGGATG TCTTCACGCT GAGCCCCAGC CCCCAGGACT GGCGTGACAC CCTTTTCTAT  1260
GGGGTCTTCA CTTCCCAGTG GCACAGGGGA ACTACAGAAG GCTCTGCCGT CTGTGTCTTC  1320
ACAATGAAGG ATGTGCAGAG AGTCTTCAGC GGCCTCTACA AGGAGGTGAA CCGTGAGACA  1380
CAGCAGTGGT ACACCGTGAC CCACCCGGTG CCCACACCCC GGCCTGGAGC GTGCATCACC  1440
AACAGTGCCC GGGAAAGGAA GATCAACTCA TCCCTGCAGC TCCCAGACCG CGTGCTGAAC  1500
TTCCTCAAGG ACCACTTCCT GATGGACGGG CAGGTCCGAA GCCGCATGCT GCTGCTGCAG  1560
CCCCAGGCTC GCTACCAGCG CGTGGCTGTA CACCGCGTCC CTGGCCTGCA CCACACCTAC  1620
GATGTCCTCT TCCTGGGCAC TGGTGACGGC CGGCTCCACA AGGCAGTGAG CGTGGGCCCC  1680
CGGGTGCACA TCATTGAGGA GCTGCAGATC TTCTCATCGG GACAGCCCGT GCAGAATCTG  1740
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CTCCTGGACA CCCACAGGGG GCTGCTGTAT GCGGCCTCAC ACTCGGGCGT AGTCCAGGTG  1800
CCCATGGCCA ACTGCAGCCT GTACAGGAGC TGTGGGGACT GCCTCCTCGC CCGGGACCCC  1860
TACTGTGCTT GGAGCGGCTC CAGCTGCAAG CACGTCAGCC TCTACCAGCC TCAGCTGGCC  1920
ACCAGGCCGT GGATCCAGGA CATCGAGGGA GCCAGCGCCA AGGACCTTTG CAGCGCGTCT  1980
TCGGTTGTGT CCCCGTCTTT TGTACCAACA GGGGAGAAGC CATGTGAGCA AGTCCAGTTC  2040
CAGCCCAACA CAGTGAACAC TTTGGCCTGC CCGCTCCTCT CCAACCTGGC GACCCGACTC  2100
TGGCTACGCA ACGGGGCCCC CGTCAATGCC TCGGCCTCCT GCCACGTGCT ACCCACTGGG  2160
GACCTGCTGC TGGTGGGCAC CCAACAGCTG GGGGAGTTCC AGTGCTGGTC ACTAGAGGAG  2220
GGCTTCCAGC AGCTGGTAGC CAGCTACTGC CCAGAGGTGG TGGAGGACGG GGTGGCAGAC  2280
CAAACAGATG AGGGTGGCAG TGTACCCGTC ATTATCAGCA CATCGCGTGT GAGTGCACCA  2340
GCTGGTGGCA AGGCCAGCTG GGGTGCAGAC AGGTCCTACT GGAAGGAGTT CCTGGTGATG  2400
TGCACGCTCT TTGTGCTGGC CGTGCTGCTC CCAGTTTTAT TCTTGCTCTA CCGGCACCGG  2460
AACAGCATGA AAGTCTTCCT GAAGCAGGGG GAATGTGCCA GCGTGCACCC CAAGACCTGC  2520
CCTGTGGTGC TGCCCCCTGA GACCCGCCCA CTCAACGGCC TAGGGCCCCC TAGCACCCCG  2580
CTCGATCACC GAGGGTACCA GTCCCTGTCA GACAGCCCCC CGGGGTCCCG AGTCTTCACT  2640
GAGTCAGAGA AGAGGCCACT CAGCATCCAA GACAGCTTCG TGGAGGTATC CCCAGTGTGC  2700
CCCCGGCCCC GGGTCCGCCT TGGCTCGGAG ATCCGTGACT CTGTGGTGTG AGAGCTGACT  2760
TCCAGAGGAC GCTGCCCTGG CTTCAGGGGC TGTGAATGCT CGGAGAGGGT CAACTGGACC  2820
TCCCCTCCGC TCTGCTCTTC GTGGAACACG ACCGTGGTGC CCGGCCCTTG GGAGCCTTGG  2880
GGCCAGCTGG CCTGCTGCTC TCCAGTCAAG TAGCGAAGCT CCTACCACCC AGACACCCAA  2940
ACAGCCGTGG CCCCAGAGGT CCTGGCCAAA TATGGGGGCC TGCCTAGGTT GGTGGAACAG  3000
TGCTCCTTAT GTAAACTGAG CCCTTTGTTT AAAAAACAAT TCCAAATGTG AAACTAGAAT  3060
GAGAGGGAAG AGATAGCATG GCATGCAGCA CACACGGCTG CTCCAGTTCA TGGCCTCCCA  3120
GGGGTGCTGG GGATGCATCC AAAGTGGTTG TCTGAGACAG AGTTGGAAAC CCTCACCAAC  3180
TGGCCTCTTC ACCTTCCACA TTATCCCGCT GCCACCGGCT GCCCTGTCTC ACTGCAGATT  3240
CAGGACCAGC TTGGGCTGCG TGCGTTCTGC CTTGCCAGTC AGCCGAGGAT GTAGTTGTTG  3300
CTGCCGTCGT CCCACCACCT CAGGGACCAG AGGGCTAGGT TGGCACTGCG GCCCTCACCA  3360
GGTCCTGGGC TCGGACCCAA CTCCTGGACC TTTCCAGCCT GTATCAGGCT GTGGCCACAC  3420
GAGAGGACAG CGCGAGCTCA GGAGAGATTT CGTGACAATG TACGCCTTTC CCTCAGAATT  3480
CAGGGAAGAG ACTGTCGCCT GCCTTCCTCC GTTGTTGCGT GAGAACCCGT GTGCCCCTTC  3540
CCACCATATC CACCCTCGCT CCATCTTTGA ACTCAAACAC GAGGAACTAA CTGCACCCTG  3600
GTCCTCTCCC CAGTCCCCAG TTCACCCTCC ATCCCTCACC TTCCTCCACT CTAAGGGATA  3660
TCAACACTGC CCAGCACAGG GGCCCTGAAT TTATGTGGTT TTTATACATT TTTTAATAAG  3720
ATGCACTTTA TGTCATTTTT TAATAAAGTC TGAAGAATTA CTGTTT
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Seq ID NO: 479 Protein sequence
Protein Accession #: XP_044533.3

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1          11         21         31         41         51
|          |          |          |          |          |
MLRTAMGLRS WLAAPWGALP PRPPLLLLLL LLLLLQPPPP TWALSPRISL PLGSEERPFL   60
RFEAEHISNY TALLLSRDGR TLYVGAREAL FALSSNLSFL PGGEYQELLW GADAEKKQQC  120
SFKGKDPQRD CQNYIKILLP LSGSHLFTCG TAAFSPMCTY INMENFTLAR DEKGNVLLED  180
GKGRCPFDPN FKSTALVVDG ELYTGTVSSF QGNDPAISRS QSLRPTKTES SLNWLQDPAF  240
VASAYIPESL GSLQGDDDKI YFFFSETGQE FEFFENTIVS RIARICKGDE GGERVLQQRW  300
TSFLKAQLLC SRPDDGFPFN VLQDVFTLSP SPQDWRDTLF YGVFTSQWHR GTTEGSAVCV  360
FTMKDVQRVF SGLYKEVNRE TQQWYTVTHP VPTPRPGACI TNSARERKIN SSLQLPDRVL  420
NFLKDHFLMD GQVRSRMLLL QPQARYQRVA VHRVPGLHHT YDVLFLGTGD GRLHKAVSVG  480
PRVHIIEELQ IFSSGQPVQN LLLDTHRGLL YAASHSGVVQ VPMANCSLYR SCGDCLLARD  540
PYCAWSGSSC KHVSLYQPQL ATRPWIQDIE GASAKDLCSA SSVVSPSFVP TGEKPCEQVQ  600
FQPNTVNTLA CPLLSNLATR LWLRNGAPVN ASASCHVLPT GDLLLVGTQQ LGEFQCWSLE  660
EGFQQLVASY CPEVVEDGVA DQTDEGGSVP VIISTSRVSA PAGGKASWGA DRSYWKEFLV  720
MCTLFVLAVL LPVLFLLYRH RNSMKVFLKQ GECASVHPKT CPVVLPPETR PLNGLGPPST  780
PLDHRGYQSL SDSPPGSRVF TESEKRPLSI QDSFVEVSPV CPRPRVRLGS EIRDSVV
```

Seq ID NO: 480 DNA sequence
Nucleic Acid Accession #: NM_004217.1
Coding sequence: 58..1092

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1          11         21         31         41         51
|          |          |          |          |          |
GGCCGGGAGA GTAGCAGTGC CTTGGACCCC AGCTCTCCTC CCCCTTTCTC TCTAAGGATG   60
GCCCAGAAGG AGAACTCCTA CCCCTGGCCC TACGGCCGAC AGACGGCTCC ATCTGGCCTG  120
AGCACCCTGC CCCAGCGAGT CCTCCGGAAA GAGCCTGTCA CCCCATCTGC ACTTGTCCTC  180
ATGAGCCGCT CCAATGTCCA GCCCACAGCT GCCCCTGGCC AGAAGGTGAT GGAGAATAGC  240
AGTGGGACAC CCGACATCTT AACGCGGCAC TTCACAATTG ATGACTTTGA GATTGGGCGT  300
CCTCTGGGCA AAGGCAAGTT TGGAAACGTG TACTTGGCTC GGGAGAAGAA AAGCCATTTC  360
ATCGTGGCGC TCAAGGTCCT CTTCAAGTCC CAGATAGAGA AGGAGGGCGT GGAGCATCAG  420
CTGCGCAGAG AGATCGAAAT CCAGGCCCAC CTGCACCATC CCAACATCCT GCGTCTCTAC  480
AACTATTTTT ATGACCGGAG GAGGATCTAC TTGATTCTAG AGTATGCCCC CCGCGGGGAG  540
CTCTACAAGG AGCTGCAGAA GAGCTGCACA TTTGACGAGC AGCGAACAGC CACGATCATG  600
GAGGAGTTGG CAGATGCTCT AATGTACTGC CATGGGAAGA AGGTGATTCA CAGAGACATA  660
AAGCCAGAAA ATCTGCTCTT AGGGCTCAAG GGAGAGCTGA AGATTGCTGA CTTCGGCTGG  720
TCTGTGCATG CGCCCTCCCT GAGGAGGAAG ACAATGTGTG GCACCCTGGA CTACCTGCCC  780
CCAGAGATGA TTGAGGGGCG CATGCACAAT GAGAAGGTGG ATCTGTGGTG CATTGGAGTG  840
CTTTGCTATG AGCTGCTGGT GGGGAACCCA CCCTTTGAGA GTGCATCACA CAACGAGACC  900
TATCGCCGCA TCGTCAAGGT GGACCTAAAG TTCCCCGCTT CTGTGCCCAC GGGAGCCCAG  960
GACCTCATCT CCAAACTGCT CAGGCATAAC CCCTCGGAAC GGCTGCCCCT GGCCCAGGTC 1020
TCAGCCCACC CTTGGGTCCG GGCCAACTCT CGGAGGGTGC TGCCTCCCTC TGCCCTTCAA 1080
TCTGTCGCCT GATGGTCCCT GTCATTCACT CGGGTGCGTG TGTTTGTATG TCTGTGTATG 1140
TATAGGGGAA AGAAGGGATC CCTAACTGTT CCCTTATCTG TTTTCTACCT CCTCCTTTGT 1200
TTAATAAAGG CTGAAGCTTT TTGT
```

Seq ID NO: 481 Protein sequence
Protein Accession #: NP_004208

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1          11         21         31         41         51
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```
|          |          |          |          |          |
MAQKENSYPW PYGRQTAPSG LSTLPQRVLR KEPVTPSALV LMSRSNVQPT AAPGQKVMEN    60
SSGTPDILTR HFTIDDFEIG RPLGKGKFGN VYLAREKKSH FIVALKVLFK SQIEKEGVEH   120
QLRREIEIQA HLHHPNILRL YNYFYDRRRI YLILEYAPRG ELYKELQKSC TFDEQRTATI   180
MEELADALMY CHGKKVIHRD IKPENLLLGL KGELKIADFG WSVHAPSLRR KTMCGTLDYL   240
PPEMIEGRMH NEKVDLWCIG VLCYELLVGN PPFESASHNE TYRRIVKVDL KFPASVPTGA   300
QDLISKLLRH NPSERLPLAQ VSAHPWVRAN SRRVLPPSAL QSVA
```

Seq ID NO: 482 DNA sequence
Nucleic Acid Accession #: AK055663
Coding sequence: 38..1423

```
1          11         21         31         41         51
|          |          |          |          |          |
AGAACGGCTT CCGGCGGGAG CTGTGCAGCT CCTTATCATG GGGACAATTC ATCTCTTTCG    60
AAAACCACAA AGATCCTTTT TTGGCAAGTT GTTACGGGAA TTTAGACTTG TAGCAGCTGA   120
CCGAAGGTCC TGGAAGATAC TGCTCTTTGG TGTAATAAAC TTGATATGTA CTGGCTTCCT   180
GCTTATGTGG TGCAGTTCTA CTAATAGTAT AGCTTTAACT GCCTATACTT ACCTGACCAT   240
TTTTGATCTT TTTAGTTTAA TGACATGTTT AATAAGTTAC TGGGTAACAT TGAGGAAACC   300
TAGCCCTGTC TATTCATTTG GGTTTGAAAG ATTAGAAGTC CTGGCTGTAT TTGCCTCCAC   360
AGTCTTGGCA CAGTTGGGAG CTCTCTTTAT ATTAAAAGAA AGTGCAGAAC GCTTTTTGGA   420
ACAGCCCGAG ATACACACGG GAAGATTATT AGTTGGTACT TTTGTGGCTC TTTGTTTCAA   480
CCTGTTCACG ATGCTTTCTA TTCGGAATAA ACCTTTTGCT TATGTCTCAG AAGCTGCTAG   540
TACGAGCTGG CTTCAAGAGC ATGTTGCAGA TCTTAGTCGA AGCTTGTGTG GAATTATTCC   600
GGGACTTAGC AGTATCTTCC TTCCCCGAAT GAATCCATTT GTTTTGATTG ATCTTGCTGG   660
AGCATTTGCT CTTTGTATTA CATATATGCT CATTGAAATT AATAATTATT TTGCCGTAGA   720
CACTGCCTCT GCTATAGCTA TTGCCTTGAT GACATTTGGC ACTATGTATC CCATGAGTGT   780
GTACAGTGGG AAAGTCTTAC TCCAGACAAC ACCACCCCAT GTTATTGGTC AGTTGGACAA   840
ACTCATCAGA GAGGTATCTA CCTTAGATGG AGTTTTAGAA GTCCGAAATG AACATTTTTG   900
GACCCTAGGT TTTGGCTCAT TGGCTGGATC AGTGCATGTA AGAATTCGAC GAGATGCCAA   960
TGAACAAATG GTTCTTGCTC ATGTGACCAA CAGGCTGTAC ACTCTAGTGT CTACTCTAAC  1020
TGTTCAAATT TTCAAGGATG ACTGGATTAG GCCTGCCTTA TTGTCTGGGC CTGTTGCAGC  1080
CAATGTCCTA AACTTTTCAG ATCATCACGT AATCCCAATG CCTCTTTTAA AGGGTACTGA  1140
TGATTTGAAC CCAGTTACAT CAACTCCAGC TAAACCTAGT AGTCCACCTC CAGAATTTTC  1200
ATTTAACACT CCTGGGAAAA ATGTGAACCC AGTTATTCTT CTAAACACAC AAACAAGGCC  1260
TTATGGTTTT GGTCTCAATC ATGGACACAC ACCTTACAGC AGCATGCTTA ATCAAGGACT  1320
TGGAGTTCCA GGAATTGGAG CAACTCAAGG ATTGAGGACT GGTTTTACAA ATATACCAAG  1380
TAGATATGGA ACTAATAATA GAATTGGACA ACCAAGACCA TGATAGACTC TAACTTATTT  1440
TTATAAGGAA TATTGACTCC TTGGCTTCCA ATTTATTTAG TAATCCAACT TTGCATTGAC  1500
TGTTTAATCA TTTACTCTAA ATGTTAGATA ATAGTAGTCT TGTTCACATT TCATGAAACC  1560
TATGAAACTA TATTTTTGTA AAATGTATTT GTGACAGTGA AATCCTCGTA AATGTTAAAG  1620
GCTTTAAATA GGCTTCCTTT AGAAAATGTG TTTCTTTAAA TTTGGATTTT GGTATCTTTG  1680
GTTTTGTAGT TGACTGCAGT GTGATGTGAC CTTACCTTTA TAAGAGCCAC TTGATGGAGT  1740
AGATCTGTCA CATTACTAAG ATACGATATT TCTTTTTTTT TCCGAGACGG AGTCTTGCTC  1800
TGCCACTGTG CCCGGCCAAT ACATTATTAT TAACTTAAGG CTGTACTTTA TTAAGGCTTC  1860
CTTAGTTTTT GTTTTGTTTT GTTTTTTGAG ATGGAGTCTC ACTCTGTCGC CCAGGCTGGA  1920
ATGCAGTGGC ATGATCTCAG CTCACTGCAA CCTCTGCCTC CTGAGTTCAA ATGATTCTCC  1980
TGCCTCAGCC TCCCGAGTAG CTGGGATTAC AGGCACCTGC CACCACGCCC AGCTAATTTT  2040
TGTATTTTTA GTAAAGACGG GGGATTTCAC CATGTTGGCC AGGCTGGTCT TGAACTCCTG  2100
ACCTCATGAT CCACCCACCT TAGCCTCCCA AAGTGCTGGG ATTAGGTGTG AGCCACCGCA  2160
CCTGGCCGAT ATTTTCTTTA ATGAAATTTA TAAATATGCT TCTTGAATAA TACACATTTT  2220
GGGAAAGGGA AAAATGTCTG TTCAAAAAGT AAAGGTCTCT TTTATAGCTT TTCCAAACTT  2280
AATTGCTAAA TTTTTCTTTG AGGTTCTCCT GAATTATGTC TTACAAACTA AAAGCAAAAA  2340
TTTTTAGCAG AAATTTTGGA ATACATTCTA TCTAGCACAA TTTGAATTTT TAATTATCAA  2400
GATTTTTGTT AAAGTTTCTC TCCTTTAAAA ATTTTAGTAC ATTTGTAAAT
```

Seq ID NO: 483 Protein sequence
Protein Accession #: BAB70980.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MGTIHLFRKP QRSFFGKLLR EFRLVAADRR SWKILLFGVI NLICTGFLLM WCSSTNSIAL    60
TAYTYLTIFD LFSLMTCLIS YWVTLRKPSP VYSFGFERLE VLAVFASTVL AQLGALFILK   120
ESAERFLEQP EIHTGRLLVG TFVALCFNLF TMLSIRNKPF AYVSEAASTS WLQEHVADLS   180
RSLCGIIPGL SSIFLPRMNP FVLIDLAGAF ALCITYMLIE INNYFAVDTA SAIAIALMTF   240
GTMYPMSVYS GKVLLQTTPP HVIGQLDKLI REVSTLDGVL EVRNEHFWTL GFGSLAGSVH   300
VRIRRDANEQ MVLAHVTNRL YTLVSTLTVQ IFKDDWIRPA LLSGPVAANV LNFSDHHVIP   360
MPLLKGTDDL NPVTSTPAKP SSPPPEFSFN TPGKNVNPVI LLNTQTRPYG FGLNHGHTPY   420
SSMLNQGLGV PGIGATQGLR TGFTNIPSRY GTNNRIGQPR P
```

Seq ID NO: 484 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..900

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGCCGCCGC GGGAGCTGAG CGAGGCCGAG CCGCCCCCGC TCCGGGCCCC GACCCCTCCC    60
CCGCGGCGGC GTAGCGCGCC CCCAGAGCTG GGCATCAAGT GCGTGCTGGT GGGCGACGGC   120
GCCGTGGGCA AGAGCAGCCT CATCGTCAGC TACACCTGCA ATGGGTACCC CGCGCGCTAC   180
CGGCCCACTG CGCTGGACAC CTTCTCTGGT ACGTACGTTC AATCGCCCGT GCGGCCGCGT   240
GGCTGCGGCG GGGCTGTGCA CCGGGGAGCT GGGGCGGGCG TCTCGGCGGG AGGGCGCAGA   300
GGACCCCGGG GAGGAGACTG GAGCAGGCCC CGAGGTGGCG CTGGTGCGGC CCAGGACGCT   360
CTTCCTAACT CAGGCTCTCC CCGCCCCGCC CCTGCAGTGC AAGTCCTGGT GGATGGAGCT   420
CCGGTGCGCA TTGAGCTCTG GGACACAGCG GGACAGGAGG ATTTTGACCG ACTTCGTTCC   480
CTTTGCTACC CGGATACCGA TGTCTTCCTG GCGTGCTTCA GCGTGGTGCA GCCCAGCTCC   540
TTTCAAAACA TCACAGAGAA ATGGCTGCCC GAGATCCGCA CGCACAACCC CCAGGCGCCT   600
GTGCTGCTGG TGGGCACCCA GGCCGACCTG AGGGACGATG TCAACGTACT AATTCAGCTG   660
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GACCAGGGGG GCCGGGAGGG CCCCGTGCCC CAACCCCAGG CTCAGGGTCT GGCCGAGAAG 720
ATCCGAGCCT GCTGCTACCT TGAGTGCTCA GCCTTGACGC AGAAGAACTT GAAGGAAGTA 780
TTTGACTCGG CTATTCTCAG TGCCATTGAG CACAAAGCCC GGCTGGAGAA GAAACTGAAT 840
GCCAAAGGTG TGCGCACCCT CTCCCGCTGC CGCTGGAAGA AGTTCTTCTG CTTCGTTTGA

Seq ID NO: 485 Protein sequence
Protein Accession #: FGENESH predicted

```
1          11         21         31         41         51
|          |          |          |          |          |
MPPRELSEAE PPPLRAPTPP PRRRSAPPEL GIKCVLVGDG AVGKSSLIVS YTCNGYPARY   60
RPTALDTFSG TYVQSPVRPR GCGGAVHRGA GAGVSAGGRR GPRGGDWSRP RGGAGAAQDA  120
LPNSGSPRPA PAVQVLVDGA PVRIELWDTA GQEDFDRLRS LCYPDTDVFL ACFSVVQPSS  180
FQNITEKWLP EIRTHNPQAP VLLVGTQADL RDDVNVLIQL DQGGREGPVP QPQAQGLAEK  240
IRACCYLECS ALTQKNLKEV FDSAILSAIE HKARLEKKLN AKGVRTLSRC RWKKFFCFV
```

Seq ID NO: 486 DNA sequence
Nucleic Acid Accession #: XM_063832.2
Coding sequence: 1..711

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGCCGCCGC GGGAGCTGAG CGAGGCCGAG CCGCCCCCGC TCCGGGCCCC GACCCCTCCC   60
CCGCGGCGGC GTAGCGCGCC CCCAGAGCTG GGCATCAAGT GCGTGCTGGT GGGCGACGGC  120
GCCGTGGGCA AGAGCAGCCT CATCGTCAGC TACACCTGCA ATGGGTACCC CGCGCGCTAC  180
CGGCCCACTG CGCTGGACAC CTTCTCTGTG CAAGTCCTGG TGGATGGAGC TCCGGTGCGC  240
ATTGAGCTCT GGGACACAGC GGGACAGGAG GATTTTGACC GACTTCGTTC CCTTTGCTAC  300
CCGGATACCG ATGTCTTCCT GGCGTGCTTC AGCGTGGTGC AGCCCAGCTC CTTTCAAAAC  360
ATCACAGAGA AATGGCTGCC CGAGATCCGC ACGCACAACC CCCAGGCGCC TGTGCTGCTG  420
GTGGGCACCC AGGCCGACCT GAGGGACGAT GTCAACGTAC TAATTCAGCT GGACCAGGGG  480
GGCCGGGAGG GCCCCGTGCC CCAACCCCAG GCTCAGGGTC TGGCCGAGAA GATCCGAGCC  540
TGCTGCTACC TTGAGTGCTC AGCCTTGACG CAGAAGAACT TGAAGGAAGT ATTTGACTCG  600
GCTATTCTCA GTGCCATTGA GCACAAAGCC CGGCTGGAGA AGAAACTGAA TGCCAAAGGT  660
GTGCGCACCC TCTCCCGCTG CCGCTGGAAG AAGTTCTTCT GCTTCGTTTG A
```

Seq ID NO: 487 Protein sequence
Protein Accession #: XP_063832.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MPPRELSEAE PPPLRAPTPP PRRRSAPPEL GIKCVLVGDG AVGKSSLIVS YTCNGYPARY   60
RPTALDTFSV QVLVDGAPVR IELWDTAGQE DFDRLRSLCY PDTDVFLACF SVVQPSSFQN  120
ITEKWLPEIR THNPQAPVLL VGTQADLRDD VNVLIQLDQG GREGPVPQPQ AQGLAEKIRA  180
CCYLECSALT QKNLKEVFDS AILSAIEHKA RLEKKLNAKG VRTLSRCRWK KFFCFV
```

Seq ID NO: 488 DNA sequence
Nucleic Acid Accession #: NM_014398.1
Coding sequence: 64..1314

```
1          11         21         31         41         51
|          |          |          |          |          |
GGCACCGATT CGGGGCCTGC CCGGACTTCG CCGCACGCTG CAGAACCTCG CCCAGCGCCC   60
ACCATGCCCC GGCAGCTCAG CGCGGCGGCC GCGCTCTTCG CGTCCCTGGC CGTAATTTTG  120
CACGATGGCA GTCAAATGAG AGCAAAAGCA TTTCCAGAAA CCAGAGATTA TTCTCAACCT  180
ACTGCAGCAG CAACAGTACA GGACATAAAA AAACCTGTCC AGCAACCAGC TAAGCAAGCA  240
CCTCACCAAA CTTTAGCAGC AAGATTCATG GATGGTCATA TCACCTTTCA AACAGCGGCC  300
ACAGTAAAAA TTCCAACAAC TACCCCAGCA ACTACAAAAA ACACTGCAAC CACCAGCCCA  360
ATTACCTACA CCCTGGTCAC AACCCAGGCC ACACCCAACA ACTCACACAC AGCTCCTCCA  420
GTTACTGAAG TTACAGTCGG CCCTAGCTTA GCCCCTTATT CACTGCCACC CACCATCACC  480
CCACCAGCTC ATACAGCTGG AACCAGTTCA TCAACCGTCA GCCACACAAC TGGGAACACC  540
ACTCAACCCA GTAACCAGAC CACCCTTCCA GCAACTTTAT CGATAGCACT GCACAAAAGC  600
ACAACCGGTC AGAAGCCTGA TCAACCCACC CATGCCCCAG GAACAACGGC AGCTGCCCAC  660
AATACCACCC GCACAGCTGC ACCTGCCTCC ACGGTTCCTG GGCCCACCCT TGCACCTCAG  720
CCATCGTCAG TCAAGACTGG AATTTATCAG GTTCTAAACG GAAGCAGACT CTGTATAAAA  780
GCAGAGATGG GGATACAGCT GATTGTTCAA GACAAGGAGT CGGTTTTTTC ACCTCGGAGA  840
TACTTCAACA TCGACCCCAA CGCAACGCAA GCCTCTGGGA ACTGTGGCAC CCGAAAATCC  900
AACCTTCTGT TGAATTTTCA GGGCGGATTT GTGAATCTCA CATTTACCAA GGATGAAGAA  960
TCATATTATA TCAGTGAAGT GGGAGCCTAT TTGACCGTCT CAGATCCAGA GACAGTTTAC 1020
CAAGGAATCA AACATGCGGT GGTGATGTTC CAGACAGCAG TCGGGCATTC CTTCAAGTGC 1080
GTGAGTGAAC AGAGCCTCCA GTTGTCAGCC CACCTGCAGG TGAAAACAAC CGATGTCCAA 1140
CTTCAAGCCT TTGATTTTGA AGATGACCAC TTTGGAAATG TGGATGAGTG CTCGTCTGAC 1200
TACACAATTG TGCTTCCTGT GATTGGGGCC ATCGTGGTTG GTCTCTGCCT TATGGGTATG 1260
GGTGTCTATA AAATCCGCCT AAGGTGTCAA TCATCTGGAT ACCAGAGAAT CTAATTGTTG 1320
CCCGGGGGGA ATGAAAATAA TGGAATTTAG AGAACTCTTT CATCCCTTCC AGGATGGATG 1380
TTGGGAAATT CCCTCAGAGT GTGGGTCCTT CAAACAATGT AAACCACCAT CTTCTATTCA 1440
AATGAAGTGA GTCATGTGTG ATTTAAGTTC AGGCAGCACA TCAATTTCTA AATACTTTTT 1500
GTTTATTTTA TGAAAGATAT AGTGAGCTGT TTATTTTCTA GTTTCCTTTA GAATATTTTA 1560
GCCACTCAAA GTCAACATTT GAGATATGTT GAATTAACAT AATATATGTA AAGTAGAATA 1620
AGCCTTCAAA TTATAAACCA AGGGTCAATT GTAACTAATA CTACTGTGTG TGCATTGAAG 1680
ATTTTATTTT ACCCTTGATC TTAACAAAGC CTTTGCTTTG TTATCAAATG GACTTTCAGT 1740
GCTTTTACTA TCTGTGTTTT ATGGTTTCAT GTAACATACA TATTCCTGGT GTAGCACTTA 1800
ACTCCTTTTC CACTTTAAAT TTGTTTTTGT TTTTTGAGAC GGAGTTTCAC TCTTGTCACC 1860
CAGGCTGGAG TACAGTGGCA CGATCTCGGC TTATGGCAAC CTCCGCCTCC CGGGTTCAAG 1920
TGATTCTCCT GCTTCAGCTT CCCGAGTAGC TGGGATTACA GGCACACACT ACCACGCCTG 1980
GCTAATTTTT GTATTTTTAT TATAGACGGG TTTCACCATG TTGGCCAGAC TGGTCTTGAA 2040
CTCTTGACCT CAGGTGATCC ACCCACCTCA GCCTCCCAAA GTGCTGGGAT TACAGGCATG 2100
AGCCATTGCG CCCGGCCTTA AATGTTTTTT TTAATCATCA AAAAGAACAA CATATCTCAG 2160
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GTTGTCTAAG TGTTTTTATG TAAAACCAAC AAAAAGAACA AATCAGCTTA TATTTTTTAT  2220
CTTGATGACT CCTGCTCCAG AATTGCTAGA CTAAGAATTA GGTGGCTACA GATGGTAGAA  2280
CTAAACAATA AGCAAGAGAC AATAATAATG GCCCTTAATT ATTAACAAAG TGCCAGAGTC  2340
TAGGCTAAGC ACTTTATCTA TATCTCATTT CATTCTCACA ACTTATAAGT GAATGAGTAA  2400
ACTGAGACTT AAGGGAACTG AATCACTTAA ATGTCACCTG GCTAACTGAT GGCAGAGCCA  2460
GAGCTTGAAT TCATGTTGGT CTGACATCAA GGTCTTTGGT CTTCTCCCTA CACCAAGTTA  2520
CCTACAAGAA CAATGACACC ACACTCTGCC TGAAGGCTCA CACCTCATAC CAGCATACGC  2580
TCACCTTACA GGGAAATGGG TTTATCCAGG ATCATGAGAC ATTAGGGTAG ATGAAAGGAG  2640
AGCTTTGCAG ATAACAAAAT AGCCTATCCT TAATAAATCC TCCACTCTCT GGAAGGAGAC  2700
TGAGGGGCTT TGTAAAACAT TAGTCAGTTG CTCATTTTTA TGGGATTGCT TAGCTGGGCT  2760
GTAAAGATGA AGGCATCAAA TAAACTCAAA GTATTTTTAA ATTTTTTTGA TAATAGAGAA  2820
ACTTCGCTAA CCAACTGTTC TTTCTTGAGT GTATAGCCCC ATCTTGTGGT AACTTGCTGC  2880
TTCTGCACTT CATATCCATA TTTCCTATTG TTCACTTTAT TCTGTAGAGC AGCCTGCCAA  2940
GAATTTTATT TCTGCTGTTT TTTTTGCTGC TAAAGAAAGG AACTAAGTCA GGATGTTAAC  3000
AGAAAAGTCC ACATAACCCT AGAATTCTTA GTCAAGGAAT AATTCAAGTC AGCCTAGAGA  3060
CCATGTTGAC TTTCCTCATG TGTTTCCTTA TGACTCAGTA AGTTGGCAAG GTCCTGACTT  3120
TAGTCTTAAT AAAACATTGA ATTGTAGTAA AGGTTTTTGC AATAAAAACT TACTTTGG
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Seq ID NO: 489 Protein sequence
Protein Accession #: NP_055213.1

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1          11         21         31         41         51
|          |          |          |          |          |
MPRQLSAAAA LFASLAVILH DGSQMRAKAF PETRDYSQPT AAATVQDIKK PVQQPAKQAP    60
HQTLAARFMD GHITFQTAAT VKIPTTTPAT TKNTATTSPI TYTLVTTQAT PNNSHTAPPV   120
TEVTVGPSLA PYSLPPTITP PAHTAGTSSS TVSHTTGNTT QPSNQTTLPA TLSIALHKST   180
TGQKPDQPTH APGTTAAAHN TTRTAAPAST VPGPTLAPQP SSVKTGIYQV LNGSRLCIKA   240
EMGIQLIVQD KESVFSPRRY FNIDPNATQA SGNCGTRKSN LLLNFQGGFV NLTFTKDEES   300
YYISEVGAYL TVSDPETVYQ GIKHAVVMFQ TAVGHSFKCV SEQSLQLSAH LQVKTTDVQL   360
QAFDFEDDHF GNVDECSSDY TIVLPVIGAI VVGLCLMGMG VYKIRLRCQS SGYQRI
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Seq ID NO: 490 DNA sequence
Nucleic Acid Accession #: NM_005409.3
Coding sequence: 94..378

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1          11         21         31         41         51
|          |          |          |          |          |
TTCCTTTCAT GTTCAGCATT TCTACTCCTT CCAAGAAGAG CAGCAAAGCT GAAGTAGCAG    60
CAACAGCACC AGCAGCAACA GCAAAAAACA AACATGAGTG TGAAGGGCAT GGCTATAGCC   120
TTGGCTGTGA TATTGTGTGC TACAGTTGTT CAAGGCTTCC CCATGTTCAA AAGAGGACGC   180
TGTCTTTGCA TAGGCCCTGG GGTAAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC   240
ATAATGTACC CAAGTAACAA CTGTGACAAA ATAGAAGTGA TTATTACCCT GAAAGAAAAT   300
AAAGGACAAC GATGCCTAAA TCCCAAATCG AAGCAAGCAA GGCTTATAAT CAAAAAAGTT   360
GAAAGAAAGA ATTTTTAAAA ATATCAAAAC ATATGAAGTC CTGGAAAAGG GCATCTGAAA   420
AACCTAGAAC AAGTTTAACT GTGACTACTG AAATGACAAG AATTCTACAG TAGGAAACTG   480
AGACTTTTCT ATGGTTTTGT GACTTTCAAC TTTTGTACAG TTATGTGAAG GATGAAAGGT   540
GGGTGAAAGG ACCAAAAACA GAAATACAGT CTTCCTGAAT GAATGACAAT CAGAATTCCA   600
CTGCCCAAAG GAGTCCAGCA ATTAAATGGA TTTCTAGGAA AAGCTACCTT AAGAAAGGCT   660
GGTTACCATC GGAGTTTACA AAGTGCTTTC ACGTTCTTAC TTGTTGTATT ATACATTCAT   720
GCATTTCTAG GCTAGAGAAC CTTCTAGATT TGATGCTTAC AACTATTCTG TTGTGACTAT   780
GAGAACATTT CTGTCTCTAG AAGTTATCTG TCTGTATTGA TCTTTATGCT ATATTACTAT   840
CTGTGGTTAC AGTGGAGACA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAAG   900
CATCTATGTG TCGTAAAGCA TTCCTCAAAC ATTTTTTCAT GCAAATACAC ACTTCTTTCC   960
CCAAATATCA TGTAGCACAT CAATATGTAG GGAAACATTC TTATGCATCA TTTGGTTTGT  1020
TTTATAACCA ATTCATTAAA TGTAATTCAT AAAATGTACT ATGAAAAAAA TTATACGCTA  1080
TGGGATACTG GCAACAGTGC ACATATTTCA TAACCAAATT AGCAGCACCG GTCTTAATTT  1140
GATGTTTTTC AACTTTTATT CATTGAGATG TTTTGAAGCA ATTAGGATAT GTGTGTTTAC  1200
TGTACTTTTT GTTTTGATCC GTTTGTATAA ATGATAGCAA TATCTTGGAC ACATTTGAAA  1260
TACAAAATGT TTTTGTCTAC CAAAGAAAAA TGTTGAAAAA TAAGCAAATG TATACCTAGC  1320
AATCACTTTT ACTTTTTGTA ATTCTGTCTC TTAGAAAAAT ACATAATCTA ATCAATTTCT  1380
TTGTTCATGC CTATATACTG TAAAATTTAG GTATACTCAA GACTAGTTTA AAGAATCAAA  1440
GTCATTTTTT TCTCTAATAA ACTACCACAA CCTTTCTTTT TTAAAAAAAA AAA
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Seq ID NO: 491 Protein sequence
Protein Accession #: NP_005400.1

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1          11         21         31         41         51
|          |          |          |          |          |
MSVKGMAIAL AVILCATVVQ GFPMFKRGRC LCIGPGVKAV KVADIEKASI MYPSNNCDKI    60
EVIITLKENK GQRCLNPKSK QARLIIKKVE RKNF
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Seq ID NO: 492 DNA sequence
Nucleic Acid Accession #: NM_000577.1
Coding sequence: 41..520

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1          11         21         31         41         51
|          |          |          |          |          |
GGCACGAGGG GAAGACCTCC TGTCCTATCA GGCCCTCCCC ATGGCTTTAG AGACGATCTG    60
CCGACCCTCT GGGAGAAAAT CCAGCAAGAT GCAAGCCTTC AGAATCTGGG ATGTTAACCA   120
GAAGACCTTC TATCTGAGGA ACAACCAACT AGTTGCCGGA TACTTGCAAG GACCAAATGT   180
CAATTTAGAA GAAAAGATAG ATGTGGTACC CATTGAGCCT CATGCTCTGT TCTTGGGAAT   240
CCATGGAGGG AAGATGTGCC TGTCCTGTGT CAAGTCTGGT GATGAGACCA GACTCCAGCT   300
GGAGGCAGTT AACATCACTG ACCTGAGCGA GAACAGAAAG CAGGACAAGC GCTTCGCCTT   360
CATCCGCTCA GACAGTGGCC CCACCACCAG TTTTGAGTCT GCCGCCTGCC CCGGTTGGTT   420
CCTCTGCACA GCGATGGAAG CTGACCAGCC CGTCAGCCTC ACCAATATGC CTGACGAAGG   480
CGTCATGGTC ACCAAATTCT ACTTCCAGGA GGACGAGTAG TACTGCCCAG GCCTGCCTGT   540
TCCCATTCTT GCATGGCAAG GACTGCAGGG ACTGCCAGTC CCCCTGCCCC AGGGCTCCCG   600
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GCTATGGGGG CACTGAGGAC CAGCCATTGA GGGGTGGACC CTCAGAAGGC GTCACAACAA   660
CCTGGTCACA GGACTCTGCC TCCTCTTCAA CTGACCAGCC TCCATGCTGC CTCCAGAATG   720
GTCTTTCTAA TGTGTGAATC AGAGCACAGC AGCCCCTGCA CAAAGCCCTT CCATGTCGCC   780
TCTGCATTCA GGATCAAACC CCGACCACCT GCCCAACCTG CTCTCCTCTT GCCACTGCCT   840
CTTCCTCCCT CATTCCACCT TCCCATGCCC TGGATCCATC AGGCCACTTG ATGACCCCCA   900
ACCAAGTGGC TCCCACACCC TGTTTTACAA AAAAGAAAAG ACCAGTCCAT GAGGGAGGTT   960
TTTAAGGGTT TGTGGAAAAT GAAAATTAGG ATTTCATGAT TTTTTTTTTT CAGTCCCCGT  1020
GAAGGAGAGC CCTTCATTTG GAGATTATGT TCTTTCGGGG AGAGGCTGAG GACTTAAAAT  1080
ATTCCTGCAT TTGTGAAATG ATGGTGAAAG TAAGTGGTAG CTTTTCCCTT CTTTTTCTTC  1140
TTTTTTTGTG ATGTCCCAAC TTGTAAAAAT TAAAAGTTAT GGTACTATGT TAGCCCCATA  1200
ATTTTTTTTT TCCTTTTAAA ACACTTCCAT AATCTGGACT CCTCTGTCCA GGCACTGCTG  1260
CCCAGCCTCC AAGCTCCATC TCCACTCCAG ATTTTTTACA GCTGCCTGCA GTACTTTACC  1320
TCCTATCAGA AGTTTCTCAG CTCCCAAGGC TCTGAGCAAA TGTGGCTCCT GGGGGTTCTT  1380
TCTTCCTCTG CTGAAGGAAT AAATTGCTCC TTGACATTGT AGAGCTTCTG GCACTTGGAG  1440
ACTTGTATGA AAGATGGCTG TGCCTCTGCC TGTCTCCCCC ACCAGGCTGG GAGCTCTGCA  1500
GAGCAGGAAA CATGACTCGT ATATGTCTCA GGTCCCTGCA GGGCCAAGCA CCTAGCCTCG  1560
CTCTTGGCAG GTACTCAGCG AATGAATGCT GTATATGTTG GGTGCAAAGT TCCCTACTTC  1620
CTGTGACTTC AGCTCTGTTT TACAATAAAA TCTTGAAAAT GCCTAAAAAA AAAAAAAAAA  1680
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA
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Seq ID NO: 493 Protein sequence
Protein Accession #: NP_000568.1

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1          11         21         31         41         51
|          |          |          |          |          |
MALETICRPS GRKSSKMQAF RIWDVNQKTF YLRNNQLVAG YLQGPNVNLE EKIDVVPIEP    60
HALFLGIHGG KMCLSCVKSG DETRLQLEAV NITDLSENRK QDKRFAFIRS DSGPTTSFES   120
AACPGWFLCT AMEADQPVSL TNMPDEGVMV TKFYFQEDE
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Seq ID NO: 494 DNA sequence
Nucleic Acid Accession #: NM_002081.1
Coding sequence: 222..1898

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1          11         21         31         41         51
|          |          |          |          |          |
GGCTGCCCGA GCGAGCGTTC GGACCTCGCA CCCCGCGCGC CCCGCGCCGC CGCCGCCGCC    60
GGCTTTTGTT GTCTCCGCCT CCTCGGCCGC CGCCGCCTCT GGACCGCGAG CCGCGCGCGC   120
CGGGACCTTG GCTCTGCCCT TCGCGGGCGG GAACTGCGCA GGACCCGGCC AGGATCCGAG   180
AGAGGCGCGG GCGGGTGGCC GGGGGCGCCG CCGGCCCCGC CATGGAGCTC CGGGCCCGAG   240
GCTGGTGGCT GCTATGTGCG GCCGCAGCGC TGGTCGCCTG CGCCCGCGGG GACCCGGCCA   300
GCAAGAGCCG GAGCTGCGGC GAGGTCCGCC AGATCTACGG AGCCAAGGGC TTCAGCCTGA   360
GCGACGTGCC CCAGGCGGAG ATCTCGGGTG AGCACCTGCG GATCTGTCCC CAGGGCTACA   420
CCTGCTGCAC CAGCGAGATG GAGGAGAACC TGGCCAACCG CAGCCATGCC GAGCTGGAGA   480
CCGCGCTCCG GGACAGCAGC CGCGTCCTGC AGGCCATGCT TGCCACCCAG CTGCGCAGCT   540
TCGATGACCA CTTCCAGCAC CTGCTGAACG ACTCGGAGCG GACGCTGCAG GCCACCTTCC   600
CCGGCGCCTT CGGAGAGCTG TACACGCAGA ACGCGAGGGC CTTCCGGGAC CTGTACTCAG   660
AGCTGCGCCT GTACTACCGC GGTGCCAACC TGCACCTGGA GGAGACGCTG GCCGAGTTCT   720
GGGCCCGCCT GCTCGAGCGC CTCTTCAAGC AGCTGCACCC CCAGCTGCTG CTGCCTGATG   780
ACTACCTGGA CTGCCTGGGC AAGCAGGCCG AGGCGCTGCG GCCCTTCGGG GAGGCCCCGA   840
GAGAGCTGCG CCTGCGGGCC ACCCGTGCCT TCGTGGCTGC TCGCTCCTTT GTGCAGGGCC   900
TGGGCGTGGC CAGCGACGTG GTCCGGAAAG TGGCTCAGGT CCCCCTGGGC CCGGAGTGCT   960
CGAGAGCTGT CATGAAGCTG GTCTACTGTG CTCACTGCCT GGGAGTCCCC GGCGCCAGGC  1020
CCTGCCCTGA CTATTGCCGA AATGTGCTCA AGGGCTGCCT TGCCAACCAG GCCGACCTGG  1080
ACGCCGAGTG GAGGAACCTC CTGGACTCCA TGGTGCTCAT CACCGACAAG TTCTGGGGTA  1140
CATCGGGTGT GGAGAGTGTC ATCGGCAGCG TGCACACGTG GCTGGCGGAG GCCATCAACG  1200
CCCTCCAGGA CAACAGGGAC ACGCTCACGG CCAAGGTCAT CCAGGGCTGC GGGAACCCCA  1260
AGGTCAACCC CCAGGGCCCT GGGCCTGAGG AGAAGCGGCG CCGGGGCAAG CTGGCCCCGC  1320
GGGAGAGGCC ACCTTCAGGC ACGCTGGAGA AGCTGGTCTC TGAAGCCAAG GCCCAGCTCC  1380
GCGACGTCCA GGACTTCTGG ATCAGCCTCC CAGGGACACT GTGCAGTGAG AAGATGGCCC  1440
TGAGCACTGC CAGTGATGAC CGCTGCTGGA ACGGGATGGC CAGAGGCCGG TACCTCCCCG  1500
AGGTCATGGG TGACGGCCTG GCCAACCAGA TCAACAACCC CGAGGTGGAG GTGGACATCA  1560
CCAAGCCGGA CATGACCATC CGGCAGCAGA TCATGCAGCT GAAGATCATG ACCAACCGGC  1620
TGCGCAGCGC CTACAACGGC AACGACGTGG ACTTCCAGGA CGCCAGTGAC GACGGCAGCG  1680
GCTCGGGCAG CGGTGATGGC TGTCTGGATG ACCTCTGCGG CCGGAAGGTC AGCAGGAAGA  1740
GCTCCAGCTC CCGGACGCCC TTGACCCATG CCCTCCCAGG CCTGTCAGAG CAGGAAGGAC  1800
AGAAGACCTC GGCTGCCAGC TGCCCCCAGC CCCCGACCTT CCTCCTGCCC CTCCTCCTCT  1860
TCCTGGCCCT TACAGTAGCC AGGCCCCGGT GGCGGTAACT GCCCCAAGGC CCCAGGGACA  1920
GAGGCCAAGG ACTGACTTTG CCAAAAATAC AACACAGACG ATATTTAATT CACCTCAGCC  1980
TGGAGAGGCC TGGGGTGGGA CAGGGAGGGC CGGCGGCTCT GAGCAGGGGC AGGCGCAGAG  2040
GTCCCAGCCC CAGGCCTGGC CTCGCCTGCC TTTCTGCCTT TTAATTTTGT ATGAGGTCCT  2100
CAGGTCAGCT GGGAGCCAGT GTGCCCAAAA GCCATGTATT TCAGGGACCT CAGGGGCACC  2160
TCCGGCTGCC TAGCCCTCCC CCCAGCTCCC TGCACCGCCG CAGAAGCAGC CCCTCGAGGC  2220
CTACAGAGGA GGCCTCAAAG CAACCCGCTG GAGCCCACAG CGAGCCTGTG CCTTCCTCCC  2280
CGCCTCCTCC CACTGGGACT CCCAGCAGAG CCCACCAGCC AGCCCTGGCC CACCCCCCAG  2340
CCTCCAGAGA AGCCCCGCAC GGGCTGTCTG GGTGTCCGCC ATCCAGGGTC TGGCAGAGCC  2400
TCTGAGATGA TGCATGATGC CCTCCCCTCA GCGCAGGCTG CAGAGCCCGG CCCCACCTCC  2460
CTGCGCCCTT GAGGGGCCCC AGCGTCTGCA GGGTGACGCC TGAGACAGCA CCACTGCTGA  2520
GGAGTCTGAG GACTGTCCTC CCACAGACCC TGCAGTGAGG GGCCCTCCAT GCGCAGATGA  2580
GGGGCCACTG ACCCACCTGC GCTTCTGCTG GAGGAGGGGA AGCTGGGCCC AAAGGCCCAG  2640
GGAGGCAGCG TGGGCTCTGC CAATGTGGGC TGCCCCTCGC ACACAGGGCT CACAGGGCAG  2700
GCCTTGCTGG GGTCCAGGGC TGTTGGAGGA CCCCGAGGGC TGAGGAGCAG CCAGGACCCG  2760
CCTGCTCCCA TCCTCACCCA GATCAGGAAC CAGGGCCTCC CTGTTCACGG TGACACAGGT  2820
CAGGGCTCAG AGTGACCCTC GGCTGTCACC TGCTCACAGG GATGCTGGTG GCTGGTGAGA  2880
CCCCGCACTG CACACGGGAA TGCCTAGGTC CCTTCCCGAC CCAGCCAGCT GCACTGCAGG  2940
GCACGGGGAC CTGGATAGTT AAGGGCTTTT CCAAACATGC ATCCATTTAC TGACACTTCC  3000
TGTCCTTGTT CATGGAGAGC TGTTCGCTCC TCCCAGATGG CTTCGGAGGC CCGCAGGGCC  3060
CACCTTGGAC CCTGGTGACC TCCTGTCACT CACTGAGGCC ATCAGGGCCC TGCCCCAGGC  3120
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CTGGACGGGC CCTCCTTCCC TCCTGTGCCC CAGCTGCCAG GTGGCCCTGG GGAGGGGTGG  3180
TGTGGTGTTG GGAAGGGGTC CTGCAGGGGG AGGAGGACTT GGAGGGTCTG GGGGCAGCTG  3240
TCCTGAACCG ACTGACCCTG AGGAGGCCGC TTAGTGCTGC TTTGCTTTTC ATCACCGTCC  3300
CGCACAGTGG ACGGAGGTCC CCGGTTGCTG GTCAGGTCCC CATGGCTTGT TCTCTGGAAC  3360
CTGACTTTAG ATGTTTTGGG ATCAGGAGCC CCCAACACAG GCAAGTCCAC CCCATAATAA  3420
CCCTGCCAGT GCCAGGGTGG GCTGGGGACT CTGGCACAGT GATGCCGGGC GCCAGGACAG  3480
CAGCACTCCC GCTGCACACA GACGGCCTAG GGGTGGCGCT CAGACCCCAC CCTACGCTCA  3540
TCTCTGGAAG GGGCAGCCCT GAGTGGTCAC TGGTCAGGGC AGTGGCCAAG CCTGCTGTGT  3600
CCTTCCTCCA CAAGGTCCCC CCACCGCTCA GTGTCAGCGG GTGACGTGTG TTCTTTTGAG  3660
TCCTTGTATG AATAAAAGGC TGGAAACCTA AA
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Seq ID NO: 495 Protein sequence
Protein Accession #: NP_002072.1

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1          11         21         31         41         51
|          |          |          |          |          |
MELRARGWWL LCAAAALVAC ARGDPASKSR SCGEVRQIYG AKGFSLSDVP QAEISGEHLR   60
ICPQGYTCCT SEMEENLANR SHAELETALR DSSRVLQAML ATQLRSFDDH FQHLLNDSER  120
TLQATFPGAF GELYTQNARA FRDLYSELRL YYRGANLHLE ETLAEFWARL LERLFKQLHP  180
QLLLPDDYLD CLGKQAEALR PFGEAPRELR LRATRAFVAA RSFVQGLGVA SDVVRKVAQV  240
PLGPECSRAV MKLVYCAHCL GVPGARPCPD YCRNVLKGCL ANQADLDAEW RNLLDSMVLI  300
TDKFWGTSGV ESVIGSVHTW LAEAINALQD NRDTLTAKVI QGCGNPKVNP QGPGPEEKRR  360
RGKLAPRERP PSGTLEKLVS EAKAQLRDVQ DFWISLPGTL CSEKMALSTA SDDRCWNGMA  420
RGRYLPEVMG DGLANQINNP EVEVDITKPD MTIRQQIMQL KIMTNRLRSA YNGNDVDFQD  480
ASDDGSGSGS
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Seq ID NO: 496 DNA sequence
Nucleic Acid Accession #: NM_001650.2
Coding sequence: 40.1011

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1          11         21         31         41         51
|          |          |          |          |          |
GGGGCAGGCA ATGAGAGCTG CACTCTGGCT GGGGAAGGCA TGAGTGACAG ACCCACAGCA    60
AGGCGGTGGG GTAAGTGTGG ACCTTTGTGT ACCAGAGAGA ACATCATGGT GGCTTTCAAA   120
GGGGTCTGGA CTCAAGCTTT CTGGAAAGCA GTCACAGCGG AATTTCTGGC CATGCTTATT   180
TTTGTTCTCC TCAGCCTGGG ATCCACCATC AACTGGGGTG GAACAGAAAA GCCTTTACCG   240
GTCGACATGG TTCTCATCTC CCTTTGCTTT GGACTCAGCA TTGCAACCAT GGTGCAGTGC   300
TTTGGCCATA TCAGCGGTGG CCACATCAAC CCTGCAGTGA CTGTGGCCAT GGTGTGCACC   360
AGGAAGATCA GCATCGCCAA GTCTGTCTTC TACATCGCAG CCCAGTGCCT GGGGGCCATC   420
ATTGGAGCAG GAATCCTCTA TCTGGTCACA CCTCCCAGTG TGGTGGGAGG CCTGGGAGTC   480
ACCATGGTTC ATGGAAATCT TACCGCTGGT CATGGTCTCC TGGTTGAGTT GATAATCACA   540
TTTCAATTGG TGTTTACTAT CTTTGCCAGC TGTGATTCCA AACGGACTGA TGTCACTGGC   600
TCAATAGCTT TAGCAATTGG ATTTTCTGTT GCAATTGGAC ATTTATTTGC AATCAATTAT   660
ACTGGTGCCA GCATGAATCC CGCCCGATCC TTTGGACCTG CAGTTATCAT GGGAAATTGG   720
GAAAACCATT GGATATATTG GGTTGGGCCC ATCATAGGAG CTGTCCTCGC TGGTGGCCTT   780
TATGAGTATG TCTTCTGTCC AGATGTTGAA TTCAAACGTC GTTTTAAAGA AGCCTTCAGC   840
AAAGCTGCCC AGCAAACAAA AGGAAGCTAC ATGGAGGTGG AGGACAACAG GAGTCAGGTA   900
GAGACGGATG ACCTGATTCT AAAACCTGGA GTGGTGCATG TGATTGACGT TGACCGGGGA   960
GAGGAGAAGA AGGGGAAAGA CCAATCTGGA GAGGTATTGT CTTCAGTATG ACTAGAAGAT  1020
CGCACTGAAA GCAGACAAGA CTCCTTAGAA CTGTCCTCAG ATTTCCTTCC ACCCATTAAG  1080
GAAACAGATT TGTTATAAAT TAGAAATGTG CAGGTTTGTT GTTTCATGTC ATATTACTCA  1140
GTCTAAACAA TAAATATTTC ATAATTTACA AAGGAGGAAC GGAAGAAACC TATTGTGAAT  1200
TCCAAATCTA AAAAAAGAAA TATTTTTAAG ATGTTCTTAA GCAAATATAT ACCTATTTTA  1260
TCTAGTTACC TTTCATTAAC AACCAATTTT AACCGTGTGT CAAGATTTGG TTAAGTCTTG  1320
CCTGACAGAA CTCAAAGACA CGTCTATCAG CTTATTCCTT CTCTACTGGA ATATTGGTAT  1380
AGTCAATTCT TATTTGAATA TTTATTCTAT TAAACTGAGT TTAACAATGG C
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Seq ID NO: 497 Protein sequence
Protein Accession #: NP_001641.1

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1          11         21         31         41         51
|          |          |          |          |          |
MSDRPTARRW GKCGPLCTRE NIMVAFKGVW TQAFWKAVTA EFLAMLIFVL LSLGSTINWG   60
GTEKPLPVDM VLISLCFGLS IATMVQCFGH ISGGHINPAV TVAMVCTRKI SIAKSVFYIA  120
AQCLGAIIGA GILYLVTPPS VVGGLGVTMV HGNLTAGHGL LVELIITFQL VFTIFASCDS  180
KRTDVTGSIA LAIGFSVAIG HLFAINYTGA SMNPARSFGP AVIMGNWENH WIYWVGPIIG  240
AVLAGGLYEY VFCPDVEFKR RFKEAFSKAA QQTKGSYMEV EDNRSQVETD DLILKPGVVH  300
VIDVDRGEEK KGKDQSGEVL SSV
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Seq ID NO: 498 DNA sequence
Nucleic Acid Accession #: AB020684.1
Coding sequence: 1..1744

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1          11         21         31         41         51
|          |          |          |          |          |
CCCCCTTGTC ATTAATACAT TAAAAAGATT CAATCTTTAC CCTGAGGTAA TTTTGGCCAG   60
TTGGTACCGG ATTTATACCA AAATAATGGA CTTGATTGGT ATTCAAACCA AGATATGTTG  120
GACGGTTACC AGAGGAGAAG GACTCAGTCC TATTGAAAGC TGTGAAGGAT TGGGAGATCC  180
TGCTTGCTTT TATGTTGCTG TAATTTTTAT TTTAAATGGA CTAATGATGG CATTATTCTT  240
CATATATGGC ACATATTTAA GTGGCAGCCG ATTAGGAGGC CTGGTTACAG TGTTGTGCTT  300
CTTTTTCAAT CATGGAGAGT GTACCCGTGT AATGTGGACA CCACCTCTCC GTGAAAGCTT  360
CTCATATCCA TTTCTTGTTC TTCAGATGTT GCTAGTGACT CATATTCTCA GGGCTACAAA  420
ACTTTATAGA GGAAGCTTGA TTGCACTCTG CATTTCCAAT GTATTTTTCA TGCTTCCTTG  480
GCAGTTTGCT CAGTTTGTAC TTCTTACTCA GATTGCATCA TTATTTGCAG TATATGTTGT  540
CGGGTACATT GATATATGTA AATTACGGAA GATCATTTAT ATACACATGA TTTCTCTTGC  600
ACTTTGTTTT GTTTTGATGT TTGGGAACTC AATGTTATTA ACTTCTTATT ATGCTTCTTC  660
TTTGGTAATT ATTTGGGGTA TTCTGGCAAT GAAACCACAT TTCCTGAAAA TAAATGTATC  720
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TGAACTTAGT TTATGGGTTA TTCAAGGATG TTTTTGGTTA TTTGGAACTG TCATACTTAA   780
ATACTTGACA TCTAAAATTT TTGGTATTGC AGATGACGCT CATATTGGCA ACTTACTAAC   840
ATCAAAATTC TTTAGTTATA AGGATTTTGA TACTTTATTG TATACCTGTG CAGCGGAGTT   900
TGACTTTATG GAAAAAGAGA CTCCACTGAG ATACACAAAG ACATTATTGC TTCCAGTTGT   960
TCTTGTAGTG TTTGTTGCTA TTGTTAGAAA GATTATTAGT GATATGTGGG GTGTCTTAGC  1020
TAAACAACAG ACACATGTAA GAAAACACCA GTTTGATCAT GGAGAGCTGG TTTACCATGC  1080
ATTGCAATTG TTAGCATATA CAGCCCTTGG TATTTTAATT ATGAGACTAA AACTCTTCTT  1140
GACACCACAC ATGTGTGTTA TGGCATCACT GATCTGCTCA AGACAGCTAT TTGGATGGCT  1200
CTTTTGCAAA GTACATCCTG GTGCTATTGT GTTTGCTATA TTAGCAGCAA TGTCAATACA  1260
AGGTTCAGCA AATCTGCAAA CCCAGTGGAA TATTGTAGGG GAGTTCAGCA ATTTGCCCCA  1320
AGAAGAACTT ATAGAATGGA TCAAATATAG TACTAAACCA GATGCAGTGT TTGCGGGTGC  1380
CATGCCCACG ATGGCAAGTG TTAAGCTCTC TGCACTTCGG CCCATTGTGA ATCATCCACA  1440
TTATGAAGAC GCAGGCTTGA GAGCCAGAAC AAAAATAGTA TACTCAATGT ATAGTCGGAA  1500
AGCAGCCGAA GAAGTGAAGC GAGAACTGAT AAAGTTAAAA GTGAACTATT ACATTCTAGA  1560
AGAGTCATGG TGTGTAAGAA GATCCAAGCC TGGTTGCAGT ATGCCTGAAA TTTGGGATGT  1620
AGAAGATCCT GCCAATGCTG GGAAAACTCC CTTATGTAAC CTCTTGGTGA AGGATTCCAA  1680
ACCTCACTTC ACCACTGTAT TCCAGAACAG TGTTTACAAA GTCCTAGAAG TTGTAAAAGA  1740
ATGACTGCTA CATGACCTGC TGCCTACGGA GAACTACATC TGTAATGGTT TTAATGTTTT  1800
GCTAAGTCAT GTGTTGTTCA TATCCCAAAA ACTTTTATAG GTAACTGTTT TCAAATAGAA  1860
AACGTTTTAT TTGGTCAATT TGAATGTCAT TCTAATTATA AAAATGACTT ACACCTTTAT  1920
CAATTGGTTA CTATTTCAAT GCACCCTTTA AAATTTGCTA TGCAAATGAG TATATGCTTG  1980
TACTTGACTT TAATATTTGT GCTAAAGTGA GCAAAGCTAC CTGTATAAAG AAAACACAGT  2040
GGGTTGTGAC AAGGATGACA TGAAAATACA GGACAATTCT GACAATGTAG GGGCTGATTT  2100
TATAGTGTAA GAACTATTAA TGCCCCTTGC TTCTTTTTTC TGCCTCTTGC TCTTGTCTTT  2160
TGGACATTTC AGTGATTGTA AGTTCTTCGG TCATGTCAGC CCCTGTCATC AACTTGAGTT  2220
ACAGTAGATG GGGCAGACAT GGAGTGTTTG CTATATAAAA CTATCTGTTT GTTTTACTTC  2280
CTTGTGCGCT TTTTGTTCTC TGTTCTCTTG TTAATGAAGC TTTTCCTGCC CATTATTAAT  2340
CCAAACTCTT GGACCTTGTG GTTAGGAAAT TCCCTTAACT TCCAGCCATA TGGCATTATC  2400
GTGTCTCTTT CTCTCTCTCT CTTGCTCTCT CTCTTCTCCT CTTCCCCATA TTTTCTGTCA  2460
AATAAGTACT GTTTACTCAT TTAGTTGCTT ATCAAGTACT TATTCTTGGT TTTAAAAAAA  2520
ATTAATGGTA ACTGTATTTT TCTCATTTTT AGCATTATTC AAATGTTTAT ATTTTAATAC  2580
CTTTAAACCA CTTTAAAGTT TTTTCATGTT TAATTATAGT TTTAAGAAAA ACTATTTTGA  2640
ACAACCCCAA ATATAGTGCA TCTAGAAACT AATGTATATT TGATTAGACA TCATTTATAG  2700
TGGAACAGTA GACTGTAGTA CATGGTAATT TTTCTTTTAC TATTAAGATA CAATAAAACA  2760
TGACTAATTT TGCTGTCAAA AATGTAAAGA ATAATGATAA ATGGAGTTTT TTATATTTTA  2820
CTTTTAAGAT TGCCTGTCTT TAATAAGACA AAGCCTTAAG CCTTATGTTA TAATTTTGGT  2880
TCTAAAAACC ATCATTTCAG TATAAGGAAT AAGTATATTT CGTCCTCCTC TTTAGTTTTT  2940
TTCTTCCTAT TTATTTTTAT TTTGAAAAAT TTCTACACCT TCTTTGAATT CCTTGTATGA  3000
ATTTTTGTTT CTTAGAAGTT AATTTGTGTG AAATGAGATT CTTCAAAACG ATGAAACCTC  3060
ATAGCTCTGA GAAAAGGTTT TAGGGTTTTA AATTCTAAGC AAAGCGTGAC TATGGCTGAC  3120
AGACTACACA TTTAATTATA CAGCTTCTCT TTCTTAACCA CAGGCAGATT AACCTCATTG  3180
TGGATTGTCC TTCAGACCTT AGTCCTCAGG CATGGTTTCT GGTGCCCACT CCTGGAAGCC  3240
GCTGTTCCCT TTCTACCTTC TTACCAGAGC CCAAGGGCAG GCCTGGTCCC GGGGAAGCAG  3300
CAGCTTGCTG ACATAAGTCA GCTGCAAAGG CTGAGGAGTG TGCCCTCAGA GAAGCACCGC  3360
CCCCCAGTCT TGTGCCAGCG CCTAGAGCCG CAGCTCCCAG GGATGCTCCT TCCCTGGAGG  3420
CAGCCCAGGA GAGGGACTCT GGCAGCGTTC TTCAGATTTG TGGCCACTGT TTCTCATTTG  3480
CTGGTTGACT GTTTTTATTT CTTAGGCTTT TGCTAGTTTT AGAAAATAGG GAAGCAGCCC  3540
TTGATTTGTG GATTAAAAGC AACATTTGAG CGATGATGCA CAACAGTCCA GGAAAATGGG  3600
CGGTGGACAC TTGAGGCTGA GGATGGGAGT TGACATGAGC AGGGAGAGGG AGGTGCGCGC  3660
TGCTTATCTG TGATTGTTGC TCACCTGAGT GTGGCTGATT GTGTACATCC AGCAGTTACA  3720
ATTTTTAAAA ATTATACTTT TACATTTATT TTATATTTTT CTCACCCCCA GTAATTTCCT  3780
TCCAAAGAAG TTCACATGTA ATAAGTAGAA ATTCTGTATA GGAAAAAAGC ATTAAAAATA  3840
CTATTATAAC TGCTTCATTT GCTGGGAACC ATTAAAAGTA ATATAAATTA GCTTTTTCCA  3900
GAAGGATCCT TTTGTAGCAG TGTTTATGAA TGTAACCCCC AGCAAAATAT GGCTATATAT  3960
TAGGGGAGCC AGTTTGGAGC AGAGGCCTGA AGGTCCCTGC TATGCAGCCG TGGCCACAGC  4020
TCGCAGCCCA AGCACTGTGG AGCATCCACA CCTTTGATGG CAATGCAGAT TGGTAGCAGG  4080
TTCCATAGGC GTACAAAACA GTATTAAAGC TCAGTGTTTT GCATATTGTT AGCATTTACA  4140
AATATTTTTG CTTTAGTATG AGGAAAGTAA GGATGGGCAA AGAAGCGATC AAAATAGCTA  4200
TTGCTACAAC ATTTTCGAAA ACAAAGTTGG GGCTGTATTT CTTTAAAAAG ATAAGCCTCT  4260
AAAAATGCTT GGCAAAAAAA ATATAGTGTT AAAATAGGCC AGTGATATTA ATGAGAAAAT  4320
GAAAGTATGT ATCAGGAATA AAGTGATATT GCATAGGAGT ATTGTATTTT TATGAATTTT  4380
ATGCCAGTTG TTTACATGTA CTATATATGT TAAATTAAAA AAAATCATGA GAAATG
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Seq ID NO: 499 Protein sequence
Protein Accession #: BAA74900.1

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1          11         21         31         41         51
|          |          |          |          |          |
PLVINTLKRF NLYPEVILAS WYRIYTKIMD LIGIQTKICW TVTRGEGLSP IESCEGLGDP    60
ACFYVAVIFI LNGLMMALFF IYGTYLSGSR LGGLVTVLCF FFNHGECTRV MWTPPLRESP   120
SYPFLVLQML LVTHILRATK LYRGSLIALC ISNVFFMLPW QFAQFVLLTQ IASLFAVYVV   180
GYIDICKLRK IIYIHMISLA LCFVLMFGNS MLLTSYYASS LVIIWGILAM KPHFLKINVS   240
ELSLWVIQGC FWLFGTVILK YLTSKIFGIA DDAHIGNLLT SKFFSYKDFD TLLYTCAAEF   300
DFMEKETPLR YTKTLLLPVV LVVFVAIVRK IISDMWGVLA KQQTHVRKHQ FDHGELVYHA   360
LQLLAYTALG ILIMRLKLFL TPHMCVMASL ICSRQLFGWL FCKVHPGAIV FAILAAMSIQ   420
GSANLQTQWN IVGEFSNLPQ EELIEWIKYS TKPDAVFAGA MPTMASVKLS ALRPIVNHPH   480
YEDAGLRART KIVYSMYSRK AAEEVKRELI KLKVNYYILE ESWCVRRSKP GCSMPEIWDV   540
EDPANAGKTP LCNLLVKDSK PHFTTVFQNS VYKVLEVVKE
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Seq ID NO: 500 DNA sequence
Nucleic Acid Accession #: NM_001276.1
Coding sequence: 127..1278

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1          11         21         31         41         51
|          |          |          |          |          |
AGTGGAGTGG GACAGGTATA TAAAGGAAGT ACAGGGCCTG GGGAAGAGGC CCTGTCTAGG    60
TAGCTGGCAC CAGGAGCCGT GGGCAAGGGA AGAGGCCACA CCCTGCCCTG CTCTGCTGCA   120
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GCCAGAATGG GTGTGAAGGC GTCTCAAACA GGCTTTGTGG TCCTGGTGCT GCTCCAGTGC   180
TGCTCTGCAT ACAAACTGGT CTGCTACTAC ACCAGCTGGT CCCAGTACCG GGAAGGCGAT   240
GGGAGCTGCT TCCCAGATGC CCTTGACCGC TTCCTCTGTA CCCACATCAT CTACAGCTTT   300
GCCAATATAA GCAACGATCA CATCGACACC TGGGAGTGGA ATGATGTGAC GCTCTACGGC   360
ATGCTCAACA CACTCAAGAA CAGGAACCCC AACCTGAAGA CTCTCTTGTC TGTCGGAGGA   420
TGGAACTTTG GGTCTCAAAG ATTTTCCAAG ATAGCCTCCA ACACCCAGAG TCGCCGGACT   480
TTCATCAAGT CAGTACCGCC ATTCCTGCGC ACCCATGGCT TTGATGGGCT GGACCTTGCC   540
TGGCTCTACC CTGGACGGAG AGACAAACAG CATTTTACCA CCCTAATCAA GGAAATGAAG   600
GCCGAATTTA TAAAGGAAGC CCAGCCAGGG AAAAAGCAGC TCCTGCTCAG CGCAGCACTG   660
TCTGCGGGGA AGGTCACCAT TGACAGCAGC TATGACATTG CCAAGATATC CCAACACCTG   720
GATTTCATTA GCATCATGAC CTACGATTTT CATGGAGCCT GGCGTGGGAC CACAGGCCAT   780
CACAGTCCCC TGTTCCGAGG TCAGGAGGAT GCAAGTCCTG ACAGATTCAG CAACACTGAC   840
TATGCTGTGG GGTACATGTT GAGGCTGGGG GCTCCTGCCA GTAAGCTGGT GATGGGCATC   900
CCCACCTTCG GGAGGAGCTT CACTCTGGCT TCTTCTGAGA CTGGTGTTGG AGCCCCAATC   960
TCAGGACCGG GAATTCCAGG CCGGTTCACC AAGGAGGCAG GGACCCTTGC CTACTATGAG  1020
ATCTGTGACT TCCTCCGCGG AGCCACAGTC CATAGAACCC TCGGCCAGCA GGTCCCCTAT  1080
GCCACCAAGG GCAACCAGTG GGTAGGATAC GACGACCAGG AAAGCGTCAA AAGCAAGGTG  1140
CAGTACCTGA AGGATAGGCA GCTGGCAGGC GCCATGGTAT GGGCCCTGGA CCTGGATGAC  1200
TTCCAGGGCT CCTTCTGCGG CCAGGATCTG CGCTTCCCTC TCACCAATGC CATCAAGGAT  1260
GCACTCGCTG CAACGTAGCC CTCTGTTCTG CACACAGCAC GGGGGCCAAG GATGCCCCGT  1320
CCCCCTCTGG CTCCAGCTGG CCGGGAGCCT GATCACCTGC CCTGCTGAGT CCCAGGCTGA  1380
GCCTCAGTCT CCCTCCCTTG GGGCCTATGC AGAGGTCCAC AACACACAGA TTTGAGCTCA  1440
GCCCTGGTGG GCAGAGAGGT AGGGATGGGG CTGTGGGGAT AGTGAGGCAT CGCAATGTAA  1500
GACTCGGGAT TAGTACACAC TTGTTGATGA TTAATGGAAA TGTTTACAGA TCCCCAAGCC  1560
TGGCAAGGGA ATTTCTTCAA CTCCCTGCCC CCTAGCCCTC CTTATCAAAG GACACCATTT  1620
TGGCAAGCTC TATCACCAAG GAGCCAAACA TCCTACAAGA CACAGTGACC ATACTAATTA  1680
TACCCCCTGC AAAGCCAGCT TGAAACCTTC ACTTAGGAAC GTAATCGTGT CCCCTATCCT  1740
ACTTCCCCTT CCTAATTCCA CAGCTGCTCA ATAAAGTACA AGAGTTTAAC AGTGTGTTGG  1800
CGCTTTGCTT TGGTCTATCT TTGAGCGCCC ACTAGACCCA CTGGACTCAC CTCCCCCATC  1860
TCTTCTGGGT TCCTTCCTCT GAGCCTTGGG ACCCCTGAGC TTGCAGAGAT GAAGGCCGCC  1920
ATGTT
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Seq ID NO: 501 Protein sequence
Protein Accession #: NP_001267.1

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1          11         21         31         41         51
|          |          |          |          |          |
MGVKASQTGF VVLVLLQCCS AYKLVCYYTS WSQYREGDGS CFPDALDRFL CTHIIYSFAN    60
ISNDHIDTWE WNDVTLYGML NTLKNRNPNL KTLLSVGGWN FGSQRFSKIA SNTQSRRTFI   120
KSVPPFLRTH GFDGLDLAWL YPGRRDKQHF TTLIKEMKAE FIKEAQPGKK QLLLSAALSA   180
GKVTIDSSYD IAKISQHLDF ISIMTYDFHG AWRGTTGHHS PLFRGQEDAS PDRFSNTDYA   240
VGYMLRLGAP ASKLVMGIPT FGRSFTLASS ETGVGAPISG PGIPGRFTKE AGTLAYYEIC   300
DFLRGATVHR TLGQQVPYAT KGNQWVGYDD QESVKSKVQY LKDRQLAGAM VWALDLDDFQ   360
GSFCGQDLRF PLTNAIKDAL AAT
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Seq ID NO: 502 DNA sequence
Nucleic Acid Accession #: NM_006474.1
Coding sequence: 181..669

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1          11         21         31         41         51
|          |          |          |          |          |
GCTGCCTAGG GTCTGGAAAG CTCGGGCACC CTCCCTCTCC GGGGCTCCTG CTCCCACCCC    60
TCCGGCCCCC CCACCGTCGC GCTCCTCCAG GCTGGGCCTG TGGCCGCGGT GCTTTTAATT   120
TTCCCCCAGC TCAGAATCTT GCTGCTCGGC CCCCAGGAGA GCAACAACTC AACGGGAACG   180
ATGTGGAAGG TGTCAGCTCT GCTCTTCGTT TTGGGAAGCG CGTCGCTCTG GGTCCTGGCA   240
GAAGGAGCCA GCACAGGCCA GCCAGAAGAT GACACTGAGA CTACAGGTTT GGAAGGCGGC   300
GTTGCCATGC CAGGTGCCGA AGATGATGTG GTGACTCCAG GAACCAGCGA AGACCGCTAT   360
AAGTCTGGCT TGACAACTCT GGTGGCAACA AGTGTCAACA GTGTAACAGG CATTCGCATC   420
GAGGATCTGC CAACTTCAGA AAGCACAGTC CACGCGCAAG AACAAAGTCC AAGCGCCACA   480
GCCTCAAACG TGGCCACCAG TCACTCCACG GAGAAAGTGG ATGGAGACAC ACAGACAACA   540
GTTGAGAAAG ATGGTTTGTC AACAGTGACC CTGGTTGGAA TCATAGTTGG GGTCTTACTA   600
GCCATCGGTT TCATTGGTGG AATCATCGTT GTGGTTATGC GAAAAATGTC GGGAAGGTAC   660
TCGCCCTAAA GAGCTGAAGG GTTACGCCCT GCTTGCCAAC GTGCTTTAAA AAAAGACCGT   720
TTCTGACTCT GTGGCCCTGT CCCTGAGCTC GTGGGGAGAA GATGACCCTG GGAACATTTG   780
CGGGCCCATT CAGATTCCAC GGTGACTTTC CGTTTGCCAA ATTAACCGAG GAAAGACCTT   840
TCACCAGATT TGGTTCTTAA ACTTT
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Seq ID NO: 503 Protein sequence
Protein Accession #: NP_006465.1

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1          11         21         31         41         51
|          |          |          |          |          |
MWKVSALLFV LGSASLWVLA EGASTGQPED DTETTGLEGG VAMPGAEDDV VTPGTSEDRY    60
KSGLTTLVAT SVNSVTGIRI EDLPTSESTV HAQEQSPSAT ASNVATSHST EKVDGDTQTT   120
VEKDGLSTVT LVGIIVGVLL AIGFIGGIIV VVMRKMSGRY SP
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Seq ID NO: 504 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 62..895

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1          11         21         31         41         51
|          |          |          |          |          |
CACTGCTCTG AGAATTTGTG AGCAGCCCCT AACAGGCTGT TACTTCACTA CAACTGACGA    60
TATGATCATC TTAATTTACT TATTTCTCTT GCTATGGGAA GACACTCAAG GATGGGGATT   120
CAAGGATGGA ATTTTTCATA ACTCCATATG GCTTGAACGA GCAGCCGGTG TGTACCACAG   180
AGAAGCACGG TCTGGCAAAT ACAAGCTCAC CTACGCAGAA GCTAAGGCGG TGTGTGAATT   240
TGAAGGCGGC CATCTCGCAA CTTACAAGCA GCTAGAGGCA GCCAGAAAAA TTGGATTTCA   300
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TGTCTGTGCT GCTGGATGGA TGGCTAAGGG CAGAGTTGGA TACCCCATTG TGAAGCCAGG   360
GCCCAACTGT GGATTTGGAA AAACTGGCAT TATTGATTAT GGAATCCGTC TCAATAGGAG   420
TGAAAGATGG GATGCCTATT GCTACAACCC ACACGCAAAG GAGTGTGGTG GCGTCTTTAC   480
AGATCCAAAG CAAATTTTTA AATCTCCAGG CTTCCCAAAT GAGTACGAAG ATAACCAAAT   540
CTGCTACTGG CACATTAGAC TCAAGTATGG TCAGCGTATT CACCTGAGTT TTTTAGATTT   600
TGACCTTGAA GATGACCCAG GTTGCTTGGC TGATTATGTT GAAATATATG ACAGTTACGA   660
TGATGTCCAT GGCTTTGTGG GAAGATACTG TGGAGATGAG CTTCCAGATG ACATCATCAG   720
TACAGGAAAT GTCATGACCT TGAAGTTTCT AAGTGATGCT TCAGTGACAG CTGGAGGTTT   780
CCAAATCAAA TATGTTGCAA TGGATCCTGT ATCCAAATCC AGTCAAGGAA AAAATACAAG   840
TACTACTTCT ACTGGAAATA AAAACTTTTT AGCTGGAAGA TTTAGCCACT TATAAAAAAA   900
AAAAAAAGGA TGATCAAAAC ACACAGTGTT TATGTTGGAA TCTTTTGGAA CTCCTTTGAT   960
CTCACTGTTA TTATTAACAT TTATTTATTA TTTTTCTAAA TGTGAAAGCA ATACATAATT  1020
TAGGGAAAAT TGGAAAATAT AGGAAACTTT AAACGAGAAA ATGAAACCTC TCATAATCCC  1080
ACTGCATAGA AATAACAAGC GTTAACATTT TCATATTTTT TTCTTTCAGT CATTTTTCTA  1140
TTTGTGGTAT ATGTATATAT GTACCTATAT GTATTTGCAT TTGAAATTTT GGAATCCTGC  1200
TCTATGTACA GTTTTGTATT ATACTTTTTA AATCTTGAAC TTTATAAACA TTTTCTGAAA  1260
TCATTGATTA TTCTACAAAA ACATGATTTT AAACAGCTGT AAAATATTCT ATGATATGAA  1320
TGTTTTATGC ATTATTTAAG CCTGTCTCTA TTGTTGGAAT TTCAGGTCAT TTTCATAAAT  1380
ATTGTTGCAA TAAATATCCT TGAACACACA AAAAAAAAAA AA
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Seq ID NO: 505 Protein sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MIILIYLFLL LWEDTQGWGF KDGIFHNSIW LERAAGVYHR EARSGKYKLT YAEAKAVCEF   60
EGGHLATYKQ LEAARKIGFH VCAAGWMAKG RVGYPIVKPG PNCGFGKTGI IDYGIRLNRS  120
ERWDAYCYNP HAKECGGVFT DPKQIFKSPG FPNEYEDNQI CYWHIRLKYG QRIHLSFLDF  180
DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPDDIIS TGNVMTLKFL SDASVTAGGF  240
QIKYVAMDPV SKSSQGKNTS TTSTGNKNFL AGRFSHL
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Seq ID NO: 506 DNA sequence
Nucleic Acid Accession #: NM_007115.1
Coding sequence: 69..902

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1          11         21         31         41         51
|          |          |          |          |          |
GAATTCGCAC TGCTCTGAGA ATTTGTGAGC AGCCCCTAAC AGGCTGTTAC TTCACTACAA   60
CTGACGATAT GATCATCTTA ATTTACTTAT TTCTCTTGCT ATGGGAAGAC ACTCAAGGAT  120
GGGGATTCAA GGATGGAATT TTTCATAACT CCATATGGCT TGAACGAGCA GCCGGTGTGT  180
ACCACAGAGA AGCACGGTCT GGCAAATACA AGCTCACCTA CGCAGAAGCT AAGGCGGTGT  240
GTGAATTTGA AGGCGGCCAT CTCGCAACTT ACAAGCAGCT AGAGGCAGCC AGAAAAATTG  300
GATTTCATGT CTGTGCTGCT GGATGGATGG CTAAGGGCAG AGTTGGATAC CCCATTGTGA  360
AGCCAGGGCC CAACTGTGGA TTTGGAAAAA CTGGCATTAT TGATTATGGA ATCCGTCTCA  420
ATAGGAGTGA AAGATGGGAT GCCTATTGCT ACAACCCACA CGCAAAGGAG TGTGGTGGCG  480
TCTTTACAGA TCCAAAGCGA ATTTTTAAAT CTCCAGGCTT CCCAAATGAG TACGAAGATA  540
ACCAAATCTG CTACTGGCAC ATTAGACTCA AGTATGGTCA GCGTATTCAC CTGAGTTTTT  600
TAGATTTTGA CCTTGAAGAT GACCCAGGTT GCTTGGCTGA TTATGTTGAA ATATATGACA  660
GTTACGATGA TGTCCATGGC TTTGTGGGAA GATACTGTGG AGATGAGCTT CCAGATGACA  720
TCATCAGTAC AGGAAATGTC ATGACCTTGA AGTTTCTAAG TGATGCTTCA GTGACAGCTG  780
GAGGTTTCCA AATCAAATAT GTTGCAATGG ATCCTGTATC CAAATCCAGT CAAGGAAAAA  840
ATACAAGTAC TACTTCTACT GGAAATAAAA ACTTTTTAGC TGGAAGATTT AGCCACTTAT  900
AAAAAAAAAA AAGGATGATC AAAACACACA GTGTTTATGT TGGAATCTTT TGGAACTCCT  960
TTGATCTCAC TGTTATTATT AACATTTATT TATTATTTTT CTAAATGTGA AAGAAATACA 1020
TAATTTAGGG AAAATTGGAA AATATAGGAA ACTTTAAACG AGAAAATGAA ACCTCTCATA 1080
ATCCCACTGC ATAGAAATAA CAAGCGTTAA CATTTCATA TTTTTTTCTT TCAGTCATTT 1140
TTGTATTTGT GGTATATGTA TATATGTACC TATATGTATT TGCATTTGAA ATTTTGGAAT 1200
CCTGCTCTAT GTACAGTTTT GTATTATACT TTTTAAATCT TGAACTTTAT GAACATTTTC 1260
TGAAATCATT GATTATTCTA CAAAAACATG ATTTTAAACA GCTGTAAAAT ATTCTATGAT 1320
ATGAATGTTT TATGCATTAT TTAAGCCTGT CTCTATTGTT GGAATTTCAG GTCATTTTCA 1380
TAAATATTGT TGCAATAAAT ATCCTTCGGA ATTC
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Seq ID NO: 507 Protein sequence
Protein Accession #: NP_009046.1

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1          11         21         31         41         51
|          |          |          |          |          |
MIILIYLFLL LWEDTQGWGF KDGIFHNSIW LERAAGVYHR EARSGKYKLT YAEAKAVCEF   60
EGGHLATYKQ LEAARKIGFH VCAAGWMAKG RVGYPIVKPG PNXXFGKTGI IDYGIRLNRS  120
ERWDAYCYNP HAKECGGVFT DPKRIFKSPG FPNEYEDNQI CYWHIRLKYG QRIHLSFLDF  180
DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPDDIIS TGNVMTLKFL SDASVTAGGF  240
QIKYVAMDPV SKSSQGKNTS TTSTGNKNFL AGRFSHL
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Seq ID NO: 508 DNA sequence
Nucleic Acid Accession #: NM_001044.1
Coding sequence: 129..1991

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1          11         21         31         41         51
|          |          |          |          |          |
ACCGCTCCGG AGCGGGAGGG GAGGCTTCGC GGAACGCTCT CGGCGCCAGG ACTCGCGTGC   60
AAAGCCCAGG CCCGGGCGGC CAGACCAAGA GGGAAGAAGC ACAGAATTCC TCAACTCCCA  120
GTGTGCCCAT GAGTAAGAGC AAATGCTCCG TGGGACTCAT GTCTTCCGTG GTGGCCCCGG  180
CTAAGGAGCC CAATGCCGTG GGCCCGAAGG AGGTGGAGCT CATCCTTGTC AAGGAGCAGA  240
ACGGAGTGCA GCTCACCAGC TCCACCCTCA CCAACCCGCG GCAGAGCCCC GTGGAGGCCC  300
AGGATCGGGA GACCTGGGGC AAGAAGATCG ACTTTCTCCT GTCCGTCATT GGCTTTGCTG  360
TGGACCTGGC CAACGTCTGG CGGTTCCCCT ACCTGTGCTA CAAAAATGGT GGCGGTGCCT  420
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TCCTGGTCCC CTACCTGCTC TTCATGGTCA TTGCTGGGAT GCCACTTTTC TACATGGAGC    480
TGGCCCTCGG CCAGTTCAAC AGGGAAGGGG CCGCTGGTGT CTGGAAGATC TGCCCCATAC    540
TGAAAGGTGT GGGCTTCACG GTCATCCTCA TCTCACTGTA TGTCGGCTTC TTCTACAACG    600
TCATCATCGC CTGGGCGCTG CACTATCTCT TCTCCTCCTT CACCACGGAG CTCCCCTGGA    660
TCCACTGCAA CAACTCCTGG AACAGCCCCA ACTGCTCGGA TGCCCATCCT GGTGACTCCA    720
GTGGAGACAG CTCGGGCCTC AACGACACTT TTGGGACCAC ACCTGCTGCC GAGTACTTTG    780
AACGTGGCGT GCTGCACCTC CACCAGAGCC ATGGCATCGA CGACCTGGGG CCTCCGCGGT    840
GGCAGCTCAC AGCCTGCCTG GTGCTGGTCA TCGTGCTGCT CTACTTCAGC CTCTGGAAGG    900
GCGTGAAGAC CTCAGGGAAG GTGGTATGGA TCACAGCCAC CATGCCATAC GTGGTCCTCA    960
CTGCCCTGCT CCTGCGTGGG GTCACCCTCC CTGGAGCCAT AGACGGCATC AGAGCATACC   1020
TGAGCGTTGA CTTCTACCGG CTCTGCGAGG CGTCTGTTTG GATTGACGCG GCCACCCAGG   1080
TGTGCTTCTC CCTGGGCGTG GGGTTCGGGG TGCTGATCGC CTTCTCCAGC TACAACAAGT   1140
TCACCAACAA CTGCTACAGG GACGCGATTG TCACCACCTC CATCAACTCC CTGACGAGCT   1200
TCTCCTCCGG CTTCGTCGTC TTCTCCTTCC TGGGGTACAT GGCACAGAAG CACAGTGTGC   1260
CCATCGGGGA CGTGGCCAAG GACGGGCCAG GGCTGATCTT CATCATCTAC CCGGAAGCCA   1320
TCGCCACGCT CCCTCTGTCC TCAGCCTGGG CCGTGGTCTT CTTCATCATG CTGCTCACCC   1380
TGGGTATCGA CAGCGCCATG GGTGGTATGG AGTCAGTGAT CACCGGGCTC ATCGATGAGT   1440
TCCAGCTGCT GCACAGACAC CGTGAGCTCT TCACGCTCTT CATCGTCCTG GCGACCTTCC   1500
TCCTGTCCCT GTTCTGCGTC ACCAACGGTG GCATCTACGT CTTCACGCTC CTGGACCATT   1560
TTGCAGCCGG CACGTCCATC CTCTTTGGAG TGCTCATCGA AGCCATCGGA GTGGCCTGGT   1620
TCTATGGTGT TGGGCAGTTC AGCGACGACA TCCAGCAGAT GACCGGGCAG CGGCCCAGCC   1680
TGTACTGGCG GCTGTGCTGG AAGCTGGTCA GCCCCTGCTT TCTCCTGTTC GTGGTCGTGG   1740
TCAGCATTGT GACCTTCAGA CCCCCCCACT ACGGAGCCTA CATCTTCCCC GACTGGGCCA   1800
ACGCGCTGGG CTGGGTCATC GCCACATCCT CCATGGCCAT GGTGCCCATC TATGCGGCCT   1860
ACAAGTTCTG CAGCCTGCCT GGGTCCTTTC GAGAGAAACT GGCCTACGCC ATTGCACCCG   1920
AGAAGGACCG TGAGCTGGTG GACAGAGGGG AGGTGCGCCA GTTCACGCTC CGCCACTGGC   1980
TCAAGGTGTA GAGGGAGCAG AGACGAAGAC CCCAGGAAGT CATCCTGCAA TGGGAGAGAC   2040
ACGAACAAAC CAAGGAAATC TAAGTTTCGA GAGAAAGGAG GGCAACTTCT ACTCTTCAAC   2100
CTCTACTGAA AACACAAACA ACAAAGCAGA AGACTCCTCT CTTCTGACTG TTTACACCTT   2160
TCCGTGCCGG GAGCGCACCT CGCCGTGTCT TGTGTTGCTG TAATAACGAC GTAGATCTGT   2220
GCAGCGAGGT CCACCCCGTT GTTGTCCCTG CAGGGCAGAA AAACGTCTAA CTTCATGCTG   2280
TCTGTGTGAG GCTCCCTCCC TCCCTGCTCC CTGCTCCCGG CTCTGAGGCT GCCCCAGGGG   2340
CACTGTGTTC TCAGGCGGGG ATCACGATCC TTGTAGACGC ACCTGCTGAG AATCCCCGTG   2400
CTCACAGTAG CTTCCTAGAC CATTTACTTT GCCCATATTA AAAAGCCAAG TGTCCTGCTT   2460
GGTTTAGCTG TGCAGAAGGT GAAATGGAGG AAACCACAAA TTCATGCAAA GTCCTTTCCC   2520
GATGCGTGGC TCCCAGCAGA GGCCGTAAAT TGAGCGTTCA GTTGACACAT TGCACACACA   2580
GTCTGTTCAG AGGCATTGGA GGATGGGGGT CCTGGTATGT CTCACCAGGA AATTCTGTTT   2640
ATGTTCTTGC AGCAGAGAGA AATAAAACTC CTTGAAACCA GCTCAGGCTA CTGCCACTCA   2700
GGCAGCCTGT GGGTCCTTGT GGTGTAGGGA ACGGCCTGAG AGGAGCGTGT CCTATCCCCG   2760
GACGCATGCA GGGCCCCCAC AGGAGCGTGT CCTATCCCCG GACGCATGCA GGGCCCCCAC   2820
AGGAGCATGT CCTATCCCTG GACGCATGCA GGGCCCCCAC AGGAGCGTGT ACTACCCCAG   2880
AACGCATGCA GGGCCCCCAC AGGAGCGTGT ACTACCCCAG GACGCATGCA GGGCCCCCAC   2940
TGGAGCGTGT ACTACCCCAG GACGCATGCA GGGCCCCCAC AGGAGCGTGT CCTATCCCCG   3000
GACCGGACGC ATGCAGGGCC CCCACAGGAG CGTGTACTAC CCCAGGACGC ATGCAGGGCC   3060
CCCACAGGAG CGTGTACTAC CCCAGGATGC ATGCAGGGCC CCCACAGGAG CGTGTACTAC   3120
CCCAGGACGC ATGCAGGGCC CCCATGCAGG CAGCCTGCAG ACCAACACTC TGCCTGGCCT   3180
TGAGCCGTGA CCTCCAGGAA GGGACCCCAC TGGAATTTTA TTTCTCTCAG GTGCGTGCCA   3240
CATCAATAAC AACAGTTTTT ATGTTTGCGA ATGGCTTTTT AAAATCATAT TTACCTGTGA   3300
ATCAAAACAA ATTCAAGAAT GCAGTATCCG CGAGCCTGCT TGCTGATATT GCAGTTTTTG   3360
TTTACAAGAA TAATTAGCAA TACTGAGTGA AGGATGTTGG CCAAAAGCTG CTTTCCATGG   3420
CACACTGCCC TCTGCCACTG ACAGGAAAGT GGATGCCATA GTTTGAATTC ATGCCTCAAG   3480
TCGGTGGGCC TGCCTACGTG CTGCCCGAGG GCAGGGGCCG TGCAGGGCCA GTCATGGCTG   3540
TCCCCTGCAA GTGGACGTGG GCTCCAGGGA CTGGAGTGTA ATGCTCGGTG GGAGCCGTCA   3600
GCCTGTGAAC TGCCAGGCAG CTGCAGTTAG CACAGAGGAT GGCTTCCCCA TTGCCTTCTG   3660
GGGAGGGACA CAGAGGACGG CTTCCCCATC GCCTTCTGGC CGCTGCAGTC AGCACAGAGA   3720
GCGGCTTCCC CATTGCCTTC TGGGGAGGGA CACAGAGGAC AGTTTCCCCA TCGCCTTCTG   3780
GTTGTTGAAG ACAGCACAGA GAGCGGCTTC CCCATCGCCT TCTGGGGAGG GGCTCCGTGT   3840
AGCAACCCAG GTGTTGTCCG TGTCTGTTGA CCAATCTCTA TTCAGCATCG TGTGGGTCCC   3900
TAAGCACAAT AAAAGACATC CACAATGGAA AAAAAAAAAG GAATTC
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Seq ID NO: 509 Protein sequence
Protein Accession #: NP_001035.1

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1          11         21         31         41         51
|          |          |          |          |          |
MSKSKCSVGL MSSVVAPAKE PNAVGPKEVE LILVKEQNGV QLTSSTLTNP RQSPVEAQDR     60
ETWGKKIDFL LSVIGFAVDL ANVWRFPYLC YKNGGGAFLV PYLLFMVIAG MPLFYMELAL    120
GQFNREGAAG VWKICPILKG VGFTVILISL YVGFFYNVII AWALHYLFSS FTTELPWIHC    180
NNSWNSPNCS DAHPGDSSGD SSGLNDTFGT TPAAEYFERG VLHLHQSHGI DDLGPPRWQL    240
TACLVLVIVL LYFSLWKGVK TSGKVVWITA TMPYVVLTAL LLRGVTLPGA IDGIRAYLSV    300
DFYRLCEASV WIDAATQVCF SLGVGFGVLI AFSSYNKFTN NCYRDAIVTT SINSLTSFSS    360
GFVVFSFLGY MAQKHSVPIG DVAKDGPGLI FIIYPEAIAT LPLSSAWAVV FFIMLLTLGI    420
DSAMGGMESV ITGLIDEFQL LHRHRELFTL FIVLATFLLS LFCVTNGGIY VFTLLDHFAA    480
GTSILFGVLI EAIGVAWFYG VGQFSDDIQQ MTGQRPSLYW RLCWKLVSPC FLLFVVVVSI    540
VTFRPPHYGA YIFPDWANAL GWVIATSSMA MVPIYAAYKF CSLPGSFREK LAYAIAPEKD    600
RELVDRGEVR QFTLRHWLKV
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Seq ID NO: 510 DNA sequence
Nucleic Acid Accession #: NM_001216.1
Coding sequence: 43..1422

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1          11         21         31         41         51
|          |          |          |          |          |
GCCCGTACAC ACCGTGTGCT GGGACACCCC ACAGTCAGCC GCATGGCTCC CCTGTGCCCC     60
AGCCCCTGGC TCCCTCTGTT GATCCCGGCC CCTGCTCCAG GCCTCACTGT GCAACTGCTG    120
CTGTCACTGC TGCTTCTGAT GCCTGTCCAT CCCCAGAGGT TGCCCCGGAT GCAGGAGGAT    180
TCCCCCTTGG GAGGAGGCTC TTCTGGGGAA GATGACCCAC TGGGCGAGGA GGATCTGCCC    240
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AGTGAAGAGG ATTCACCCAG AGAGGAGGAT CCACCCGGAG AGGAGGATCT ACCTGGAGAG   300
GAGGATCTAC CTGGAGAGGA GGATCTACCT GAAGTTAAGC CTAAATCAGA AGAAGAGGGC   360
TCCCTGAAGT TAGAGGATCT ACCTACTGTT GAGGCTCCTG GAGATCCTCA AGAACCCCAG   420
AATAATGCCC ACAGGGACAA AGAAGGGGAT GACCAGAGTC ATTGGCGCTA TGGAGGCGAC   480
CCGCCCTGGC CCCGGGTGTC CCCAGCCTGC GCGGGCCGCT TCCAGTCCCC GGTGGATATC   540
CGCCCCCAGC TCGCCGCCTT CTGCCCGGCC CTGCGCCCCC TGGAACTCCT GGGCTTCCAG   600
CTCCCGCCGC TCCCAGAACT GCGCCTGCGC AACAATGGCC ACAGTGTGCA ACTGACCCTG   660
CCTCCTGGGC TAGAGATGGC TCTGGGTCCC GGGCGGGAGT ACCGGGCTCT GCAGCTGCAT   720
CTGCACTGGG GGGCTGCAGG TCGTCCGGGC TCGGAGCACA CTGTGGAAGG CCACCGTTTC   780
CCTGCCGAGA TCCACGTGGT TCACCTCAGC ACCGCCTTTG CCAGAGTTGA CGAGGCCTTG   840
GGGCGCCCGG GAGGCCTGGC CGTGTTGGCC GCCTTTCTGG AGGAGGGCCC GGAAGAAAAC   900
AGTGCCTATG AGCAGTTGCT GTCTCGCTTG GAAGAAATCG CTGAGGAAGG CTCAGAGACT   960
CAGGTCCCAG GACTGGACAT ATCTGCACTC CTGCCCTCTG ACTTCAGCCG CTACTTCCAA  1020
TATGAGGGGT CTCTGACTAC ACCGCCCTGT GCCCAGGGTG TCATCTGGAC TGTGTTTAAC  1080
CAGACAGTGA TGCTGAGTGC TAAGCAGCTC CACACCCTCT CTGACACCCT GTGGGGACCT  1140
GGTGACTCTC GGCTACAGCT GAACTTCCGA GCGACGCAGC CTTTGAATGG GCGAGTGATT  1200
GAGGCCTCCT TCCCTGCTGG AGTGGACAGC AGTCCTCGGG CTGCTGAGCC AGTCCAGCTG  1260
AATTCCTGCC TGGCTGCTGG TGACATCCTA GCCCTGGTTT TTGGCCTCCT TTTTGCTGTC  1320
ACCAGCGTCG CGTTCCTTGT GCAGATGAGA AGGCAGCACA GAAGGGGAAC CAAAGGGGGT  1380
GTGAGCTACC GCCCAGCAGA GGTAGCCGAG ACTGGAGCCT AGAGGCTGGA TCTTGGAGAA  1440
TGTGAGAAGC CAGCCAGAGG CATCTGAGGG GGAGCCGGTA ACTGTCCTGT CCTGCTCATT  1500
ATGCCACTTC CTTTTAACTG CCAAGAAATT TTTTAAAATA AATATTTATA AT
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Seq ID NO: 511 Protein sequence
Protein Accession #: NP_001207.1

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1          11         21         31         41         51
|          |          |          |          |          |
MAPLCPSPWL PLLIPAPAPG LTVQLLLSLL LLMPVHPQRL PRMQEDSPLG GGSSGEDDPL    60
GEEDLPSEED SPREEDPPGE EDLPGEEDLP GEEDLPEVKP KSEEEGSLKL EDLPTVEAPG   120
DPQEPQNNAH RDKEGDDQSH WRYGGDPPWP RVSPACAGRF QSPVDIRPQL AAFCPALRPL   180
ELLGFQLPPL PELRLRNNGH SVQLTLPPGL EMALGPGREY RALQLHLHWG AAGRPGSEHT   240
VEGHRFPAEI HVVHLSTAFA RVDEALGRPG GLAVLAAFLE EGPEENSAYE QLLSRLEEIA   300
EEGSETQVPG LDISALLPSD FSRYFQYEGS LTTPPCAQGV IWTVFNQTVM LSAKQLHTLS   360
DTLWGPGDSR LQLNFRATQP LNGRVIEASF PAGVDSSPRA AEPVQLNSCL AAGDILALVF   420
GLLFAVTSVA FLVQMRRQHR RGTKGGVSYR PAEVAETGA
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Seq ID NO: 512 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..3978

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TTTGCAGAAA GATATGACCC CAGCCTGAAG ACCATGATCC CAGTGCGACC CTGTGCAAGG   120
TTAGCACCCA ACCCGGTGGA TGATGCCGGG CTACTCTCCT TCGCCACATT TTCCTGGCTC   180
ACGCCGGTGA TGGTGAAAGG CTACCGGCAA AGGCTGACCG TAGACACCCT GCCCCCATTG   240
TCGACATATG ACTCATCTGA CACCAATGCC AAAAGATTTC GAGTCCTTTG GGATGAAGAG   300
GTAGCAAGGG TGGGTCCTGA GAAGGCCTCT CTGAGCCACG TGGTGTGGAA ATTCCAGAGG   360
ACACGCGTGT TGATGGACAT CGTGGCCAAC ATCCTGTGCA TCATCATGGC AGCCATAGGG   420
CCGACAGTTC TCATTCACCA AATCCTCCAG CAGACTGAGA GGACCTCTGG GAAAGTCTGG   480
GTTGGCATTG GACTGTGCAT AGCCCTTTTT GCCACCGAGT TTACCAAAGT CTTCTTTTGG   540
GCCCTTGCCT GGGCCATCAA CTACCGCACG GCCATCCGGT TGAAGGTGGC GCTCTCCACC   600
TTGGTTTTTG AAAACCTAGT GTCCTTCAAG ACATTGACCC ACATCTCTGT TGGCGAGGTG   660
CTCAATATAC TGTCAAGTGA TAGCTATTCT TTGTTTGAAG CTGCCTTGTT TTGTCCTTTG   720
CCAGCCACCA TCCCGATCCT AATGGTCTTT TGTGCGGCGT ACGCCTTTTT CATTCTGGGG   780
CCCACAGCTC TCATCGGGAT ATCAGTGTAT GTCATATTCA TACCCGTCCA GATGTTTATG   840
GCCAAGCTCA ATTCAGCTTT CCGAAGGTCA GCAATTTTGG TGACAGACAA GCGAGTTCAG   900
ACAATGAATG AGTTTCTGAC CTGCATCAGG CTGATCAAAA TGTATGCCTG GGAGAAATCT   960
TTTACCAACA CTATCCAAGA TATAAGAAGG AGGGAAAGAA AATTACTGGA AAAAGCTGGA  1020
TTTGTCCAAA GTGGAAACTC TGCCCTGGCC CCCATCGTGT CCACCATAGC CATCGTGCTG  1080
ACATTATCCT GCCACATCCT CCTGAGACGC AAACTCACCG CACCCGTGGC ATTTAGTGTG  1140
ATTGCCATGT TTAATGTAAT GAAGTTTTCC ATTGCAATCT TGCCCTTCTC CATCAAAGCA  1200
ATGGCTGAAG CGAATGTCTC TCTAAGGAGA ATGAAGAAAA TTCTCATAGA TAAAAGCCCC  1260
CCATCTTACA TCACCCAACC AGAAGACCCA GATACTGTCT TGCTTTTAGC AAATGCCACC  1320
TTGACATGGG AGCATGAAGC CAGCAGGAAA AGTACCCCAA AGAAATTGCA GAACCAGAAA  1380
AGGCATTTAT GCAAGAAACA GAGGTCAGAG GCATACAGTG AGAGGAGTCC ACCAGCCAAG  1440
GGAGCCACTG GCCCAGAGGA GCAAAGTGAC AGCCTCAAAT CGGTTCTGCA CAGCATAAGC  1500
TTTGTGGTGA GAAAGTTATG TCGTTATCCC GAAGCCCAGC TCCTGGCTTG GAGGTGGCCA  1560
GCAGTGTTTG TTGGGAGAAT CATCAGAGGA TACAGGCCTC ATGGATTTTC TGCTAAAGAC  1620
AAGGATGAAT CTAGAAGGCT TCTTACTTGG CCCCAAGAAG TGGATAGGAC TCAAAGGGCA  1680
GCCAAATACC TGGGGAAGAT CTTGGGAATA TGTGGGAATG TGGGAAGTGG AAAGAGCTCC  1740
CTCCTTGCAG CTCTCCTAGG ACAGATGCAG CTGCAGAAAG GGGTGGTGGC AGTCAATGGA  1800
ACTTTGGCCT ACGTTTCACA GCAGGCATGG ATCTTTCATG GAAATGTGAG AGAAAACATA  1860
CTCTTTGGAG AAAAGTATGA TCACCAAAGG TATCAGCACA CAGTCCGCGT CTGTGGCCTC  1920
CAGAAGGACC TGAGCAACCT CCCCTATGGA GACCTGACTG AGATTGGGGA GCGGGGCCTC  1980
AACCTCTCTG GGGGGCAGAG GCAGAGGATT AGCCTGGCCC GCGCTGTCTA CTCCGACCGT  2040
CAGCTCTACC TGCTGGACGA CCCCCTGTCG GCCGTGGACG CCCACGTGGG GAAGCACGTC  2100
TTTGAGGAGT GCATTAAGAA GACGCTCAGG GGAAAGACAG TCGTCCTGGT GACCCACCAG  2160
CTACAGTTCT TAGAGTCTTG TGATGAAGTT ATTTTATTAG AAGATGGAGA GATTTGTGAA  2220
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CTGCGAGGAT TGCAGTTCAA GGATCCTGAA CACCTTTACA ATGCAGCAAT GGTGGAAGCC  2340
TTCAAGGAGA GCCCTGCTGA GAGAGAGGAA GATGCTGGTA TAATCGGGTA CCTCCTTTCT  2400
CTCTTCACTG TGTTCCTCTT CCTCCTGATG ATTGGCAGCG CTGCCTTCAG CAACTGGTGG  2460
CTGGGTCTCT GGTTGGACAA GGGCTCACGG ATGACCTGTG GGCCCCAGGG CAACAGGACC  2520
ATGTGTGAGG TCGGCGCGGT GCTGGCAGAC ATCGGTCAGC ATGTGTACCA GTGGGTGTAC  2580
ACTGCAAGCA TGGTGTTCAT GCTGGTGTTT GGCGTCACCA AAGGCTTCGT CTTCACCAAG  2640
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ACCACACTGA TGGCATCCTC CTCTCTGCAT GACACGGTGT TTGATAAGAT CTTAAAGAGC 2700
CCAATGAGTT TCTTTGACAC GACTCCCACT GGCAGGCTAA TGAACCGTTT TTCCAAGGAT 2760
ATGGACGAGC TGGATGTGAG GCTGCCGTTT CACGCAGAGA ACTTTCTGCA GCAGTTTTTT 2820
ATGGTGGTGT TTATTCTCGT GATCTTGGCT GCTGTGTTTC CTGCTGTCCT TTTAGTCGTG 2880
GCCAGCCTTG CTGTAGGCTT CTTCATTCTG TTACGCATTT TCCACAGAGG AGTCCAGGAG 2940
CTCAAGAAGG TGGAGAATGT CAGCCGGTCA CCCTGGTTCA CCCACATCAC CTCCTCCATG 3000
CAGGGCCTGG GCATCATTCA CGCCTATGGC AAGAAGGAGA GCTGCATCAC CTATACTTCA 3060
TCCAAAGGCC TGTCATTGTC ATACATCATC CAGCTGAGCG GACTGCTCCA AGTGTGTGTG 3120
CGAACGGGAA CAGAGACGCA AGCCAAATTC ACCTCCGTGG AGCTGCTCAG GGAATACATT 3180
TCGACCTGTG TTCCTGAATG CACTCATCCC CTCAAAGTGG GGACCTGTCC CAAGGACTGG 3240
CCCAGCTGTG GGGAGATCAC CTTCAGAGAC TATCAGATGA GATACAGAGA CAACACCCCC 3300
CTTGTTCTCG ACAGCCTGAA CTTGAACATA CAAAGTGGGC AGACAGTCGG GATTGTTGGA 3360
AGAACAGGTT CCGGAAAGTC ATCGTTAGGA ATGGCTTTGT TTCGTCTGGT GGAGCCAGCC 3420
AGTGGCACAA TCTTTATTGA TGAGGTGGAT ATCTGCATTC TCAGCTTGGA AGACCTCAGA 3480
ACCAAGCTGA CTGTGATCCC ACAGGATCCT GTCCTGTTTG TAGGTACAGT AAGGTACAAC 3540
TTGGATCCCT TTGAGAGTCA CACCGATGAG ATGCTCTGGC AGGTTCTGGA GAGAACATTC 3600
ATGAGAGACA CAATAATGAA ACTCCCAGAA AAATTACAGG CAGAAGTCAC AGAAAATGGA 3660
GAAAACTTCT CAGTAGGGGA ACGTCAGCTG CTTTGTGTGG CCCGAGCTCT TCTCCGTAAT 3720
TCAAAGATCA TTCTCCTTGA TGAAGCCACC GCCTCTATGG ACTCCAAGAC TGACACCCTG 3780
GTTCAGAACA CCATCAAAGA TGCCTTCAAG GGCTGCACTG TGCTGACCAT CGCCCACCGC 3840
CTCAACACAG TTCTCAACTG CGATCACGTC CTGGTTATGG AAAATGGGAA GGTGATTGAG 3900
TTTGACAAGC CTGAAGTCCT TGCAGAGAAG CCAGATTCTG CATTTGCGAT GTTACTAGCA 3960
GCAGAAGTCA GATTGTAG

Seq ID NO: 513 Protein sequence
Protein Accession #: Eos sequence

1 11 21 31 41 51
| | | | | |
MVGEGPYLIS DLDQRGRRRS FAERYDPSLK TMIPVRPCAR LAPNPVDDAG LLSFATFSWL 60
TPVMVKGYRQ RLTVDTLPPL STYDSSDTNA KRFRVLWDEE VARVGPEKAS LSHVVWKFQR 120
TRVLMDIVAN ILCIIMAAIG PTVLIHQILQ QTERTSGKVW VGIGLCIALF ATEFTKVFFW 180
ALAWAINYRT AIRLKVALST LVFENLVSFK TLTHISVGEV LNILSSDSYS LFEAALFCPL 240
PATIPILMVF CAAYAFFILG PTALIGISVY VIFIPVQMFM AKLNSAFRRS AILVTDKRVQ 300
TMNEFLTCIR LIKMYAWEKS FTNTIQDIRR RERKLLEKAG FVQSGNSALA PIVSTIAIVL 360
TLSCHILLRR KLTAPVAFSV IAMFNVMKFS IAILPFSIKA MAEANVSLRR MKKILIDKSP 420
PSYITQPEDP DTVLLLANAT LTWEHEASRK STPKKLQNQK RHLCKKQRSE AYSERSPPAK 480
GATGPEEQSD SLKSVLHSIS FVVRKLCRYP EAQLLAWRWP AVFVGRIIRG YRPHGFSAKD 540
KDESRRLLTW PQEVDRTQRA AKYLGKILGI CGNVGSGKSS LLAALLGQMQ LQKGVVAVNG 600
TLAYVSQQAW IFHGNVRENI LFGEKYDHQR YQHTVRVCGL QKDLSNLPYG DLTEIGERGL 660
NLSGGQRQRI SLARAVYSDR QLYLLDDPLS AVDAHVGKHV FEECIKKTLR GKTVVLVTHQ 720
LQFLESCDEV ILLEDGEICE KGTHKELMEE RGRYAKLIHN LRGLQFKDPE HLYNAAMVEA 780
FKESPAEREE DAGIIGYLLS LFTVFLFLLM IGSAAFSNWW LGLWLDKGSR MTCGPQGNRT 840
MCEVGAVLAD IGQHVYQWVY TASMVFMLVF GVTKGFVFTK TTLMASSSLH DTVFDKILKS 900
PMSFFDTTPT GRLMNRFSKD MDELDVRLPF HAENFLQQFF MVVFILVILA AVFPAVLLVV 960
ASLAVGFFIL LRIFHRGVQE LKKVENVSRS PWFTHITSSM QGLGIIHAYG KKESCITYTS 1020
SKGLSLSYII QLSGLLQVCV RTGTETQAKF TSVELLREYI STCVPECTHP LKVGTCPKDW 1080
PSCGEITFRD YQMRYRDNTP LVLDSLNLNI QSGQTVGIVG RTGSGKSSLG MALFRLVEPA 1140
SGTIFIDEVD ICILSLEDLR TKLTVIPQDP VLFVGTVRYN LDPFESHTDE MLWQVLERTF 1200
MRDTIMKLPE KLQAEVTENG ENFSVGERQL LCVARALLRN SKIILLDEAT ASMDSKTDTL 1260
VQNTIKDAFK GCTVLTIAHR LNTVLNCDHV LVMENGKVIE FDKPEVLAEK PDSAFAMLLA 1320
AEVRL

Seq ID NO: 514 DNA sequence
Nucleic Acid Accession #: Z31560
Coding sequence: 1-966

1 11 21 31 41 51
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CACAGCGCCC GCATGTACAA CATGATGGAG ACGGAGCTGA AGCCGCCGGG CCCGCAGCAA 60
ACTTCGGGGG GCGGCGGCGG CAACTCCACC GCGGCGGCGG CCGGCGGCAA CCAGAAAAAC 120
AGCCCGGACC GCGTCAAGCG GCCCATGAAT GCCTTCATGG TGTGGTCCCG CGGGCAGCGG 180
CGCAAGATGG CCCAGGAGAA CCCCAAGATG CACAACTCGG AGATCAGCAA GCGCCTGGGC 240
GCCGAGTGGA AACTTTTGTC GGAGACGGAG AAGCGGCCGT TCATCGACGA GGCTAAGCGG 300
CTGCGAGCGC TGCACATGAA GGAGCACCCG GATTATAAAT ACCGGCCCCG GCGGAAAACC 360
AAGACGCTCA TGAAGAAGGA TAAGTACACG CTGCCCGGCG GGCTGCTGGC CCCCGGCGGC 420
AATAGCATGG CGAGCGGGGT CGGGGTGGGC GCCGGCCTGG GCGCGGGCGT GAACCAGCGC 480
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CAGCTGGGCT ACCCGCAGCA CCCGGGCCTC AATGCGCACG GCGCAGCGCA GATGCAGCCC 600
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ATGAACGGCT CGCCCACCTA CAGCATGTCC TACTCGCAGC AGGGCACCCC TGGCATGGCT 720
CTTGGCTCCA TGGGTTCGGT GGTCAAGTCC GAGGCCAGCT CCAGCCCCCC TGTGGTTACC 780
TCTTCCTCCC ACTCCAGGGC GCCCTGCCAG GCCGGGGACC TCCGGGACAT GATCAGCATG 840
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CACTACCAGA GCGGCCCGGT GCCCGGCACG GCCATTAACG GCACACTGCC CCTCTCACAC 960
ATGTGAGGGC CGGACAGCGA ACTGGAGGGG GGAGAAATTT TCAAAGAAAA ACGAGGGAAA 1020
TGGGAGGGGT GCAAAAGAGG AGAGTAAGAA ACAGCATGGA GAAAACCCGG TACGCTCAAA 1080
AAAAA

Seq ID NO: 515 Protein sequence
Protein Accession #: CAA83435

1 11 21 31 41 51
| | | | | |
HSARMYNMME TELKPPGPQQ TSGGGGGNST AAAAGGNQKN SPDRVKRPMN AFMVWSRGQR 60
RKMAQENPKM HNSEISKRLG AEWKLLSETE KRPFIDEAKR LRALHMKEHP DYKYRPRRKT 120
KTLMKKDKYT LPGGLLAPGG NSMASGVGVG AGLGAGVNQR MDSYAHMNGW SNGSYSMMQD 180

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QLGYPQHPGL NAHGAAQMQP MHRYDVSALQ YNSMTSSQTY MNGSPTYSMS YSQQGTPGMA   240
LGSMGSVVKS EASSSPPVVT SSSHSRAPCQ AGDLRDMISM YLPGAEVPEP AAPSRLHMSQ   300
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Seq ID NO: 516 DNA sequence
Nucleic Acid Accession #: U91618
Coding sequence: 29..541

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CATGCTACTC CTGGCTTTCA GCTCCTGGAG TCTGTGCTCA GATTCAGAAG AGGAAATGAA   120
AGCATTAGAA GCAGATTTCT TGACCAATAT GCATACATCA AAGATTAGTA AAGCACATGT   180
TCCCTCTTGG AAGATGACTC TGCTAAATGT TTGCAGTCTT GTAAATAATT TGAACAGCCC   240
AGCTGAGGAA ACAGGAGAAG TTCATGAAGA GGAGCTTGTT GCAAGAAGGA AACTTCCTAC   300
TGCTTTAGAT GGCTTTAGCT TGGAAGCAAT GTTGACAATA TACCAGCTCC ACAAAATCTG   360
TCACAGCAGG GCTTTTCAAC ACTGGGAGTT AATCCAGGAA GATATTCTTG ATACTGGAAA   420
TGACAAAAAT GGAAAGGAAG AAGTCATAAA GAGAAAAATT CCTTATATTC TGAAACGGCA   480
GCTGTATGAG AATAAACCCA GAAGACCCTA CATACTCAAA AGAGATTCTT ACTATTACTG   540
AGAGAATAAA TCATTTATTT ACATGTGATT GTGATTCATC ATCCCTTAAT TAAATATCAA   600
ATTATATTTG TGTGAAAATG TGACAAACAC ACTTATCTGT CTCTTCTACA ATTGTGGTTT   660
ATTGAATGTG TTTTTCTGCA CTAATAGAAA TTAGACTAAG TGTTTTCAAA TAAATCTAAA   720
TCTTCAAAAA AAAAAAAAAA AAATGGGGCC GCAATT
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Seq ID NO: 517 Protein sequence
Protein Accession #: AAB50564

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1          11         21         31         41         51
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MMAGMKIQLV CMLLLAFSSW SLCSDSEEEM KALEADFLTN MHTSKISKAH VPSWKMTLLN    60
VCSLVNNLNS PAEETGEVHE EELVARRKLP TALDGFSLEA MLTIYQLHKI CHSRAFQHWE   120
LIQEDILDTG NDKNGKEEVI KRKIPYILKR QLYENKPRRP YILKRDSYYY
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Seq ID NO: 518 DNA sequence
Nucleic Acid Accession #: NM_006536.2
Coding sequence: 109..2940

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ACCTAAAACC TTGCAAGTTC AGGAAGAAAC CATCTGCATC CATATTGAAA ACCTGACACA    60
ATGTATGCAG CAGGCTCAGT GTGAGTGAAC TGGAGGCTTC TCTACAACAT GACCCAAAGG   120
AGCATTGCAG GTCCTATTTG CAACCTGAAG TTTGTGACTC TCCTGGTTGC CTTAAGTTCA   180
GAACTCCCAT TCCTGGGAGC TGGAGTACAG CTTCAAGACA ATGGGTATAA TGGATTGCTC   240
ATTGCAATTA ATCCTCAGGT ACCTGAGAAT CAGAACCTCA TCTCAAACAT TAAGGAAATG   300
ATAACTGAAG CTTCATTTTA CCTATTTAAT GCTACCAAGA GAAGAGTATT TTTCAGAAAT   360
ATAAAGATTT TAATACCTGC CACATGGAAA GCTAATAATA ACAGCAAAAT AAAACAAGAA   420
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Seq ID NO: 519 Protein sequence
Protein Accession #: NP_006527.1

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Seq ID NO: 520 DNA sequence
Nucleic Acid Accession #: NM_000228.1
Coding sequence: 82..3600

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Seq ID NO: 521 Protein sequence
Protein Accession #: NP_000219.1

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NARLNGGKVQ LNLMDLVSGI PATQSQKIQE VGEITNLRVN FTRLAPVPQR GYHPPSAYYA   240
VSQLRLQGSC FCHGHADRCA PKPGASAGPS TAVQVHDVCV CQHNTAGPNC ERCAPFYNNR   300
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HYFRNRRPGA SIQETCISCE CDPDGAVPGA PCDPVTGQCV CKEHVQGERC DLCKPGFTGL   420
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CACDPHNSPQ PTVQPVHRAV PCREGFGGLM CSAAAIRQCP DRTYGDVATG CRACDCDFRG   540
TEGPGCDKAS GRCLCRPGLT GPRCDQCQRG YCNRYPVCVA CHPCFQTYDA DLREQALRFG   600
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Seq ID NO: 522 DNA sequence
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Seq ID NO: 523 Protein sequence
Protein Accession #: NP_001935.1

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LDDSFLDSLG PKFKKLAEIS LGVDGEGKEV QPPSKDSGYG IESCGHPIEV QQTGFVKCQT   900
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Seq ID NO: 525 Protein sequence
Protein Accession #: P39900

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Seq ID NO: 526 DNA sequence
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Coding sequence: 64..2590

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CTCTATTGCT GTTTCTATTC TCTCTTATAG TGACCAACAT CTTTTTAATT TAGATCCAAA 3840
TAACCATGTC CTCCTAGAGT TTAGAGGCTA GAGGGAGCTG AGGGGAGGAT CTTACTGAAA 3900
GCACCCTGGG GAGATTGATT GTCCTTAAAC CTAAGCCCCA CAAACTTGAC ACCTGATCAG 3960
GTCTGGGAGC TACAAAATTT CATTTTTCTC CTCACTGCCC TTCTTCTGAG TGGCATTGGC 4020
CTGAATCAAG GAAAGCCAGG CCTTGTGGGC CCCCTTCTTT CGGCTTTCTG CTAAAGCAAC 4080
ACCTCCAGCA GAGATTCCCT TAAGTGACTC CAGGTTTTCC ACCATCCTTC AGCGTGAATT 4140
AATTTTTAAT CAGTTTGCTT TCTCCAGAGA AATTTTAAAA TAATAGAAGA AATAGAAATT 4200
TTGAATGTAT AAAAGAAAAA GATCAAGTTG TCATTTTAGA ACAGAGGGAA CTTTGGGAGA 4260
AAGCAGCCCA AGTAGGTTAT TTGTACAGTC AGAGGGCAAC AGGAAGATGC AGGCCTTCAA 4320
GGGCAAGGAG AGGCCACAAG GAATATGGGT GGGAGTAAAA GCAACATCGT CTGCTTCATA 4380
CTTTTTCCTA GGCTTGGCAC TGCCTTTTCC TTTCTCAGGC CAATGGCAAC TGCCATTTGA 4440
GTCCGGTGAG GGATCAGCCA ACCTCTTCTC TATGGCTCAC CTTATTTGGA GTGAGAAATC 4500
AAGGAGACAG AGCTGACTGC ATGATGAGTC TGAAGGCATT TGCAGGATGA GCCTGAACTG 4560
GTTGTGCAGA ACAAACAAGG CATTCATGGG AATTGTTGTA TTCCTTCTGC AGCCCTCCTT 4620
CTGGGCACTA AGAAGGTCTA TGAATTAAAT GCCTATCTAA AATTCTGATT TATTCCTACA 4680
TTTTCTGTTT TCTAATTTGA CCCTAAAATC TATGTGTTTT AGACTTAGAC TTTTTATTGC 4740
CCCCCCCCCC TTTTTTTTTG AGACGGAGTC TCGCTCTGAC GCACAGGCTG GAGTGCAGTG 4800
GCTCCGATCT CTGCTCACTG AAAGCTCCGC CTCCCGGGTT CATGCCATTC TCCTGCCTCA 4860
GCCTCCTGAG TAGCTGGGAC TACAGGCGCC CACCACCACG CCCGGCTAAT TTTTTGTATT 4920
TTTAATAGAG ACGGGGTTTC ACTGTGTTAG CCAGGATGGT CTCGATCTCC TGACCTCGTG 4980
ATCCGCCTGC CTCGGCCTCC CAAAGTGCTG GGATTACAGG CATGACCCAC CGCTCCCGGC 5040
CTTGTTTTCC GTTTAAAGTC GTCTTCTTTT AATGTAATCA TTTTGAACAT GTGTGAAAGT 5100
TGATCATACG AATTGGATCA ATCTTGAAAT ACTCAACCAA AAGACAGTCG AGAAGCCAGG 5160
GGGAGAAAGA ACTCAGGGCA CAAAATATTG GTCTGAGAAT GGAATTCTCT GTAAGCCTAG 5220
TTGCTGAAAT TTCCTGCTGT AACCAGAAGC CAGTTTTATC TAACGGCTAC TGAAACACCC 5280
ACTGTGTTTT GCTCACTCCC TCACTCACCG ATCAAAACCT GCTACCTCCC CAAGACTTTA 5340
CTAGTGCCGA TAAACTTTCT CAAAGAGCAA CCAGTATCAC TTCCCTGTTT ATAAAACCTC 5400
TAACCATCTC TTTGTTCTTT GAACATGCTG AAAACCACCT GGTCTGCATG TATGCCCGAA 5460
TTTGTAATTC TTTTCTCTCA AATGAAAATT TAATTTTAGG GATTCATTTC TATATTTTCA 5520
CATATGTAGT ATTATTATTT CCTTATATGT GTAAGGTGAA ATTTATGGTA TTTGAGTGTG 5580
CAAGAAAATA TATTTTTAAA GCTTTCATTT TTCCCCCAGT GAATGATTTA GAATTTTTTA 5640
TGTAAATATA CAGAATGTTT TTTCTTACTT TTATAAGGAA GCAGCTGTCT AAAATGCAGT 5700
GGGGTTTGTT TTGCAATGTT TTAAACAGAG TTTTAGTATT GCTATTAAAA GAAGTTACTT 5760
TGCTTTTAAA GAAACTTGGC TGCTTAAAAT AAGCAAAAAT TGGATGCATA AAGTAATATT 5820
TACAGATGTG GGGAGATGTA ATAAAACAAT ATTAACTTGG TTTCTTGTTT TTGCTGTATT 5880
TAGAGATTAA ATAATTCTAA GATGATCACT TTGCAAAATT ATGCTTATGG CTGGCATGGA 5940
AATAGAAATA CTCAATTATG TCTTTGTTGT ATTAATGGGG AATATTTTGG ACAATGTTTC 6000
ATTATCAAAT TGTCGACATC ATTAATATAT ATTGTAATGT TGGGAAGAGA TCACTATTTT 6060
GAAGCACAGC TTTACAGATG AGTATCTATG ATACATATGT ATAATAAATT TTGATCGGGT 6120
ATTAAAAGTA TTAGAAGGTG GTTATAATTG CAGAGTATTC CATGAATAGT ACACTGACAC 6180

AGGGGTTTTA CTTTGAGGAC CAGTGTAGTC AAGGGAAAAC ATGAGTTAAA AAGAAAAGCA 6240
GGCAATATTG CAGTCTTGAT TCTGCCACTT ACAGGATAGA TAATGCCTGA ACTTTAATGA 6300
CAAGATGATC CAACCATAAA GGTGCTCTGT GCTTCACAGT GAATCTTTTC CCCATGCAGG 6360
AGTGTGCTCC CCTACAAACG TTAAGACTGA TCATTTCAAA AATCTATTAG CTATATCAAA 6420
AGCCTTACAT TTTAATATAG GTTGAACCAA AATTTCAATT CCAGTAACTT CTATTGTAAC 6480
CATTATTTTT GTGTATGTCT TCAAGAATGT TCATTGGATT TTTGTTTGTA ATAGTAAAAT 6540
ACCGGATACA TTTCACGTGT CCTTCAGTAT TGATTTGGTT GAATATTGGG TCATAATGGT 6600
TGAGAAGCAT GGACACTAGA GCCAGAATGC TTGGATATGA ATCCTGGATC TGTCACTTAC 6660
TTCTGTGTGA CCTTTGAAAG GCTACTTATT TCCTCTCTTA GCTTTCTCAT TAAAATCAAT 6720
GAACAATGCC AGCCTCATGG GGTTGTTGAA TGATTAAATT AGTTAATATA CCTAAAGTAC 6780
ATAGAACACT GCCTGCACAT AGTAAAAGAA TTATAAGTGT GAGGTAGTTG GTAAAATTAT 6840
GTAGTTGGAT ATACTACCGA ACAATATCTA ATCTCTTTTT AGGAAATAA AGTTTGTGCA 6900
TATATATAAT CCCGAAACAT G

Seq ID NO: 529 Protein sequence
Protein Accession #: NP_001932.1

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1          11         21         31         41         51
|          |          |          |          |          |
MAAAGPRRSV RGAVCLHLLL TLVIFSRDGE ACKKVILNVP SKLEADKIIG RVNLEECFRS   60
ADLIRSSDPD FRVLNDGSVY TARAVALSDK KRSFTIWLSD KRKQTQKEVT VLLEHQKKVS  120
KTRHTRETVL RRAKRRWAPI PCSMQENSLG PFPLFLQQVE SDAAQNYTVF YSISGRGVDK  180
EPLNLFYIER DTGNLFCTRP VDREEYDVFD LIAYASTADG YSADLPLPLP IRVEDENDNH  240
PVFTEAIYNF EVLESSRPGT TVGVVCATDR DEPDTMHTRL KYSILQQTPR SPGLFSVHPS  300
TGVITTVSHY LDREVVDKYS LIMKVQDMDG QFFGLIGTST CIITVTDSND NAPTFRQNAY  360
EAFVEENAFN VEILRIPIED KDLINTANWR VNFTILKGNE NGHFKISTDK ETNEGVLSVV  420
KPLNYEENRQ VNLEIGVNNE APFARDIPRV TALNRALVTV HVRDLDEGPE CTPAAQYVRI  480
KENLAVGSKI NGYKAYDPEN RNGNGLRYKK LHDPKGWITI DEISGSIITS KILDREVETP  540
KNELYNITVL AIDKDDRSCT GTLAVNIEDV NDNPPEILQE YVVICKPKMG YTDILAVDPD  600
EPVHGAPFYF SLPNTSPEIS RLWSLTKVND TAARLSYQKN AGFQEYTIPI TVKDRAGQAA  660
TKLLRVNLCE CTHPTQCRAT SRSTGVILGK WAILAILLGI ALLFSVLLTL VCGVFGATKG  720
KRFPEDLAQQ NLIISNTEAP GDDRVCSANG FMTQTTNNSS QGFCGTMGSG MKNGGQETIE  780
MMKGGNQTLE SCRGAGHHHT LDSCRGGHTE VDNCRYTYSE WHSFTQPRLG EKLHRCNQNE  840
DRMPSQDYVL TYNYEGRGSP AGSVGCCSEK QEEDGLDFLN NLEPKFITLA EACTKR
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Seq ID NO: 530 DNA sequence
Nucleic Acid Accession #: NM_016583.2
Coding sequence: 72..842

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1          11         21         31         41         51
|          |          |          |          |          |
GGAGTGGGGG AGAGAGAGGA GACCAGGACA GCTGCTGAGA CCTCTAAGAA GTCCAGATAC    60
TAAGAGCAAA GATGTTTCAA ACTGGGGGCC TCATTGTCTT CTACGGGCTG TTAGCCCAGA   120
CCATGGCCCA GTTTGGAGGC CTGCCCGTGC CCCTGGACCA GACCCTGCCC TTGAATGTGA   180
ATCCAGCCCT GCCCTTGAGT CCCACAGGTC TTGCAGGAAG CTTGACAAAT GCCCTCAGCA   240
ATGGCCTGCT GTCTGGGGGC CTGTTGGGCA TTCTGGAAAA CCTTCCGCTC CTGGACATCC   300
TGAAGCCTGG AGGAGGTACT TCTGGTGGCC TCCTTGGGGG ACTGCTTGGA AAAGTGACGT   360
CAGTGATTCC TGGCCTGAAC AACATCATTG ACATAAAGGT CACTGACCCC CAGCTGCTGG   420
AACTTGGCCT TGTGCAGAGC CCTGATGGCC ACCGTCTCTA TGTCACCATC CCTCTCGGCA   480
TAAAGCTCCA AGTGAATACG CCCCTGGTCG GTGCAAGTCT GTTGAGGCTG GCTGTGAAGC   540
TGGACATCAC TGCAGAAATC TTAGCTGTGA GAGATAAGCA GGAGAGGATC CACCTGGTCC   600
TTGGTGACTG CACCCATTCC CCTGGAAGCC TGCAAATTTC TCTGCTTGAT GGACTTGGCC   660
CCCTCCCCAT TCAAGGTCTT CTGGACAGCC TCACAGGGAT CTTGAATAAA GTCCTGCCTG   720
AGTTGGTTCA GGGCAACGTG TGCCCTCTGG TCAATGAGGT TCTCAGAGGC TTGGACATCA   780
CCCTGGTGCA TGACATTGTT AACATGCTGA TCCACGGACT ACAGTTTGTC ATCAAGGTCT   840
AAGCCTTCCA GGAAGGGGCT GGCCTCTGCT GAGCTGCTTC CCAGTGCTCA CAGATGGCTG   900
GCCCATGTGC TGGAAGATGA CACAGTTGCC TTCTCTCCGA GGAACCTGCC CCCTCTCCTT   960
TCCCACCAGG CGTGTGTAAC ATCCCATGTG CCTCACCTAA TAAAATGGCT CTTCTTCTGC  1020
AAAAAAAAAA AAAAAAAAAA AAAAAAAAA
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Seq ID NO: 531 Protein sequence
Protein Accession #: NP_057667.1

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1          11         21         31         41         51
|          |          |          |          |          |
MFQTGGLIVF YGLLAQTMAQ FGGLPVPLDQ TLPLNVNPAL PLSPTGLAGS LTNALSNGLL   60
SGGLLGILEN LPLLDILKPG GGTSGGLLGG LLGKVTSVIP GLNNIIDIKV TDPQLLELGL  120
VQSPDGHRLY VTIPLGIKLQ VNTPLVGASL LRLAVKLDIT AEILAVRDKQ ERIHLVLGDC  180
THSPGSLQIS LLDGLGPLPI QGLLDSLTGI LNKVLPELVQ GNVCPLVNEV LRGLDITLVH  240
DIVNMLIHGL QFVIKV
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Seq ID NO: 532 DNA sequence
Nucleic Acid Accession #: NM_004363.1
Coding sequence: 115..2223

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1          11         21         31         41         51
|          |          |          |          |          |
CTCAGGGCAG AGGGAGGAAG GACAGCAGAC CAGACAGTCA CAGCAGCCTT GACAAAACGT   60
TCCTGGAACT CAAGCTCTTC TCCACAGAGG AGGACAGAGC AGACAGCAGA GACCATGGAG  120
TCTCCCTCGG CCCCTCCCCA CAGATGGTGC ATCCCCTGGC AGAGGCTCCT GCTCACAGCC  180
TCACTTCTAA CCTTCTGGAA CCCGCCCACC ACTGCCAAGC TCACTATTGA ATCCACGCCG  240
TTCAATGTCG CAGAGGGGAA GGAGGTGCTT CTACTTGTCC ACAATCTGCC CCAGCATCTT  300
TTTGGCTACA GCTGGTACAA AGGTGAAAGA GTGGATGGCA ACCGTCAAAT TATAGGATAT  360
GTAATAGGAA CTCAACAAGC TACCCCAGGG CCCGCATACA GTGGTCGAGA GATAATATAC  420
CCCAATGCAT CCCTGCTGAT CCAGAACATC ATCCAGAATG ACACAGGATT CTACACCCTA  480
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CACGTCATAA AGTCAGATCT TGTGAATGAA GAAGCAACTG GCCAGTTCCG GGTATACCCG    540
GAGCTGCCCA AGCCCTCCAT CTCCAGCAAC AACTCCAAAC CCGTGGAGGA CAAGGATGCT    600
GTGGCCTTCA CCTGTGAACC TGAGACTCAG GACGCAACCT ACCTGTGGTG GGTAAACAAT    660
CAGAGCCTCC CGGTCAGTCC CAGGCTGCAG CTGTCCAATG GCAACAGGAC CCTCACTCTA    720
TTCAATGTCA CAAGAAATGA CACAGCAAGC TACAAATGTG AAACCCAGAA CCCAGTGAGT    780
GCCAGGCGCA GTGATTCAGT CATCCTGAAT GTCCTCTATG GCCCGGATGC CCCCACCATT    840
TCCCCTCTAA ACACATCTTA CAGATCAGGG GAAAATCTGA ACCTCTCCTG CCACGCAGCC    900
TCTAACCCAC CTGCACAGTA CTCTTGGTTT GTCAATGGGA CTTTCCAGCA ATCCACCCAA    960
GAGCTCTTTA TCCCCAACAT CACTGTGAAT AATAGTGGAT CCTATACGTG CCAAGCCCAT   1020
AACTCAGACA CTGGCCTCAA TAGGACCACA GTCACGACGA TCACAGTCTA TGCAGAGCCA   1080
CCCAAACCCT TCATCACCAG CAACAACTCC AACCCCGTGG AGGATGAGGA TGCTGTAGCC   1140
TTAACCTGTG AACCTGAGAT TCAGAACACA ACCTACCTGT GGTGGGTAAA TAATCAGAGC   1200
CTCCCGGTCA GTCCCAGGCT GCAGCTGTCC AATGACAACA GGACCCTCAC TCTACTCAGT   1260
GTCACAAGGA ATGATGTAGG ACCCTATGAG TGTGGAATCC AGAACGAATT AAGTGTTGAC   1320
CACAGCGACC CAGTCATCCT GAATGTCCTC TATGGCCCAG ACGACCCCAC CATTTCCCCC   1380
TCATACACCT ATTACCGTCC AGGGGTGAAC CTCAGCCTCT CCTGCCATGC AGCCTCTAAC   1440
CCACCTGCAC AGTATTCTTG GCTGATTGAT GGGAACATCC AGCAACACAC ACAAGAGCTC   1500
TTTATCTCCA ACATCACTGA GAAGAACAGC GGACTCTATA CCTGCCAGGC CAATAACTCA   1560
GCCAGTGGCC ACAGCAGGAC TACAGTCAAG ACAATCACAG TCTCTGCGGA GCTGCCCAAG   1620
CCCTCCATCT CCAGCAACAA CTCCAAACCC GTGGAGGACA AGGATGCTGT GGCCTTCACC   1680
TGTGAACCTG AGGCTCAGAA CACAACCTAC CTGTGGTGGG TAAATGGTCA GAGCCTCCCA   1740
GTCAGTCCCA GGCTGCAGCT GTCCAATGGC AACAGGACCC TCACTCTATT CAATGTCACA   1800
AGAAATGACG CAAGAGCCTA TGTATGTGGA ATCCAGAACT CAGTGAGTGC AAACCGCAGT   1860
GACCCAGTCA CCCTGGATGT CCTCTATGGG CCGGACACCC CCATCATTTC CCCCCCAGAC   1920
TCGTCTTACC TTTCGGGAGC GAACCTCAAC CTCTCCTGCC ACTCGGCCTC TAACCCATCC   1980
CCGCAGTATT CTTGGCGTAT CAATGGGATA CCGCAGCAAC ACACACAAGT TCTCTTTATC   2040
GCCAAAATCA CGCCAAATAA TAACGGGACC TATGCCTGTT TTGTCTCTAA CTTGGCTACT   2100
GGCCGCAATA ATTCCATAGT CAAGAGCATC ACAGTCTCTG CATCTGGAAC TTCTCCTGGT   2160
CTCTCAGCTG GGGCCACTGT CGGCATCATG ATTGGAGTGC TGGTTGGGGT TGCTCTGATA   2220
TAGCAGCCCT GGTGTAGTTT CTTCATTTCA GGAAGACTGA CAGTTGTTTT GCTTCTTCCT   2280
TAAAGCATTT GCAACAGCTA CAGTCTAAAA TTGCTTCTTT ACCAAGGATA TTTACAGAAA   2340
AGACTCTGAC CAGAGATCGA GACCATCCTA GCCAACATCG TGAAACCCCA TCTCTACTAA   2400
AAATACAAAA ATGAGCTGGG CTTGGTGGCG CGCACCTGTA GTCCCAGTTA CTCGGGAGGC   2460
TGAGGCAGGA GAATCGCTTG AACCCGGGAG GTGGAGATTG CAGTGAGCCC AGATCGCACC   2520
ACTGCACTCC AGTCTGGCAA CAGAGCAAGA CTCCATCTCA AAAAGAAAAG AAAAGAAGAC   2580
TCTGACCTGT ACTCTTGAAT ACAAGTTTCT GATACCACTG CACTGTCTGA GAATTTCCAA   2640
AACTTTAATG AACTAACTGA CAGCTTCATG AAACTGTCCA CCAAGATCAA GCAGAGAAAA   2700
TAATTAATTT CATGGGACTA AATGAACTAA TGAGGATTGC TGATTCTTTA AATGTCTTGT   2760
TTCCCAGATT TCAGGAAACT TTTTTTCTTT TAAGCTATCC ACTCTTACAG CAATTTGATA   2820
AAATATACTT TTGTGAACAA AAATTGAGAC ATTTACATTT TCTCCCTATG TGGTCGCTCC   2880
AGACTTGGGA AACTATTCAT GAATATTTAT ATTGTATGGT AATATAGTTA TTGCACAAGT   2940
TCAATAAAAA TCTGCTCTTT GTATAACAGA AAAA
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Seq ID NO: 533 Protein sequence
Protein Accession #: NP_004354.1

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1          11         21         31         41         51
|          |          |          |          |          |
MESPSAPPHR WCIPWQRLLL TASLLTFWNP PTTAKLTIES TPFNVAEGKE VLLLVHNLPQ     60
HLFGYSWYKG ERVDGNRQII GYVIGTQQAT PGPAYSGREI IYPNASLLIQ NIIQNDTGFY    120
TLHVIKSDLV NEEATGQFRV YPELPKPSIS SNNSKPVEDK DAVAFTCEPE TQDATYLWWV    180
NNQSLPVSPR LQLSNGNRTL TLFNVTRNDT ASYKCETQNP VSARRSDSVI LNVLYGPDAP    240
TISPLNTSYR SGENLNLSCH AASNPPAQYS WFVNGTFQQS TQELFIPNIT VNNSGSYTCQ    300
AHNSDTGLNR TTVTTITVYA EPPKPFITSN NSNPVEDEDA VALTCEPEIQ NTTYLWWVNN    360
QSLPVSPRLQ LSNDNRTLTL LSVTRNDVGP YECGIQNELS VDHSDPVILN VLYGPDDPTI    420
SPSYTYYRPG VNLSLSCHAA SNPPAQYSWL IDGNIQQHTQ ELFISNITEK NSGLYTCQAN    480
NSASGHSRTT VKTITVSAEL PKPSISSNNS KPVEDKDAVA FTCEPEAQNT TYLWWVNGQS    540
LPVSPRLQLS NGNRTLTLFN VTRNDARAYV CGIQNSVSAN RSDPVTLDVL YGPDTPIISP    600
PDSSYLSGAN LNLSCHSASN PSPQYSWRIN GIPQQHTQVL FIAKITPNNN GTYACFVSNL    660
ATGRNNSIVK SITVSASGTS PGLSAGATVG IMIGVLVGVA LI
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Seq ID NO: 534 DNA sequence
Nucleic Acid Accession #: NM_006952.1
Coding sequence: 11..793

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1          11         21         31         41         51
|          |          |          |          |          |
AATCCCGACA ATGGCGAAAG ACAACTCAAC TGTTCGTTGC TTCCAGGGCC TGCTGATTTT     60
TGGAAATGTG ATTATTGGTT GTTGCGGCAT TGCCCTGACT GCGGAGTGCA TCTTCTTTGT    120
ATCTGACCAA CACAGCCTCT ACCCACTGCT TGAAGCCACC GACAACGATG ACATCTATGG    180
GGCTGCCTGG ATCGGCATAT TTGTGGGCAT CTGCCTCTTC TGCCTGTCTG TTCTAGGCAT    240
TGTAGGCATC ATGAAGTCCA GCAGGAAAAT TCTTCTGGCG TATTTCATTC TGATGTTTAT    300
AGTATATGCC TTTGAAGTGG CATCTTGTAT CACAGCAGCA ACACAACGAG ACTTTTTCAC    360
ACCCAACCTC TTCCTGAAGC AGATGCTAGA GAGGTACCAA AACAACAGCC CTCCAAACAA    420
TGATGACCAG TGGAAAAACA ATGGAGTCAC CAAAACCTGG GACAGGCTCA TGCTCCAGGA    480
CAATTGCTGT GGCGTAAATG GTCCATCAGA CTGGCAAAAA TACACATCTG CCTTCCGGAC    540
TGAGAATAAT GATGCTGACT ATCCCTGGCC TCGTCAATGC TGTGTTATGA ACAATCTTAA    600
AGAACCTCTC AACCTGGAGG CTTGTAAACT AGGCGTGCCT GGTTTTTATC ACAATCAGGG    660
CTGCTATGAA CTGATCTCTG GTCCAATGAA CCGACACGCC TGGGGGGTTG CCTGGTTTGG    720
ATTTGCCATT CTCTGCTGGA CTTTTTGGGT TCTCCTGGGT ACCATGTTCT ACTGGAGCAG    780
AATTGAATAT TAAGAA
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Seq ID NO: 535 Protein sequence
Protein Accession #: NP_008883.1

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1          11         21         31         41         51
|          |          |          |          |          |
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MAKDNSTVRC FQGLLIFGNV IIGCCGIALT AECIFFVSDQ HSLYPLLEAT DNDDIYGAAW    60
IGIFVGICLF CLSVLGIVGI MKSSRKILLA YFILMFIVYA FEVASCITAA TQRDFFTPNL   120
FLKQMLERYQ NNSPPNNDDQ WKNNGVTKTW DRLMLQDNCC GVNGPSDWQK YTSAFRTENN   180
DADYPWPRQC CVMNNLKEPL NLEACKLGVP GFYHNQGCYE LISGPMNRHA WGVAWFGFAI   240
LCWTFWVLLG TMFYWSRIEY
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Seq ID NO: 536 DNA sequence
Nucleic Acid Accession #: NM_002638.1
Coding sequence: 120..473

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1          11         21         31         41         51
|          |          |          |          |          |
CAATACAGCT AAGGAATTAT CCCTTGTAAA TACCACAGAC CCGCCCTGGA GCCAGGCCAA    60
GCTGGACTGC ATAAAGATTG GTATGGCCTT AGCTCTTAGC CAAACACCTT CCTGACACCA   120
TGAGGGCCAG CAGCTTCTTG ATCGTGGTGG TGTTCCTCAT CGCTGGGACG CTGGTTCTAG   180
AGGCAGCTGT CACGGGAGTT CCTGTTAAAG GTCAAGACAC TGTCAAAGGC CGTGTTCCAT   240
TCAATGGACA AGATCCCGTT AAAGGACAAG TTTCAGTTAA AGGTCAAGAT AAAGTCAAAG   300
CGCAAGAGCC AGTCAAAGGT CCAGTCTCCA CTAAGCCTGG CTCCTGCCCC ATTATCTTGA   360
TCCGGTGCGC CATGTTGAAT CCCCCTAACC GCTGCTTGAA AGATACTGAC TGCCCAGGAA   420
TCAAGAAGTG CTGTGAAGGC TCTTGCGGGA TGGCCTGTTT CGTTCCCCAG TGAAGGGAGC   480
CGGTCCTTGC TGCACCTGTG CCGTCCCCAG AGCTACAGGC CCCATCTGGT CCTAAGTCCC   540
TGCTGCCCTT CCCCTTCCCA CACTGTCCAT TCTTCCTCCC ATTCAGGATG CCCACGGCTG   600
GAGCTGCCTC TCTCATCCAC TTTCCAATAA A
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Seq ID NO: 537 Protein sequence
Protein Accession #: NP_002629.1

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1          11         21         31         41         51
|          |          |          |          |          |
MRASSFLIVV VFLIAGTLVL EAAVTGVPVK GQDTVKGRVP FNGQDPVKGQ VSVKGQDKVK    60
AQEPVKGPVS TKPGSCPIIL IRCAMLNPPN RCLKDTDCPG IKKCCEGSCG MACFVPQ
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Seq ID NO: 538 DNA sequence
Nucleic Acid Accession #: NM_001793.2
Coding sequence: 71..2560

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1          11         21         31         41         51
|          |          |          |          |          |
AAAGGGGCAA GAGCTGAGCG GAACACCGGC CCGCCGTCGC GGCAGCTGCT TCACCCCTCT    60
CTCTGCAGCC ATGGGGCTCC CTCGTGGACC TCTCGCGTCT CTCCTCCTTC TCCAGGTTTG   120
CTGGCTGCAG TGCGCGGCCT CCGAGCCGTG CCGGGCGGTC TTCAGGGAGG CTGAAGTGAC   180
CTTGGAGGCG GGAGGCGCGG AGCAGGAGCC CGGCCAGGCG CTGGGGAAAG TATTCATGGG   240
CTGCCCTGGG CAAGAGCCAG CTCTGTTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA   300
TGGCGAGACA GTCCAGGAAA GAAGGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC   360
ATCCAAACGT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCCAA TATCTGTCCC   420
TGAAAATGGC AAGGGTCCCT TCCCCCAGAG ACTGAATCAG CTCAAGTCTA ATAAAGATAG   480
AGACACCAAG ATTTTCTACA GCATCACGGG GCCGGGGGCA GACAGCCCCC CTGAGGGTGT   540
CTTCGCTGTA GAGAAGGAGA CAGGCTGGTT GTTGTTGAAT AAGCCACTGG ACCGGGAGGA   600
GATTGCCAAG TATGAGCTCT TTGGCCACGC TGTGTCAGAG AATGGTGCCT CAGTGGAGGA   660
CCCCATGAAC ATCTCCATCA TCGTGACCGA CCAGAATGAC CACAAGCCCA AGTTTACCCA   720
GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCCTACCA GGTACTTCTG TGATGCAGGT   780
GACAGCCACG GATGAGGATG ATGCCATCTA CACCTACAAT GGGGTGGTTG CTTACTCCAT   840
CCATAGCCAA GAACCAAAGG ACCCACACGA CCTCATGTTC ACCATTCACC GGAGCACAGG   900
CACCATCAGC GTCATCTCCA GTGGCCTGGA CCGGGAAAAA GTCCCTGAGT ACACACTGAC   960
CATCCAGGCC ACAGACATGG ATGGGGACGG CTCCACCACC ACGGCAGTGG CAGTAGTGGA  1020
GATCCTTGAT GCCAATGACA ATGCTCCCAT GTTTGACCCC CAGAAGTACG AGGCCCATGT  1080
GCCTGAGAAT GCAGTGGGCC ATGAGGTGCA GAGGCTGACG GTCACTGATC TGGACGCCCC  1140
CAACTCACCA GCGTGGCGTG CCACCTACCT TATCATGGGC GGTGACGACG GGGACCATTT  1200
TACCATCACC ACCCACCCTG AGAGCAACCA GGGCATCCTG ACAACCAGGA AGGGTTTGGA  1260
TTTTGAGGCC AAAAACCAGC ACACCCTGTA CGTTGAAGTG ACCAACGAGG CCCCTTTTGT  1320
GCTGAAGCTC CCAACCTCCA CAGCCACCAT AGTGGTCCAC GTGGAGGATG TGAATGAGGC  1380
ACCTGTGTTT GTCCCACCCT CCAAAGTCGT TGAGGTCCAG GAGGGCATCC CCACTGGGGA  1440
GCCTGTGTGT GTCTACACTG CAGAAGACCC TGACAAGGAG AATCAAAAGA TCAGCTACCG  1500
CATCCTGAGA GACCCAGCAG GGTGGCTAGC CATGGACCCA GACAGTGGGC AGGTCACAGC  1560
TGTGGGCACC CTCGACCGTG AGGATGAGCA GTTTGTGAGG AACAACATCT ATGAAGTCAT  1620
GGTCTTGGCC ATGGACAATG GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGCTAAC  1680
ACTGATTGAT GTCAATGACC ATGGCCCAGT CCCTGAGCCC CGTCAGATCA CCATCTGCAA  1740
CCAAAGCCCT GTGCGCCAGG TGCTGAACAT CACGGACAAG GACCTGTCTC CCCACACCTC  1800
CCCTTTCCAG GCCCAGCTCA CAGATGACTC AGACATCTAC TGGACGGCAG AGGTCAACGA  1860
GGAAGGTGAC ACAGTGGTCT TGTCCCTGAA GAAGTTCCTG AAGCAGGATA CATATGACGT  1920
GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT  1980
GTGCGACTGC CATGGCCATG TCGAAACCTG CCCTGGACCC TGGAAGGGAG GTTTCATCCT  2040
CCCTGTGCTG GGGGCTGTCC TGGCTCTGCT GTTCCTCCTG CTGGTGCTGC TTTTGTTGGT  2100
GAGAAAGAAG CGGAAGATCA AGGAGCCCCT CCTACTCCCA GAAGATGACA CCCGTGACAA  2160
CGTCTTCTAC TATGGCGAAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCACCCA  2220
GCTCCACCGA GGTCTGGAGG CCAGGCCGGA GGTGGTTCTC CGCAATGACG TGGCACCAAC  2280
CATCATCCCG ACACCCATGT ACCGTCCTCG GCCAGCCAAC CCAGATGAAA TCGGCAACTT  2340
TATAATTGAG AACCTGAAGG CGGCTAACAC AGACCCCACA GCCCCGCCCT ACGACACCCT  2400
CTTGGTGTTC GACTATGAGG GCAGCGGCTC CGACGCCGCG TCCCTGAGCT CCCTCACCTC  2460
CTCCGCCTCC GACCAAGACC AAGATTACGA TTATCTGAAC GAGTGGGGCA GCCGCTTCAA  2520
GAAGCTGGCA GACATGTACG GTGGCGGGGA GGACGACTAG GCGGCCTGCC TGCAGGGCTG  2580
GGGACCAAAC GTCAGGCCAC AGAGCATCTC CAAGGGGTCT CAGTTCCCCC TTCAGCTGAG  2640
GACTTCGGAG CTTGTCAGGA AGTGGCCGTA GCAACTTGGC GGAGACAGGC TATGAGTCTG  2700
ACGTTAGAGT GGTTGCTTCC TTAGCCTTTC AGGATGGAGG AATGTGGGCA GTTTGACTTC  2760
AGCACTGAAA ACCTCTCCAC CTGGGCCAGG GTTGCCTCAG AGGCCAAGTT TCCAGAAGCC  2820
TCTTACCTGC CGTAAAATGC TCAACCCTGT GTCCTGGGCC TGGGCCTGCT GTGACTGACC  2880
TACAGTGGAC TTTCTCTCTG GAATGGAACC TTCTTAGGCC TCCTGGTGCA ACTTAATTTT  2940
```

```
TTTTTTTAAT GCTATCTTCA AAACGTTAGA GAAAGTTCTT CAAAAGTGCA GCCCAGAGCT  3000
GCTGGGCCCA CTGGCCGTCC TGCATTTCTG GTTTCCAGAC CCCAATGCCT CCCATTCGGA  3060
TGGATCTCTG CGTTTTTATA CTGAGTGTGC CTAGGTTGCC CCTTATTTTT TATTTTCCCT  3120
GTTGCGTTGC TATAGATGAA GGGTGAGGAC AATCGTGTAT ATGTACTAGA ACTTTTTTAT  3180
TAAAGAAACT TTTCCCAGAA AAAAA
```

Seq ID NO: 539 Protein sequence
Protein Accession #: NP_001784.2

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1          11         21         31         41         51
|          |          |          |          |          |
MGLPRGPLAS LLLLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVPMGCPG   60
QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG  120
KGPFPQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLLLN KPLDREEIAK  180
YELFGHAVSE NGASVEDPMN ISIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT  240
DEDDAIYTYN GVVAYSIHSQ EPKDPHDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA  300
TDMDGDGSTT TAVAVVEILD ANDNAPMFDP QKYEAHVPEN AVGHEVQRLT VTDLDAPNSP  360
AWRATYLIMG GDDGDHFTIT THPESNQGIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL  420
PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR  480
DPAGWLAMDP DSGQVTAVGT LDREDEQFVR NNIYEVMVLA MDNGSPPTTG TGTLLLTLID  540
VNDHGPVPEP RQITICNQSP VRQVLNITDK DLSPHTSPFQ AQLTDDSDIY WTAEVNEEGD  600
TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDC HGHVETCPGP WKGGFILPVL  660
GAVLALLFLL LVLLLLVRKK RKIKEPLLLP EDDTRDNVFY YGEEGGGEED QDYDITQLHR  720
GLEARPEVVL RNDVAPTIIP TPMYRPRPAN PDEIGNFIIE NLKAANTDPT APPYDTLLVF  780
DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD
```

Seq ID NO: 540 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..672

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGAGGCTCC AAAGACCCCG ACAGGCCCCG GCGGGTGGGA GGCGCGCGCC CCGGGGCGGG   60
CGGGGCTCCC CCTACCGGCC AGACCCGGGG AGAGGCGCGC GGAGGCTGCG AAGGTTCCAG  120
AAGGGCGGGG AGGGGGCGCC GCGCGCTGAC CCTCCCTGGG CACCGCTGGG GACGATGGCG  180
CTGCTCGCCT TGCTGCTGGT CGTGGCCCTA CCGCGGGTGT GGACAGACGC CAACCTGACT  240
GCGAGACAAC GAGATCCAGA GGACTCCCAG CGAACGGACG AGGGTGACAA TAGAGTGTGG  300
TGTCATGTTT GTGAGAGAGA AAACACTTTC GAGTGCCAGA ACCCAAGGAG GTGCAAATGG  360
ACAGAGCCAT ACTGCGTTAT AGCGGCCGTG AAAATATTTC CACGTTTTTT CATGGTTGCG  420
AAGCAGTGCT CCGCTGGTTG TGCAGCGATG GAGAGACCCA AGCCAGAGGA GAAGCGGTTT  480
CTCCTGGAAG AGCCCATGCC CTTCTTTTAC CTCAAGTGTT GTAAAATTCG CTACTGCAAT  540
TTAGAGGGGC CACCTATCAA CTCATCAGTG TTCAAAGAAT ATGCTGGGAG CATGGGTGAG  600
AGCTGTGGTG GCTGTGGCT GGCCATCCTC CTGCTGCTGG CCTCCATTGC AGCCGGCCTC  660
AGCCTGTCTT GA
```

Seq ID NO: 541 Protein sequence
Protein Accession #: Eos sequence

```
1          11         21         31         41         51
|          |          |          |          |          |
MRLQRPRQAP AGGRRAPRGG RGSPYRPDPG RGARRLRRPQ KGGEGAPRAD PPWAPLGTMA   60
LLALLLVVAL PRVWTDANLT ARQRDPEDSQ RTDEGDNRVW CHVCERENTF ECQNPRRCKW  120
TEPYCVIAAV KIFPRFFMVA KQCSAGCAAM ERPKPEEKRF LLEEPMPFFY LKCCKIRYCN  180
LEGPPINSSV FKEYAGSMGE SCGGLWLAIL LLLASIAAGL SLS
```

Seq ID NO: 542 DNA sequence
Nucleic Acid Accession #: XM_035292.2
Coding sequence: 53..1576

```
1          11         21         31         41         51
|          |          |          |          |          |
GCTCGCTGGG CCGCGGCTCC CGGGTGTCCC AGGCCCGGCC GGTGCGCAGA GCATGGCGGG   60
TGCGGGCCCG AAGCGGCGCG CGCTAGCGGC GCCGGCGGCC GAGGAGAAGG AAGAGGCGCG  120
GGAGAAGATG CTGGCCGCCA AGAGCGCGGA CGGCTCGGCG CCGGCAGGCG AGGGCGAGGG  180
CGTGACCCTG CAGCGGAACA TCACGCTGCT CAACGGCGTG GCCATCATCG TGGGGACCAT  240
TATCGGCTCG GGCATCTTCG TGACGCCCAC GGGCGTGCTC AAGGAGGCAG GCTCGCCGGG  300
GCTGGCGCTG GTGGTGTGGG CCGCGTGCGG CGTCTTCTCC ATCGTGGGCG CGCTCTGCTA  360
CGCGGAGCTC GGCACCACCA TCTCCAAATC GGGCGGCGAC TACGCCTACA TGCTGGAGGT  420
CTACGGCTCG CTGCCCGCCT TCCTCAAGCT CTGGATCGAG CTGCTCATCA TCCGGCCTTC  480
ATCGCAGTAC ATCGTGGCCC TGGTCTTCGC CACCTACCTG CTCAAGCCGC TCTTCCCCAC  540
CTGCCCGGTG CCCGAGGAGG CAGCCAAGCT CGTGGCCTGC CTCTGCGTGC TGCTGCTCAC  600
GGCCGTGAAC TGCTACAGCG TGAAGGCCGC CACCCGGGTC CAGGATGCCT TTGCCGCCGC  660
CAAGCTCCTG GCCCTGGCCC TGATCATCCT GCTGGGCTTC GTCCAGATCG GAAAGGGTGA  720
TGTGTCCAAT CTAGATCCCA ACTTCTCATT TGAAGGCACC AAACTGGATG TGGGGAACAT  780
TGTGCTGGCA TTATACAGCG GCCTCTTTGC CTATGGAGGA TGGAATTACT TGAATTTCGT  840
CACAGAGGAA ATGATCAACC CCTACAGAAA CCTGCCCCTG GCCATCATCA TCTCCCTGCC  900
CATCGTGACG CTGGTGTACG TGCTGACCAA CCTGGCCTAC TTCACCACCC TGTCCACCGA  960
GCAGATGCTG TCGTCCGAGG CCGTGGCCGT GGACTTCGGG AACTATCACC TGGGCGTCAT 1020
GTCCTGGATC ATCCCCGTCT TCGTGGGCCT GTCCTGCTTC GGCTCCGTCA ATGGGTCCCT 1080
GTTCACATCC TCCAGGCTCT TCTTCGTGGG GTCCCGGGAA GGCCACCTGC CCTCCATCCT 1140
CTCCATGATC CACCCACAGC TCCTCACCCC CGTGCCGTCC CTCGTGTTCA CGTGTGTGAT 1200
GACGCTGCTC TACGCCTTCT CCAAGGACAT CTTCTCCGTC ATCAACTTCT TCAGCTTCTT 1260
CAACTGGCTC TGCGTGGCCC TGGCCATCAT CGGCATGATC TGGCTGCGCC ACAGAAAGCC 1320
TGAGCTTGAG CGGCCCATCA AGGTGAACCT GGCCCTGCCT GTGTTCTTCA TCCTGGCCTG 1380
CCTCTTCCTG ATCGCCGTCT CCTTCTGGAA GACACCCGTG GAGTGTGGCA TCGGCTTCAC 1440
CATCATCCTC AGCGGGCTGC CCGTCTACTT CTTCGGGGTC TGGTGGAAAA ACAAGCCCAA 1500
GTGGCTCCTC CAGGGCATCT TCTCCACGAC CGTCCTGTGT CAGAAGCTCA TGCAGGTGGT 1560
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CCCCCAGGAG ACATAGCCAG GAGGCCGAGT GGCTGCCGGA GGAGCATGC
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Seq ID NO: 543 Protein sequence
Protein Accession #: XP_035292.2

```
1          11         21         31         41         51
|          |          |          |          |          |
MAGAGPKRRA LAAPAAEEKE EAREKMLAAK SADGSAPAGE GEGVTLQRNI TLLNGVAIIV    60
GTIIGSGIFV TPTGVLKEAG SPGLALVVWA ACGVFSIVGA LCYAELGTTI SKSGGDYAYM   120
LEVYGSLPAF LKLWIELLII RPSSQYIVAL VFATYLLKPL FPTCPVPEEA AKLVACLCVL   180
LLTAVNCYSV KAATRVQDAF AAAKLLALAL IILLGFVQIG KGDVSNLDPN FSFEGTKLDV   240
GNIVLALYSG LFAYGGWNYL NFVTEEMINP YRNLPLAIII SLPIVTLVYV LTNLAYFTTL   300
STEQMLSSEA VAVDFGNYHL GVMSWIIPVF VGLSCFGSVN GSLFTSSRLF FVGSREGHLP   360
SILSMIHPQL LTPVPSLVFT CVMTLLYAFS KDIFSVINFF SFFNWLCVAL AIIGMIWLRH   420
RKPELERPIK VNLALPVFFI LACLFLIAVS FWKTPVECGI GFTIILSGLP VYFFGVWWKN   480
KPKWLLQGIF STTVLCQKLM QVVPQET
```

Seq ID NO: 544 DNA sequence
Nucleic Acid Accession #: NM_005268.1
Coding sequence: 168..989

```
1          11         21         31         41         51
|          |          |          |          |          |
TAAAAAGCAA AAGAATTCGC GGCCGCGTCG ACACGGGCTT CCCCGAAAAC CTTCCCCGCT    60
TCTGGATATG AAATTCAAGC TGCTTGCTGA GTCCTATTGC CGGCTGCTGG GAGCCAGGAG   120
AGCCCTGAGG AGTAGTCACT CAGTAGCAGC TGACGCGTGG GTCCACCATG AACTGGAGTA   180
TCTTTGAGGG ACTCCTGAGT GGGGTCAACA AGTACTCCAC AGCCTTTGGG CGCATCTGGC   240
TGTCTCTGGT CTTCATCTTC CGCGTGCTGG TGTACCTGGT GACGGCCGAG CGTGTGTGGA   300
GTGATGACCA CAAGGACTTC GACTGCAATA CTCGCCAGCC CGGCTGCTCC AACGTCTGCT   360
TTGATGAGTT CTTCCCTGTG TCCCATGTGC GCCTCTGGGC CCTGCAGCTT ATCCTGGTGA   420
CATGCCCCTC ACTGCTCGTG GTCATGCACG TGGCCTACCG GGAGGTTCAG GAGAAGAGGC   480
ACCGAGAAGC CCATGGGGAG AACAGTGGGC GCCTCTACCT GAACCCCGGC AAGAAGCGGG   540
GTGGGCTCTG GTGGACATAT GTCTGCAGCC TAGTGTTCAA GGCGAGCGTG GACATCGCCT   600
TTCTCTATGT GTTCCACTCA TTCTACCCCA AATATATCCT CCCTCCTGTG GTCAAGTGCC   660
ACGCAGATCC ATGTCCCAAT ATAGTGGACT GCTTCATCTC CAAGCCCTCA GAGAAGAACA   720
TTTTCACCCT CTTCATGGTG GCCACAGCTG CCATCTGCAT CCTGCTCAAC CTCGTGGAGC   780
TCATCTACCT GGTGAGCAAG AGATGCCACG AGTGCCTGGC AGCAAGGAAA GCTCAAGCCA   840
TGTGCACAGG TCATCACCCC CACGGTACCA CCTCTTCCTG CAAACAAGAC GACCTCCTTT   900
CGGGTGACCT CATCTTTCTG GGCTCAGACA GTCATCCTCC TCTCTTACCA GACCGCCCCC   960
GAGACCATGT GAAGAAAACC ATCTTGTGAG GGGCTGCCTG GACTGGTCTG GCAGGTTGGG  1020
CCTGGATGGG GAGGCTCTAG CATCTCTCAT AGGTGCAACC TGAGAGTGGG GGAGCTAAGC  1080
CATGAGGTAG GGGCAGGCAA GAGAGAGGAT TCAGACGCTC TGGGAGCCAG TTCCTAGTCC  1140
TCAACTCCAG CCACCTGCCC CAGCTCGACG GCACTGGGCC AGTTCCCCCT CTGCTCTGCA  1200
GCTCGGTTTC CTTTTCTAGA ATGGAAATAG TGAGGGCCAA TGC
```

Seq ID NO: 545 Protein sequence
Protein Accession #: NP_005259.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MNWSIFEGLL SGVNKYSTAF GRIWLSLVFI FRVLVYLVTA ERVWSDDHKD FDCNTRQPGC    60
SNVCFDEFFP VSHVRLWALQ LILVTCPSLL VVMHVAYREV QEKRHREAHG ENSGRLYLNP   120
GKKRGGLWWT YVCSLVFKAS VDIAFLYVFH SFYPKYILPP VVKCHADPCP NIVDCFISKP   180
SEKNIFTLFM VATAAICILL NLVELIYLVS KRCHECLAAR KAQAMCTGHH PHGTTSSCKQ   240
DDLLSGDLIF LGSDSHPPLL PDRPRDHVKK TIL
```

Seq ID NO: 546 DNA sequence
Nucleic Acid Accession #: NM_002391.1
Coding sequence: 26..457

```
1          11         21         31         41         51
|          |          |          |          |          |
CGGGCGAAGC AGCGCGGGCA GCGAGATGCA GCACCGAGGC TTCCTCCTCC TCACCCTCCT    60
CGCCCTGCTG GCGCTCACCT CCGCGGTCGC CAAAAAGAAA GATAAGGTGA AGAAGGGCGG   120
CCCGGGGAGC GAGTGCGCTG AGTGGGCCTG GGGGCCCTGC ACCCCCAGCA GCAAGGATTG   180
CGGCGTGGGT TTCCGCGAGG GCACCTGCGG GGCCCAGACC CAGCGCATCC GGTGCAGGGT   240
GCCCTGCAAC TGGAAGAAGG AGTTTGGAGC CGACTGCAAG TACAAGTTTG AGAACTGGGG   300
TGCGTGTGAT GGGGGCACAG GCACCAAAGT CCGCCAAGGC ACCCTGAAGA AGGCGCGCTA   360
CAATGCTCAG TGCCAGGAGA CCATCCGCGT CACCAAGCCC TGCACCCCCA AGACCAAAGC   420
AAAGGCCAAA GCCAAGAAAG GGAAGGGAAA GGACTAGACG CCAAGCCTGG ATGCCAAGGA   480
GCCCCTGGTG TCACATGGGG CCTGGCCACG CCCTCCCTCT CCCAGGCCCG AGATGTGACC   540
CACCAGTGCC TTCTGTCTGC TCGTTAGCTT TAATCAATCA TGCCCTGCCT TGTCCCTCTC   600
ACTCCCCAGC CCCACCCCTA AGTGCCCAAA GTGGGGAGGG ACAAGGGATT CTGGGAAGCT   660
TGAGCCTCCC CCAAAGCAAT GTGAGTCCCA GAGCCCGCTT TTGTTCTTCC CCACAATTCC   720
ATTACTAAGA AACACATCAA ATAAACTGAC TTTTTCCCCC CAATAAAAGC TCTTCTTTTT   780
TAATAT
```

Seq ID NO: 547 Protein sequence
Protein Accession #: NP_002382.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MQHRGFLLLT LLALLALTSA VAKKKDKVKK GGPGSECAEW AWGPCTPSSK DCGVGFREGT    60
CGAQTQRIRC RVPCNWKKEF GADCKYKFEN WGACDGGTGT KVRQGTLKKA RYNAQCQETI   120
RVTKPCTPKT KAKAKAKKGK GKD
```

Seq ID NO: 548 DNA sequence

Nucleic Acid Accession #: NM_006783.1
Coding sequence: 1..786

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGGATTGGG GGACGCTGCA CACTTTCATC GGGGGTGTCA ACAAACACTC CACCAGCATC     60
GGGAAGGTGT GGATCACAGT CATCTTTATT TTCCGAGTCA TGATCCTAGT GGTGGCTGCC    120
CAGGAAGTGT GGGGTGACGA GCAAGAGGAC TTCGTCTGCA ACACACTGCA ACCGGGATGC    180
AAAAATGTGT GCTATGACCA CTTTTTCCCG GTGTCCCACA TCCGGCTGTG GGCCCTCCAG    240
CTGATCTTCG TCTCCACCCC AGCGCTGCTG GTGGCCATGC ATGTGGCCTA CTACAGGCAC    300
GAAACCACTC GCAAGTTCAG GCGAGGAGAG AAGAGGAATG ATTTCAAAGA CATAGAGGAC    360
ATTAAAAAGC ACAAGGTTCG GATAGAGGGG TCGCTGTGGT GGACGTACAC CAGCAGCATC    420
TTTTTCCGAA TCATCTTTGA AGCAGCCTTT ATGTATGTGT TTTACTTCCT TTACAATGGG    480
TACCACCTGC CCTGGGTGTT GAAATGTGGG ATTGACCCCT GCCCCAACCT TGTTGACTGC    540
TTTATTTCTA GGCCAACAGA GAAGACCGTG TTTACCATTT TTATGATTTC TGCGTCTGTG    600
ATTTGCATGC TGCTTAACGT GGCAGAGTTG TGCTACCTGC TGCTGAAAGT GTGTTTTAGG    660
AGATCAAAGA GAGCACAGAC GCAAAAAAAT CACCCCAATC ATGCCCTAAA GGAGAGTAAG    720
CAGAATGAAA TGAATGAGCT GATTTCAGAT AGTGGTCAAA ATGCAATCAC AGGTTTCCCA    780
AGCTAA
```

Seq ID NO: 549 Protein sequence
Protein Accession #: NP_006774.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MDWGTLHTFI GGVNKHSTSI GKVWITVIFI FRVMILVVAA QEVWGDEQED FVCNTLQPGC     60
KNVCYDHFFP VSHIRLWALQ LIFVSTPALL VAMHVAYYRH ETTRKFRRGE KRNDFKDIED    120
IKKHKVRIEG SLWWTYTSSI FFRIIFEAAF MYVFYFLYNG YHLPWVLKCG IDPCPNLVDC    180
FISRPTEKTV FTIFMISASV ICMLLNVAEL CYLLLKVCFR RSKRAQTQKN HPNHALKESK    240
QNEMNELISD SGQNAITGFP S
```

Seq ID NO: 550 DNA sequence
Nucleic Acid Accession #: NM_002571.1
Coding sequence: 99..587

```
1          11         21         31         41         51
|          |          |          |          |          |
CATCCCTCTG GCTCCAGAGC TCAGAGCCAC CCACAGCCGC AGCCATGCTG TGCCTCCTGC     60
TCACCCTGGG CGTGGCCCTG GTCTGTGGTG TCCCGGCCAT GGACATCCCC CAGACCAAGC    120
AGGACCTGGA GCTCCCAAAG TTGGCAGGGA CCTGGCACTC CATGGCCATG GCGACCAACA    180
ACATCTCCCT CATGGCGACA CTGAAGGCCC CTCTGAGGGT CCACATCACC TCACTGTTGC    240
CCACCCCCGA GGACAACCTG GAGATCGTTC TGCACAGATG GGAGAACAAC AGCTGTGTTG    300
AGAAGAAGGT CCTTGGAGAG AAGACTGGGA ATCCAAAGAA GTTCAAGATC AACTATACGG    360
TGGCGAACGA GGCCACGCTG CTCGATACTG ACTACGACAA TTTCCTGTTT CTCTGCCTAC    420
AGGACACCAC CACCCCCATC CAGAGCATGA TGTGCCAGTA CCTGGCCAGA GTCCTGGTGG    480
AGGACGATGA GATCATGCAG GGATTCATCA GGGCTTTCAG GCCCCTGCCC AGGCACCTAT    540
GGTACTTGCT GGACTTGAAA CAGATGGAAG AGCCGTGCCG TTTCTAGCTC ACCTCCGCCT    600
CCAGGAAGAC CAGACTCCCA CCCTTCCACA CCTCCAGAGC AGTGGGACTT CCTCCTGCCC    660
TTTCAAAGAA TAACCACAGC TCAGAAGACG ATGACGTGGT CATCTGTGTC GCCATCCCCT    720
TCCTGCTGCA CACCTGCACC ATTGCCATGG GGAGGCTGCT CCCTGGGGGC AGAGTCTCTG    780
GCAGAGGTTA TTAATAAACC CTTGGAGCAT G
```

Seq ID NO: 551 Protein sequence
Protein Accession #: NP_002562.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MDIPQTKQDL ELPKLAGTWH SMAMATNNIS LMATLKAPLR VHITSLLPTP EDNLEIVLHR     60
WENNSCVEKK VLGEKTGNPK KFKINYTVAN EATLLDTDYD NFLFLCLQDT TTPIQSMMCQ    120
YLARVLVEDD EIMQGFIRAF RPLPRHLWYL LDLKQMEEPC RF
```

Seq ID NO: 552 DNA sequence
Nucleic Acid Accession #: NM_006500.1
Coding sequence: 27..1967

```
1          11         21         31         41         51
|          |          |          |          |          |
ACTTGCGTCT CGCCCTCCGG CCAAGCATGG GGCTTCCCAG GCTGGTCTGC GCCTTCTTGC     60
TCGCCGCCTG CTGCTGCTGT CCTCGCGTCG CGGGTGTGCC CGGAGAGGCT GAGCAGCCTG    120
CGCCTGAGCT GGTGGAGGTG GAAGTGGGCA GCACAGCCCT TCTGAAGTGC GGCCTCTCCC    180
AGTCCCAAGG CAACCTCAGC CATGTCGACT GGTTTTCTGT CCACAAGGAG AAGCGGACGC    240
TCATCTTCCG TGTGCGCCAG GGCCAGGGCC AGAGCGAACC TGGGGAGTAC GAGCAGCGGC    300
TCAGCCTCCA GGACAGAGGG GCTACTCTGG CCCTGACTCA AGTCACCCCC CAAGACGAGC    360
GCATCTTCTT GTGCCAGGGC AAGCGCCCTC GGTCCCAGGA GTACCGCATC CAGCTCCGCG    420
TCTACAAAGC TCCGGAGGAG CCAAACATCC AGGTCAACCC CCTGGGCATC CCTGTGAACA    480
GTAAGGAGCC TGAGGAGGTC GCTACCTGTG TAGGGAGGAA CGGGTACCCC ATTCCTCAAG    540
TCATCTGGTA CAAGAATGGC CGGCCTCTGA AGGAGGAGAA GAACCGGGTC CACATTCAGT    600
CGTCCCAGAC TGTGGAGTCG AGTGGTTTGT ACACCTTGCA GAGTATTCTG AAGGCACAGC    660
TGGTTAAAGA AGACAAAGAT GCCCAGTTTT ACTGTGAGCT CAACTACCGG CTGCCCAGTG    720
GGAACCACAT GAAGGAGTCC AGGGAAGTCA CCGTCCCTGT TTTCTACCCG ACAGAAAAAG    780
TGTGGCTGGA AGTGGAGCCC GTGGGAATGC TGAAGGAAGG GGACCGCGTG GAAATCAGGT    840
GTTTGGCTGA TGGCAACCCT CCACCACACT TCAGCATCAG CAAGCAGAAC CCCAGCACCA    900
GGGAGGCAGA GGAAGAGACA ACCAACGACA ACGGGGTCCT GGTGCTGGAG CCTGCCCGGA    960
AGGAACACAG TGGGCGCTAT GAATGTCAGG CCTGGAACTT GGACACCATG ATATCGCTGC   1020
TGAGTGAACC ACAGGAACTA CTGGTGAACT ATGTGTCTGA CGTCCGAGTG AGTCCCGCAG   1080
CCCCTGAGAG ACAGGAAGGC AGCAGCCTCA CCCTGACCTG TGAGGCAGAG AGTAGCCAGG   1140
ACCTCGAGTT CCAGTGGCTG AGAGAAGAGA CAGACCAGGT GCTGGAAAGG GGGCCTGTGC   1200
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TTCAGTTGCA TGACCTGAAA CGGGAGGCAG GAGGCGGCTA TCGCTGCGTG GCGTCTGTGC  1260
CCAGCATACC CGGCCTGAAC CGCACACAGC TGGTCAAGCT GGCCATTTTT GGCCCCCCTT  1320
GGATGGCATT CAAGGAGAGG AAGGTGTGGG TGAAAGAGAA TATGGTGTTG AATCTGTCTT  1380
GTGAAGCGTC AGGGCACCCC CGGCCCACCA TCTCCTGGAA CGTCAACGGC ACGGCAAGTG  1440
AACAAGACCA AGATCCACAG CGAGTCCTGA GCACCCTGAA TGTCCTCGTG ACCCCGGAGC  1500
TGTTGGAGAC AGGTGTTGAA TGCACGGCCT CCAACGACCT GGGCAAAAAC ACCAGCATCC  1560
TCTTCCTGGA GCTGGTCAAT TTAACCACCC TCACACCAGA CTCCAACACA ACCACTGGCC  1620
TCAGCACTTC CACTGCCAGT CCTCATACCA GAGCCAACAG CACCTCCACA GAGAGAAAGC  1680
TGCCGGAGCC GGAGAGCCGG GGCGTGGTCA TCGTGGCTGT GATTGTGTGC ATCCTGGTCC  1740
TGGCGGTGCT GGGCGCTGTC CTCTATTTCC TCTATAAGAA GGGCAAGCTG CCGTGCAGGC  1800
GCTCAGGGAA GCAGGAGATC ACGCTGCCCC CGTCTCGTAA GACCGAACTT GTAGTTGAAG  1860
TTAAGTCAGA TAAGCTCCCA GAAGAGATGG GCCTCCTGCA GGGCAGCAGC GGTGACAAGA  1920
GGGCTCCGGG AGACCAGGGA GAGAAATACA TCGATCTGAG GCATTAGCCC CGAATCACTT  1980
CAGCTCCCTT CCCTGCCTGG ACCATTCCCA GCTCCCTGCT CACTCTTCTC TCAGCCAAAG  2040
CCTCCAAAGG GACTAGAGAG AAGCCTCCTG CTCCCCTCAC CTGCACACCC CCTTTCAGAG  2100
GGCCACTGGG TTAGGACCTG AGGACCTCAC TTGGCCCTGC AAGCCGCTTT TCAGGGACCA  2160
GTCCACCACC ATCTCCTCCA CGTTGAGTGA AGCTCATCCC AAGCAAGGAG CCCCAGTCTC  2220
CCGAGCGGGT AGGAGAGTTT CTTGCAGAAC GTGTTTTTTC TTTACACACA TTATGGCTGT  2280
AAATACCTGG CTCCTGCCAG CAGCTGAGCT GGGTAGCCTC TCTGAGCTGG TTTCCTGCCC  2340
CAAAGGCTGG CTTCCACCAT CCAGGTGCAC CACTGAAGTG AGGACACACC GGAGCCAGGC  2400
GCCTGCTCAT GTTGAAGTGC GCTGTTCACA CCCGCTCCGG AGAGCACCCC AGCGGCATCC  2460
AGAAGCAGCT GCAGTGTTGC TGCCACCACC CTCCTGCTCG CCTCTTCAAA GTCTCCTGTG  2520
ACATTTTTTC TTTGGTCAGA AGCCAGGAAC TGGTGTCATT CCTTAAAAGA TACGTGCCGG  2580
GGCCAGGTGT GGTGGCTCAC GCCTGTAATC CCAGCACTTT GGGAGGCCGA GGCGGGCGGA  2640
TCACAAAGTC AGGACGAGAC CATCCTGGCT AACACGGTGA AACCCTGTCT CTACTAAAAA  2700
TACAAAAAAA AATTAGCTAG GCGTAGTGGT TGGCACCTAT AGTCCCAGCT ACTCGGAAGG  2760
CTGAAGCAGG AGAATGGTAT GAATCCAGGA GGTGGAGCTT GCAGTGAGCC GAGACCGTGC  2820
CACTGCACTC CAGCCTGGGC AACACAGCGA GACTCCGTCT CGAGGAAAAA AAAAGAAAAG  2880
ACGCGTACCT GCGGTGAGGA AGCTGGGCGC TGTTTTCGAG TTCAGGTGAA TTAGCCTCAA  2940
TCCCCGTGTT CACTTGCTCC CATAGCCCTC TTGATGGATC ACGTAAAACT GAAAGGCAGC  3000
GGGGAGCAGA CAAAGATGAG GTCTACACTG TCCTTCATGG GGATTAAAGC TATGGTTATA  3060
TTAGCACCAA ACTTCTACAA ACCAAGCTCA GGGCCCCAAC CCTAGAAGGG CCCAAATGAG  3120
AGAATGGTAC TTAGGGATGG AAAACGGGGC CTGGCTAGAG CTTCGGGTGT GTGTGTCTGT  3180
CTGTGTGTAT GCATACATAT GTGTGTATAT ATGGTTTTGT CAGGTGTGTA AATTTGCAAA  3240
TTGTTTCCTT TATATATGTA TGTATATATA TATATGAAAA TATATATATA TATGAAAAAT  3300
AAAGCTTAAT TGTCCCAGAA AATCATACAT TGCTTTTTTA TTCTACATGG GTACCACAGG  3360
AACCTGGGGG CCTGTGAAAC TACAACCAAA AGGCACACAA AACCGTTTCC AGTTGGCAGC  3420
AGAGATCAGG GGTTACCTCT GCTTCTGAGC AAATGGCTCA AGCTCTACCA GAGCAGACAG  3480
CTACCCTACT TTTCAGCAGC AAAACGTCCC GTATGACGCA GCACGAAGGG CCTGGCAGGC  3540
TGTTAGCAGG AGCTATGTCC CTTCCTATCG TTTCCGTCCA CTT
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Seq ID NO: 553 Protein sequence
Protein Accession #: NP_006491.1

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1          11         21         31         41         51
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GLPRLVCAFL LAACCCCPRV AGVPGEAEQP APELVEVEVG STALLKCGLS QSQGNLSHVD    60
WFSVHKEKRT LIFRVRQGQG QSEPGEYEQR LSLQDRGATL ALTQVTPQDE RIFLCQGKRP   120
RSQEYRIQLR VYKAPEEPNI QVNPLGIPVN SKEPEEVATC VGRNGYPIPQ VIWYKNGRPL   180
KEEKNRVHIQ SSQTVESSGL YTLQSILKAQ LVKEDKDAQF YCELNYRLPS GNHMKESREV   240
TVPVFYPTEK VWLEVEPVGM LKEGDRVEIR CLADGNPPPH FSISKQNPST REAEEETTND   300
NGVLVLEPAR KEHSGRYECQ AWNLDTMISL LSEPQELLVN YVSDVRVSPA APERQEGSSL   360
TLTCEAESSQ DLEFQWLREE TDQVLERGPV LQLHDLKREA GGGYRCVASV PSIPGLNRTQ   420
LVKLAIFGPP WMAFKERKVW VKENMVLNLS CEASGHPRPT ISWNVNGTAS EQDQDPQRVL   480
STLNVLVTPE LLETGVECTA SNDLGKNTSI LFLELVNLTT LTPDSNTTTG LSTSTASPHT   540
RANSTSTERK LPEPESRGVV IVAVIVCILV LAVLGAVLYF LYKKGKLPCR RSGKQEITLP   600
PSRKTELVVE VKSDKLPEEM GLLQGSSGDK RAPGDQGEKY IDLRH
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Seq ID NO: 554 DNA sequence
Nucleic Acid Accession #: NM_003183.3
Coding sequence: 165..2639

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GCTAGGCCGG GCGGATCCCG TCCTCCCCCG ATGTGAGCAG TTTTCCGAAA CCCCGTCAGG   120
CGAAGGCTGC CCAGAGAGGT GGAGTCGGTA GCGGGGCCGG GAACATGAGG CAGTCTCTCC   180
TATTCCTGAC CAGCGTGGTT CCTTTCGTGC TGGCGCCGCG ACCTCCGGAT GACCCGGGCT   240
TCGGCCCCCA CCAGAGACTC GAGAAGCTTG ATTCTTTGCT CTCAGACTAC GATATTCTCT   300
CTTTATCTAA TATCCAGCAG CATTCGGTAA GAAAAAGAGA TCTACAGACT TCAACACATG   360
TAGAAACACT ACTAACTTTT TCAGCTTTGA AAAGGCATTT TAAATTATAC CTGACATCAA   420
GTACTGAACG TTTTTCACAA AATTTCAAGG TCGTGGTGGT GGATGGTAAA AACGAAAGCG   480
AGTACACTGC AAAATGGCAG GACTTCTTCA CTGGACACGT GGTTGGTGAG CCTGACTCTA   540
GGGTTCTAGC CCACATAAGA GATGATGATG TTATAATCAG AATCAACACA GATGGGGCCG   600
AATATAACAT AGAGCCACTT TGGAGATTTG TTAATGATAC CAAAGACAAA AGAATGTTAG   660
TTTATAAATC TGAAGATATC AAGAATGTTT CACGTTTGCA GTCTCCAAAA GTGTGTGGTT   720
ATTTAAAAGT GGATAATGAA GAGTTGCTCC CAAAAGGGTT AGTAGACAGA GAACCACCTG   780
AAGAGCTTGT TCATCGAGTG AAAAGAAGAG CTGACCCAGA TCCCATGAAG AACACGTGTA   840
AATTATTGGT GGTAGCAGAT CATCGCTTCT ACAGATACAT GGGCAGAGGG GAAGAGAGTA   900
CAACTACAAA TTACTTAATA GAGCTAATTG ACAGAGTTGA TGACATCTAT CGGAACACTT   960
CATGGGATAA TGCAGGTTTT AAAGGCTATG GAATACAGAT AGAGCAGATT CGCATTCTCA  1020
AGTCTCCACA AGAGGTAAAA CCTGGTGAAA AGCACTACAA CATGGCAAAA AGTTACCCAA  1080
ATGAAGAAAA GGATGCTTGG GATGTGAAGA TGTTGCTAGA GCAATTTAGC TTTGATATAG  1140
CTGAGGAAGC ATCTAAAGTT TGCTTGGCAC ACCTTTTCAC ATACCAAGAT TTTGATATGG  1200
GAACTCTTGG ATTAGCTTAT GTTGGCTCTC CCAGAGCAAA CAGCCATGGA GGTGTTTGTC  1260
CAAAGGCTTA TTATAGCCCA GTTGGGAAGA AAAATATCTA TTTGAATAGT GGTTTGACGA  1320
GCACAAAGAA TTATGGTAAA ACCATCCTTA CAAAGGAAGC TGACCTGGTT ACAACTCATG  1380
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AATTGGGACA TAATTTTGGA GCAGAACATG ATCCGGATGG TCTAGCAGAA TGTGCCCCGA  1440
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CCCAGGAGTG TTTTCAAGAA CGCAGCAATA AAGTTTGTGG GAACTCGAGG GTGGATGAAG  1620
GAGAAGAGTG TGATCCTGGC ATCATGTATC TGAACAACGA CACCTGCTGC AACAGCGACT  1680
GCACGTTGAA GGAAGGTGTC CAGTGCAGTG ACAGGAACAG TCCTTGCTGT AAAAACTGTC  1740
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CCTACTGCAC AGGTAATAGC AGTGAGTGCC CGCCTCCAGG AAATGCTGAA AATGACACTG  1860
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ACCTTTCTGG CCGCTGTGTG CCCTATGTCG ATGCTGAACA AAAGAACTTA TTTTTGAGGA  2040
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AGGATGTAAT TGAACGATTT TGGGATTTCA TTGACCAGCT GAGCATCAAT ACTTTTGGAA  2160
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CTCTGTTTCA CCCCAGTAAC GTCGAAATGC TGAGCAGCAT GGATTCTGCA TCGGTTCGCA  2340
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CTGCCTCCTT TAAACTGCAG CGTCAGAATC GTGTTAACAG CAAAGAAACA GAGTGCTAAT  2640
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TGTAAATTAA TCTTTTATAT TGATAACAGC ACTGACTAGG GAAATGATCA GTTTTTTTTT  3000
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ATAGTTTTTT TTTTTTTTTT TTTTTTTTGC CTTCAACTAA AAACAAAGGA GATAAATTTA  3120
GTATACATTG TATCTAAATT GTGGGTCTAT TTCTAGTTAT TACCCAGAGT TTTTATGTAG  3180
CAGGGAAAAT ATATATCTAA ATTTAGAAAT CATTTGGGTT AATATGGCTC TTCATAATTC  3240
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TTTTATAAGT ATCTTCATGT ATCCCTGTTA CTGATAGGGA TACATGTCTT AGAAAATTCA  3420
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CGCCACTACA CTCCAGCCTG GGTGACAGAG TGAGATCTGC CTC
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Seq ID NO: 555 Protein sequence
Protein Accession #: NP_003174.2

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GEPDSRVLAH IRDDDVIIRI NTDGAEYNIE PLWRFVNDTK DKRMLVYKSE DIKNVSRLQS   180
PKVCGYLKVD NEELLPKGLV DREPPEELVH RVKRRADPDP MKNTCKLLVV ADHRFYRYMG   240
RGEESTTTNY LIELIDRVDD IYRNTSWDNA GFKGYGIQIE QIRILKSPQE VKPGEKHYNM   300
AKSYPNEEKD AWDVKMLLEQ FSFDIAEEAS KVCLAHLFTY QDFDMGTLGL AYVGSPRANS   360
HGGVCPKAYY SPVGKKNIYL NSGLTSTKNY GKTILTKEAD LVTTHELGHN FGAEHDPDGL   420
AECAPNEDQG GKYVMYPIAV SGDHENNKMF SNCSKQSIYK TIESKAQECF QERSNKVCGN   480
SRVDEGEECD PGIMYLNNDT CCNSDCTLKE GVQCSDRNSP CCKNCQFETA QKKCQEAINA   540
TCKGVSYCTG NSSECPPPGN AENDTVCLDL GKCKDGKCIP FCEREQQLES CACNETDNSC   600
KVCCRDLSGR CVPYVDAEQK NLFLRKGKPC TVGFCDMNGK CEKRVQDVIE RFWDFIDQLS   660
INTFGKFLAD NIVGSVLVFS LIFWIPFSIL VHCVDKKLDK QYESLSLFHP SNVEMLSSMD   720
SASVRIIKPF PAPQTPGRLQ PAPVIPSAPA APKLDHQRMD TIQEDPSTDS HMDEDGFEKD   780
PFPNSSTAAK SFEDLTDHPV ARSEKAASFK LQRQNRVNSK ETEC
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Seq ID NO: 556 DNA sequence
Nucleic Acid Accession #: NM_021832.1
Coding sequence: 164..2248

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GAAGGCTGCC CAGAGAGGTG GAGTCGGTAG CGGGGCCGGG AACATGAGGC AGTCTCTCCT   180
ATTCCTGACC AGCGTGGTTC CTTTCGTGCT GGCGCCGCGA CCTCCGGATG ACCCGGGCTT   240
CGGCCCCCAC CAGAGACTCG AGAAGCTTGA TTCTTTGCTC TCAGACTACG ATATTCTCTC   300
TTTATCTAAT ATCCAGCAGC ATTCGGTAAG AAAAAGAGAT CTACAGACTT CAACACATGT   360
AGAAACACTA CTAACTTTTT CAGCTTTGAA AAGGCATTTT AAATTATACC TGACATCAAG   420
TACTGAACGT TTTTCACAAA ATTTCAAGGT CGTGGTGGTG GATGGTAAAA ACGAAAGCGA   480
GTACACTGTA AAATGGCAGG ACTTCTTCAC TGGACACGTG GTTGGTGAGC CTGACTCTAG   540
GGTTCTAGCC CACATAAGAG ATGATGATGT TATAATCAGA ATCAACACAG ATGGGGCCGA   600
ATATAACATA GAGCCACTTT GGAGATTTGT TAATGATACC AAAGACAAAA GAATGTTAGT   660
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TTTAAAAGTG GATAATGAAG AGTTGCTCCC AAAAGGGTTA GTAGACAGAG AACCACCTGA   780
AGAGCTTGTT CATCGAGTGA AAAGAAGAGC TGACCCAGAT CCCATGAAGA ACACGTGTAA   840
ATTATTGGTG GTAGCAGATC ATCGCTTCTA CAGATACATG GGCAGAGGGG AAGAGAGTAC   900
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TGAGGAAGCA TCTAAAGTTT GCTTGGCACA CCTTTTCACA TACCAAGATT TTGATATGGG  1200
AACTCTTGGA TTAGCTTATG TTGGCTCTCC CAGAGCAAAC AGCCATGGAG GTGTTTGTCC  1260
AAAGGCTTAT TATAGCCCAG TTGGGAAGAA AAATATCTAT TTGAATAGTG GTTTGACGAG  1320
CACAAAGAAT TATGGTAAAA CCATCCTTAC AAAGGAAGCT GACCTGGTTA CAACTCATGA  1380
ATTGGGACAT AATTTTGGAG CAGAACATGA TCCGGATGGT CTAGCAGAAT GTGCCCCGAA  1440
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TGAGGACCAG GGAGGGAAAT ATGTCATGTA TCCCATAGCT GTGAGTGGCG ATCACGAGAA  1500
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CACGTTGAAG GAAGGTGTCC AGTGCAGTGA CAGGAACAGT CCTTGCTGTA AAAACTGTCA  1740
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CCTTTCCGGC CGCTGTGTGC CCTATGTCGA TGCTGAACAA AAGAACTTAT TTTTGAGGAA  2040
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CTGTGATCCC TTCGGCGCCA GCAGCTCCAA AACTGGACCA CCAGAGAATG GACACCATCC  2400
AGGAAGACCC CAGCACAGAC TCACATATGG ACGAGGATGG GTTTGAGAAG GACCCCTTCC  2460
CAAATAGCAG CACAGCTGCC AAGTCATTTG AGGATCTCAC GGACCATCCG GTCACCAGAA  2520
GTGAAAAGGC TGCCTCCTTT AAACTGCAGC GTCAGAATCG TGTTGACAGC AAAGAAACAG  2580
AGTGCTAATT TAGTTCTCAG CTCTTCTGAC TTAAGTGTGC AAAATATTTT TATAGATTTG  2640
ACCTACAATC AATCACAGCT TATATTTTGT GAAGACTGGG AAGTGACTTA GCAGATGCTG  2700
GTCATGTGTT TGAACTTCCT GCAGGTAAAC AGTTCTTGTG TGGTTTGGCC CTTCTCCTTT  2760
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TTACGTTTTT GTAAATTAAT CTTTTATATT GATAACAGGC ACTGACTAGG GAAATGATCA  2940
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TTTTATGTAG CAGGGAAAAT ATATATCTAA ATTTAGAAAT CATTTGGGTT AATATGGCTC  3180
TTCATAATTC TAAGACTAAT GCTCAGAACC TAACCACTAC CTTACAGTGA GGGCTATACA  3240
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AGAAAATTCA CTATTGGCTG GGAGTGGTGG CTCATGCCTG TAATCCCAGC ACTTGGAGAG  3420
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Seq ID NO: 557 Protein sequence
Protein Accession #: NP_068604.1

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QTSTHVETLL TFSALKRHFK LYLTSSTERF SQNFKVVVVD GKNESEYTVK WQDFFTGHVV  120
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PKVCGYLKVD NEELLPKGLV DREPPEELVH RVKRRADPDP MKNTCKLLVV ADHRFYRYMG  240
RGEESTTTNY LIELIDRVDD IYRNTSWDNA GFKGYGIQIE QIRILKSPQE VKPGEKHYNM  300
AKSYPNEEKD AWDVKMLLEQ FSFDIAEEAS KVCLAHLFTY QDFDMGTLGL AYVGSPRANS  360
HGGVCPKAYY SPVGKKNIYL NSGLTSTKNY GKTILTKEAD LVTTHELGHN FGAEHDPDGL  420
AECAPNEDQG GKYVMYPIAV SGDHENNKMF SNCSKQSIYK TIESKAQECF QERSNKVCGN  480
SRVDEGEECD PGIMYLNNDT CCNSDCTLKE GVQCSDRNSP CCKNCQFETA QKKCQEAINA  540
TCKGVSYCTG NSSECPPPGN AEDDTVCLDL GKCKDGKCIP FCEREQQLES CACNETDNSC  600
KVCCRDLSGR CVPYVDAEQK NLFLRKGKPC TVGFCDMNGK CEKRVQDVIE RFWDFIDQLS  660
INTFGKFLAD NIVGSVLVFS LIFWIPFSIL VHCV
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Seq ID NO: 558 DNA sequence
Nucleic Acid Accession #: NM_004994.1
Coding sequence: 20..2143

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CCTGAGAACC AATCTCACCG ACAGGCAGCT GGCAGAGGAA TACCTGTACC GCTATGGTTA   180
CACTCGGGTG GCAGAGATGC GTGGAGAGTC GAAATCTCTG GGGCCTGCGC TGCTGCTTCT   240
CCAGAAGCAA CTGTCCCTGC CCGAGACCGG TGAGCTGGAT AGCGCCACGC TGAAGGCCAT   300
GCGAACCCCA CGGTGCGGGG TCCCAGACCT GGGCAGATTC CAAACCTTTG AGGGCGACCT   360
CAAGTGGCAC CACCACAACA TCACCTATTG GATCCAAAAC TACTCGGAAG ACTTGCCGCG   420
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CACCTTCACT CGCGTGTACA GCCGGGACGC AGACATCGTC ATCCAGTTTG GTGTCGCGGA   540
GCACGGAGAC GGGTATCCCT TCGACGGGAA GGACGGGCTC CTGGCACACG CCTTTCCTCC   600
TGGCCCCGGC ATTCAGGGAG ACGCCCATTT CGACGATGAC GAGTTGTGGT CCCTGGGCAA   660
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CATCTTCGAG GGCCGCTCCT ACTCTGCCTG CACCACCGAC GGTCGCTCCG ACGGCTTGCC   780
CTGGTGCAGT ACCACGGCCA ACTACGACAC CGACGACCGG TTTGGCTTCT GCCCCAGCGA   840
GAGACTCTAC ACCCGGGACG GCAATGCTGA TGGGAAACCC TGCCAGTTTC CATTCATCTT   900
CCAAGGCCAA TCCTACTCCG CCTGCACCAC GGACGGTCGC TCCGACGGCT ACCGCTGGTG   960
CGCCACCACC GCCAACTACG ACCGGGACAA GCTCTTCGGC TTCTGCCCGA CCCGAGCTGA  1020
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GCAGTGCCAT GTAAATCCCC ACTGGGACCA ACCCTGGGGA AGGAGCCAGT TTGCCGGATA  2220
CAAACTGGTA TTCTGTTCTG GAGGAAAGGG AGGAGTGGAG GTGGGCTGGG CCCTCTCTTC  2280
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Seq ID NO: 559 Protein sequence
Protein Accession #: NP_004985.1

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RGESKSLGPA LLLLQKQLSL PETGELDSAT LKAMRTPRCG VPDLGRFQTF EGDLKWHHHN   120
ITYWIQNYSE DLPRAVIDDA FARAFALWSA VTPLTFTRVY SRDADIVIQF GVAEHGDGYP   180
FDGKDGLLAH AFPPGPGIQG DAHFDDDELW SLGKGVVVPT RFGNADGAAC HFPFIFEGRS   240
YSACTTDGRS DGLPWCSTTA NYDTDDRFGF CPSERLYTRD GNADGKPCQF PFIFQGQSYS   300
ACTTDGRSDG YRWCATTANY DRDKLFGFCP TRADSTVMGG NSAGELCVFP FTFLGKEYST   360
CTSEGRGDGR LWCATTSNFD SDKKWGFCPD QGYSLFLVAA HEFGHALGLD HSSVPEALMY   420
PMYRFTEGPP LHKDDVNGIR HLYGPRPEPE PRPPTTTTPQ PTAPPTVCPT GPPTVHPSER   480
PTAGPTGPPS AGPTGPPTAG PSTATTVPLS PVDDACNVNI FDAIAEIGNQ LYLFKDGKYW   540
RFSEGRGSRP QGPFLIADKW PALPRKLDSV FEEPLSKKLF FFSGRQVWVY TGASVLGPRR   600
LDKLGLGADV AQVTGALRSG RGKMLLFSGR RLWRFDVKAQ MVDPRSASEV DRMFPGVPLD   660
THDVFQYREK AYFCQDRFYW RVSSRSELNQ VDQVGYVTYD ILQCPED
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Seq ID NO: 560 DNA sequence
Nucleic Acid Accession #: NM_000213.1
Coding sequence: 127..5385

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AAGAGGATGG CAGGGCCACG CCCCAGCCCA TGGGCCAGGC TGCTCCTGGC AGCCTTGATC   180
AGCGTCAGCC TCTCTGGGAC CTTGGCAAAC CGCTGCAAGA AGGCCCCAGT GAAGAGCTGC   240
ACGGAGTGTG TCCGTGTGGA TAAGGACTGC GCCTACTGCA CAGACGAGAT GTTCAGGGAC   300
CGGCGCTGCA ACACCCAGGC GGAGCTGCTG GCCGCGGGCT GCCAGCGGGA GAGCATCGTG   360
GTCATGGAGA GCAGCTTCCA AATCACAGAG GAGACCCAGA TTGACACCAC CCTGCGGCGC   420
AGCCAGATGT CCCCCCAAGG CCTGCGGGTC CGTCTGCGGC CCGGTGAGGA GCGGCATTTT   480
GAGCTGGAGG TGTTTGAGCC ACTGGAGAGC CCCGTGGACC TGTACATCCT CATGGACTTC   540
TCCAACTCCA TGTCCGATGA TCTGGACAAC CTCAAGAAGA TGGGGCAGAA CCTGGCTCGG   600
GTCCTGAGCC AGCTCACCAG CGACTACACT ATTGGATTTG GCAAGTTTGT GGACAAAGTC   660
AGCGTCCCGC AGACGGACAT GAGGCCTGAG AAGCTGAAGG AGCCCTGGCC CAACAGTGAC   720
CCCCCCTTCT CCTTCAAGAA CGTCATCAGC CTGACAGAAG ATGTGGATGA GTTCCGGAAT   780
AAACTGCAGG GAGAGCGGAT CTCAGGCAAC CTGGATGCTC CTGAGGGCGG CTTCGATGCC   840
ATCCTGCAGA CAGCTGTGTG CACGAGGGAC ATTGGCTGGC GCCCGGACAG CACCCACCTG   900
CTGGTCTTCT CCACCGAGTC AGCCTTCCAC TATGAGGCTG ATGGCGCCAA CGTGCTGGCT   960
GGCATCATGA GCCGCAACGA TGAACGGTGC CACCTGGACA CCACGGGCAC CTACACCCAG  1020
TACAGGACAC AGGACTACCC GTCGGTGCCC ACCCTGGTGC GCCTGCTCGC CAAGCACAAC  1080
ATCATCCCCA TCTTTGCTGT CACCAACTAC TCCTATAGCT ACTACGAGAA GCTTCACACC  1140
TATTTCCCTG TCTCCTCACT GGGGGTGCTG CAGGAGGACT CGTCCAACAT CGTGGAGCTG  1200
CTGGAGGAGG CCTTCAATCG GATCCGCTCC AACCTGGACA TCCGGGCCCT AGACAGCCCC  1260
CGAGGCCTTC GGACAGAGGT CACCTCCAAG ATGTTCCAGA AGACGAGGAC TGGGTCCTTT  1320
CACATCCGGC GGGGGGAAGT GGGTATATAC CAGGTGCAGC TGCGGGCCCT TGAGCACGTG  1380
GATGGGACGC ACGTGTGCCA GCTGCCGGAG GACCAGAAGG GCAACATCCA TCTGAAACCT  1440
TCCTTCTCCG ACGGCCTCAA GATGGACGCG GGCATCATCT GTGATGTGTG CACCTGCGAG  1500
CTGCAAAAAG AGGTGCGGTC AGCTCGCTGC AGCTTCAACG GAGACTTCGT GTGCGGACAG  1560
TGTGTGTGCA GCGAGGGCTG GAGTGGCCAG ACCTGCAACT GCTCCACCGG CTCTCTGAGT  1620
GACATTCAGC CCTGCCTGCG GGAGGGCGAG GACAAGCCGT GCTCCGGCCG TGGGGAGTGC  1680
CAGTGCGGGC ACTGTGTGTG CTACGGCGAA GGCCGCTACG AGGGTCAGTT CTGCGAGTAT  1740
GACAACTTCC AGTGTCCCCG CACTTCCGGG TTCCTCTGCA ATGACCGAGG ACGCTGCTCC  1800
ATGGGCCAGT GTGTGTGTGA GCCTGGTTGG ACAGGCCCAA GCTGTGACTG TCCCCTCAGC  1860
AATGCCACCT GCATCGACAG CAATGGGGGC ATCTGTAATG GACGTGGCCA CTGTGAGTGT  1920
GGCCGCTGCC ACTGCCACCA GCAGTCGCTC TACACGGACA CCATCTGCGA GATCAACTAC  1980
TCGGCGATCC ACCCGGGCCT CTGCGAGGAC CTACGCTCCT GCGTGCAGTG CCAGGCGTGG  2040
GGCACCGGCG AGAAGAAGGG GCGCACGTGT GAGGAATGCA ACTTCAAGGT CAAGATGGTG  2100
GACGAGCTTA AGAGAGCCGA GGAGGTGGTG GTGCGCTGCT CCTTCCGGGA CGAGGATGAC  2160
GACTGCACCT ACAGCTACAC CATGGAAGGT GACGGCGCCC CTGGGCCCAA CAGCACTGTC  2220
CTGGTGCACA AGAAGAAGGA CTGCCCTCCG GGCTCCTTCT GGTGGCTCAT CCCCCTGCTC  2280
CTCCTCCTCC TGCCGCTCCT GGCCCTGCTA CTGCTGCTAT GCTGGAAGTA CTGTGCCTGC  2340
TGCAAGGCCT GCCTGGCACT TCTCCCGTGC TGCAACCGAG GTCACATGGT GGGCTTTAAG  2400
GAAGACCACT ACATGCTGCG GGAGAACCTG ATGGCCTCTG ACCACTTGGA CACGCCCATG  2460
CTGCGCAGCG GGAACCTCAA GGGCCGTGAC GTGGTCCGCT GGAAGGTCAC CAACAACATG  2520
CAGCGGCCTG GCTTTGCCAC TCATGCCGCC AGCATCAACC CCACAGAGCT GGTGCCCTAC  2580
GGGCTGTCCT TGCGCCTGGC CCGCCTTTGC ACCGAGAACC TGCTGAAGCC TGACACTCGG  2640
GAGTGCGCCC AGCTGCGCCA GGAGGTGGAG GAGAACCTGA ACGAGGTCTA CAGGCAGATC  2700
TCCGGTGTAC ACAAGCTCCA GCAGACCAAG TTCCGGCAGC AGCCCAATGC CGGGAAAAAG  2760
CAAGACCACA CCATTGTGGA CACAGTGCTG ATGGCGCCCC GCTCGGCCAA GCCGGCCCTG  2820
CTGAAGCTTA CAGAGAAGCA GGTGGAACAG AGGGCCTTCC ACGACCTCAA GGTGGCCCCC  2880
GGCTACTACA CCCTCACTGC AGACCAGGAC GCCCGGGGCA TGGTGGAGTT CCAGGAGGGC  2940
GTGGAGCTGG TGGACGTACG GGTGCCCCTC TTTATCCGGC CTGAGGATGA CGACGAGAAG  3000
CAGCTGCTGG TGGAGGCCAT CGACGTGCCC GCAGGCACTG CCACCCTCGG CCGCCGCCTG  3060
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GTAAACATCA CCATCATCAA GGAGCAAGCC AGAGACGTGG TGTCCTTTGA GCAGCCTGAG  3120
TTCTCGGTCA GCCGCGGGGA CCAGGTGGCC CGCATCCCTG TCATCCGGCG TGTCCTGGAC  3180
GGCGGGAAGT CCCAGGTCTC CTACCGCACA CAGGATGGCA CCGCGCAGGG CAACCGGGAC  3240
TACATCCCCG TGGAGGGTGA GCTGCTGTTC CAGCCTGGGG AGGCCTGGAA AGAGCTGCAG  3300
GTGAAGCTCC TGGAGCTGCA AGAAGTTGAC TCCCTCCTGC GGGGCCGCCA GGTCCGCCGT  3360
TTCCACGTCC AGCTCAGCAA CCCTAAGTTT GGGGCCCACC TGGGCCAGCC CCACTCCACC  3420
ACCATCATCA TCAGGGACCC AGATGAACTG GACCGGAGCT TCACGAGTCA GATGTTGTCA  3480
TCACAGCCAC CCCCTCACGG CGACCTGGGC GCCCCGCAGA ACCCCAATGC TAAGGCCGCT  3540
GGGTCCAGGA AGATCCATTT CAACTGGCTG CCCCCTTCTG GCAAGCCAAT GGGGTACAGG  3600
GTAAAGTACT GGATTCAGGG TGACTCCGAA TCCGAAGCCC ACCTGCTCGA CAGCAAGGTG  3660
CCCTCAGTGG AGCTCACCAA CCTGTACCCG TATTGCGACT ATGAGATGAA GGTGTGCGCC  3720
TACGGGGCTC AGGGCGAGGG ACCCTACAGC TCCCTGGTGT CCTGCCGCAC CCACCAGGAA  3780
GTGCCCAGCG AGCCAGGGCG TCTGGCCTTC AATGTCGTCT CCTCCACGGT GACCCAGCTG  3840
AGCTGGGCTG AGCCGGCTGA GACCAACGGT GAGATCACAG CCTACGAGGT CTGCTATGGC  3900
CTGGTCAACG ATGACAACCG ACCTATTGGG CCCATGAAGA AAGTGCTGGT TGACAACCCT  3960
AAGAACCGGA TGCTGCTTAT TGAGAACCTT CGGGAGTCCC AGCCCTACCG CTACACGGTG  4020
AAGGCGCGCA ACGGGGCCGG CTGGGGGCCT GAGCGGGAGG CCATCATCAA CCTGGCCACC  4080
CAGCCCAAGA GGCCCATGTC CATCCCCATC ATCCCTGACA TCCCTATCGT GGACGCCCAG  4140
AGCGGGGAGG ACTACGACAG CTTCCTTATG TACAGCGATG ACGTTCTACG CTCTCCATCG  4200
GGCAGCCAGA GGCCCAGCGT CTCCGATGAC ACTGAGCACC TGGTGAATGG CCGGATGGAC  4260
TTTGCCTTCC CGGGCAGCAC CAACTCCCTG CACAGGATGA CCACGACCAG TGCTGCTGCC  4320
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GACACGCCCA CCCGCCTGGT GTTCTCTGCC CTGGGGCCCA CATCTCTCAG AGTGAGCTGG  4560
CAGGAGCCGC GGTGCGAGCG GCCGCTGCAG GGCTACAGTG TGGAGTACCA GCTGCTGAAC  4620
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GACCTCCTGC CCAACCACTC CTACGTGTTC CGCGTGCGGG CCCAGAGCCA GGAAGGCTGG  4740
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TTCACTGCCC TGAGCCCAGA CTCGCTGCAG CTGAGCTGGG AGCGGCCACG GAGGCCCAAT  4920
GGGGATATCG TCGGCTACCT GGTGACCTGT GAGATGGCCC AAGGAGGAGG GCCAGCCACC  4980
GCATTCCGGG TGGATGGAGA CAGCCCCGAG AGCCGGCTGA CCGTGCCGGG CCTCAGCGAG  5040
AACGTGCCCT ACAAGTTCAA GGTGCAGGCC AGGACCACTG AGGGCTTCGG GCCAGAGCGC  5100
GAGGGCATCA TCACCATAGA GTCCCAGGAT GGAGGACCCT TCCCGCAGCT GGGCAGCCGT  5160
GCCGGGCTCT TCCAGCACCC GCTGCAAAGC GAGTACAGCA GCATCACCAC CACCCACACC  5220
AGCGCCACCG AGCCCTTCCT AGTGGATGGG CCGACCCTGG GGGCCCAGCA CCTGGAGGCA  5280
GGCGGCTCCC TCACCCGGCA TGTGACCCAG GAGTTTGTGA GCCGGACACT GACCACCAGC  5340
GGAACCCTTA GCACCCACAT GGACCAACAG TTCTTCCAAA CTTGACCGCA CCCTGCCCCA  5400
CCCCCGCCAT GTCCCACTAG GCGTCCTCCC GACTCCTCTC CCGGAGCCTC CTCAGCTACT  5460
CCATCCTTGC ACCCCTGGGG GCCCAGCCCA CCCGCATGCA CAGAGCAGGG GCTAGGTGTC  5520
TCCTGGGAGG CATGAAGGGG GCAAGGTCCG TCCTCTGTGG GCCCAAACCT ATTTGTAACC  5580
AAAGAGCTGG GAGCAGCACA AGGACCCAGC CTTTGTTCTG CACTTAATAA ATGGTTTTGC  5640
TACTG
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Seq ID NO: 561 Protein sequence
Protein Accession #: NP_000204.1

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MAGPRPSPWA RLLLAALISV SLSGTLANRC KKAPVKSCTE CVRVDKDCAY CTDEMFRDRR    60
CNTQAELLAA GCQRESIVVM ESSFQITEET QIDTTLRRSQ MSPQGLRVRL RPGEERHFEL   120
EVFEPLESPV DLYILMDFSN SMSDDLDNLK KMGQNLARVL SQLTSDYTIG FGKFVDKVSV   180
PQTDMRPEKL KEPWPNSDPP FSFKNVISLT EDVDEFRNKL QGERISGNLD APEGGFDAIL   240
QTAVCTRDIG WRPDSTHLLV FSTESAFHYE ADGANVLAGI MSRNDERCHL DTTGTYTQYR   300
TQDYPSVPTL VRLLAKHNII PIFAVTNYSY SYYEKLHTYF PVSSLGVLQE DSSNIVELLE   360
EAFNRIRSNL DIRALDSPRG LRTEVTSKMF QKTRTGSFHI RRGEVGIYQV QLRALEHVDG   420
THVCQLPEDQ KGNIHLKPSF SDGLKMDAGI ICDVCTCELQ KEVRSARCSF NGDFVCGQCV   480
CSEGWSGQTC NCSTGSLSDI QPCLREGEDK PCSGRGECQC GHCVCYGEGR YEGQFCEYDN   540
FQCPRTSGFL CNDRGRCSMG QCVCEPGWTG PSCDCPLSNA TCIDSNGGIC NGRGHCECGR   600
CHCHQQSLYT DTICEINYSA IHPGLCEDLR SCVQCQAWGT GEKKGRTCEE CNFKVKMVDE   660
LKRAEEVVVR CSFRDEDDDC TYSYTMEGDG APGPNSTVLV HKKKDCPPGS FWWLIPLLLL   720
LLPLLALLLL LCWKYCACCK ACLALLPCCN RGHMVGFKED HYMLRENLMA SDHLDTPMLR   780
SGNLKGRDVV RWKVTNNMQR PGFATHAASI NPTELVPYGL SLRLARLCTE NLLKPDTREC   840
AQLRQEVEEN LNEVYRQISG VHKLQQTKFR QQPNAGKKQD HTIVDTVLMA PRSAKPALLK   900
LTEKQVEQRA FHDLKVAPGY YTLTADQDAR GMVEFQEGVE LVDVRVPLFI RPEDDDEKQL   960
LVEAIDVPAG TATLGRRLVN ITIIKEQARD VVSFEQPEFS VSRGDQVARI PVIRRVLDGG  1020
KSQVSYRTQD GTAQGNRDYI PVEGELLFQP GEAWKELQVK LLELQEVDSL LRGRQVRRFH  1080
VQLSNPKFGA HLGQPHSTTI IIRDPDELDR SFTSQMLSSQ PPPHGDLGAP QNPNAKAAGS  1140
RKIHFNWLPP SGKPMGYRVK YWIQGDSESE AHLLDSKVPS VELTNLYPYC DYEMKVCAYG  1200
AQGEGPYSSL VSCRTHQEVP SEPGRLAFNV VSSTVTQLSW AEPAETNGEI TAYEVCYGLV  1260
NDDNRPIGPM KKVLVDNPKN RMLLIENLRE SQPYRYTVKA RNGAGWGPER EAIINLATQP  1320
KRPMSIPIIP DIPIVDAQSG EDYDSFLMYS DDVLRSPSGS QRPSVSDDTE HLVNGRMDFA  1380
FPGSTNSLHR MTTTSAAAYG THLSPHVPHR VLSTSSTLTR DYNSLTRSEH SHSTTLPRDY  1440
STLTSVSSHD SRLTAGVPDT PTRLVFSALG PTSLRVSWQE PRCERPLQGY SVEYQLLNGG  1500
ELHRLNIPNP AQTSVVVEDL LPNHSYVFRV RAQSQEGWGR EREGVITIES QVHPQSPLCP  1560
LPGSAFTLST PSAPGPLVFT ALSPDSLQLS WERPRRPNGD IVGYLVTCEM AQGGGPATAF  1620
RVDGDSPESR LTVPGLSENV PYKFKVQART TEGFGPEREG IITIESQDGG PFPQLGSRAG  1680
LPQHPLQSEY SSITTTHTSA TEPFLVDGPT LGAQHLEAGG SLTRHVTQEF VSRTLTTSGT  1740
LSTHMDQQFF QT
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Seq ID NO: 562 DNA sequence
Nucleic Acid Accession #: NM_013332.1
Coding sequence: 1..63

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1          11         21         31         41         51
|          |          |          |          |          |
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GCACGAGGGC GCTTTTGTCT CCGGTGAGTT TTGTGGCGGG AAGCTTCTGC GCTGGTGCTT     60
AGTAACCGAC TTTCCTCCGG ACTCCTGCAC GACCTGCTCC TACAGCCGGC GATCCACTCC    120
CGGCTGTTCC CCCGGAGGGT CCAGAGGCCT TTCAGAAGGA GAAGGCAGCT CTGTTTCTCT    180
GCAGAGGAGT AGGGTCCTTT CAGCCATGAA GCATGTGTTG AACCTCTACC TGTTAGGTGT    240
GGTACTGACC CTACTCTCCA TCTTCGTTAG AGTGATGGAG TCCCTAGAAG GCTTACTAGA    300
GAGCCCATCG CCTGGGACCT CCTGGACCAC CAGAAGCCAA CTAGCCAACA CAGAGCCCAC    360
CAAGGGCCTT CCAGACCATC CATCCAGAAG CATGTGATAA GACCTCCTTC CATACTGGCC    420
ATATTTTGGA ACACTGACCT AGACATGTCC AGATGGGAGT CCCATTCCTA GCAGACAAGC    480
TGAGCACCGT TGTAACCAGA GAACTATTAC TAGGCCTTGA AGAACCTGTC TAACTGGATG    540
CTCATTGCCT GGGCAAGGCC TGTTTAGGCC GGTTGCGGTG GCTCATGCCT GTAATCCTAG    600
CACTTTGGGA GGCTGAGGTG GGTGGATCAC CTGAGGTCAG GAGTTCGAGA CCAGCCTCGC    660
CAACATGGCG AAACCCCATC TCTACTAAAA ATACAAAAGT TAGCTGGGTG TGGTGGCAGA    720
GGCCTGTAAT CCCAGTTCCT TGGGAGGCTG AGGCGGGAGA ATTGCTTGAA CCCGGGGACG    780
GAGGTTGCAG TGAACCGAGA TCGCACTGCT GTACCCAGCC TGGGCCACAG TGCAAGACTC    840
CATCTCAAAA AAAAAAAGAA AAGAAAAAGC CTGTTTAATG CACAGGTGTG AGTGGATTGC    900
TTATGGCTAT GAGATAGGTT GATCTCGCCC TTACCCCGGG GTCTGGTGTA TGCTGTGCTT    960
TCCTCAGCAG TATGGCTCTG ACATCTCTTA GATGTCCCAA CTTCAGCTGT TGGGAGATGG   1020
TGATATTTTC AACCCTACTT CCTAAACATC TGTCTGGGGT TCCTTTAGTC TTGAATGTCT   1080
TATGCTCAAT TATTTGGTGT TGAGCCTCTC TTCCACAAGA GCTCCTCCAT GTTTGGATAG   1140
CAGTTGAAGA GGTTGTGTGG GTGGGCTGTT GGGAGTGAGG ATGGAGTGTT CAGTGCCCAT   1200
TTCTCATTTT ACATTTTAAA GTCGTTCCTC CAACATAGTG TGTATTGGTC TGAAGGGGGT   1260
GGTGGGATGC CAAAGCCTGC TCAAGTTATG GACATTGTGG CCACCATGTG GCTTAAATGA   1320
TTTTTTCTAA CTAATAAAGT GGAATATATA TTTCAAAAAA AAAAAAAAAA AA
```

Seq ID NO: 563 Protein sequence
Protein Accession #: NP_037464.1

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1          11         21         31         41         51
|          |          |          |          |          |
MKHVLNLYLL GVVLTLLSIF VRVMESLEGL LESPSPGTSW TTRSQLANTE PTKGLPDHPS     60
RSM
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Seq ID NO: 564 DNA sequence
Nucleic Acid Accession #: NM_023915.1
Coding sequence: 250..1326

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1          11         21         31         41         51
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TCAAAGCTTA TTCTTAATTA GAGACAAGAA ACCTGTTTCA ACTTGAAGAC ACCGTATGAG    120
GTGAATGGAC AGCCAGCCAC CACAATGAAA GAAATCAAAC CAGGAATAAC CTATGCTGAA    180
CCCACGCCTC AATCGTCCCC AAGTGTTTCC TGACACGCAT CTTTGCTTAC AGTGCATCAC    240
AACTGAAGAA TGGGGTTCAA CTTGACGCTT GCAAAATTAC CAAATAACGA GCTGCACGGC    300
CAAGAGAGTC ACAATTCAGG CAACAGGAGC GACGGGCCAG GAAAGAACAC CACCCTTCAC    360
AATGAATTTG ACACAATTGT CTTGCCGGTG CTTTATCTCA TTATATTTGT GGCAAGCATC    420
TTGCTGAATG GTTTAGCAGT GTGGATCTTC TTCCACATTA GGAATAAAAC CAGCTTCATA    480
TTCTATCTCA AAAACATAGT GGTTGCAGAC CTCATAATGA CGCTGACATT TCCATTTCGA    540
ATAGTCCATG ATGCAGGATT TGGACCTTGG TACTTCAAGT TTATTCTCTG CAGATACACT    600
TCAGTTTTGT TTTATGCAAA CATGTATACT TCCATCGTGT TCCTTGGGCT GATAAGCATT    660
GATCGCTATC TGAAGGTGGT CAAGCCATTT GGGGACTCTC GGATGTACAG CATAACCTTC    720
ACGAAGGTTT TATCTGTTTG TGTTTGGGTG ATCATGGCTG TTTTGTCTTT GCCAAACATC    780
ATCCTGACAA ATGGTCAGCC AACAGAGGAC AATATCCATG ACTGCTCAAA ACTTAAAAGT    840
CCTTTGGGGG TCAAATGGCA TACGGCAGTC ACCTATGTGA ACAGCTGCTT GTTTGTGGCC    900
GTGCTGGTGA TTCTGATCGG ATGTTACATA GCCATATCCA GGTACATCCA CAAATCCAGC    960
AGGCAATTCA TAAGTCAGTC AAGCCGAAAG CGAAAACATA ACCAGAGCAT CAGGGTTGTT   1020
GTGGCTGTGT TTTTTACCTG CTTTCTACCA TATCACTTGT GCAGAATTCC TTTTACTTTT   1080
AGTCACTTAG ACAGGCTTTT AGATGAATCT GCACAAAAAA TCCTATATTA CTGCAAAGAA   1140
ATTACACTTT TCTTGTCTGC GTGTAATGTT TGCCTGGATC CAATAATTTA CTTTTTCATG   1200
TGTAGGTCAT TTTCAAGAAG GCTGTTCAAA AAATCAAATA TCAGAACCAG GAGTGAAAGC   1260
ATCAGATCAC TGCAAAGTGT GAGAAGATCG GAAGTTCGCA TATATTATGA TTACACTGAT   1320
GTGTAGGCCT TTTATTGTTT GTTGGAATCG ATATGTACAA AGTGTAAATA AATGTTTCTT   1380
TTCATTATCC TTAAAAAAAA AA
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Seq ID NO: 565 Protein sequence
Protein Accession #: NP_076404

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1          11         21         31         41         51
|          |          |          |          |          |
MGFNLTLAKL PNNELHGQES HNSGNRSDGP GKNTTLHNEF DTIVLPVLYL IIFVASILLN     60
GLAVWIFFHI RNKTSFIFYL KNIVVADLIM TLTFPFRIVH DAGFGPWYFK FILCRYTSVL    120
FYANMYTSIV FLGLISIDRY LKVVKPFGDS RMYSITFTKV LSVCVWVIMA VLSLPNIILT    180
NGQPTEDNIH DCSKLKSPLG VKWHTAVTYV NSCLFVAVLV ILIGCYIAIS RYIHKSSRQF    240
ISQSSRKRKH NQSIRVVVAV FFTCFLPYHL CRIPFTFSHL DRLLDESAQK ILYYCKEITL    300
FLSACNVCLD PIIYFFMCRS FSRRLFKKSN IRTRSESIRS LQSVRRSEVR IYYDYTDV
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Seq ID NO: 566 DNA sequence
Nucleic Acid Accession #: NM_005365.1
Coding sequence: 1..948

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1          11         21         31         41         51
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GAGGACTTGG GCCTGATGGG TGCACAGGAA CCCACAGGCG AGGAGGAGGA GACTACCTCC    120
TCCTCTGACA GCAAGGAGGA GGAGGTGTCT GCTGCTGGGT CATCAAGTCC TCCCCAGAGT    180
CCTCAGGGAG GCGCTTCCTC CTCCATTTCC GTCTACTACA CTTTATGGAG CCAATTCGAT    240
GAGGGCTCCA GCAGTCAAGA AGAGGAAGAG CCAAGCTCCT CGGTCGACCC AGCTCAGCTG    300
GAGTTCATGT TCCAAGAAGC ACTGAAATTG AAGGTGGCTG AGTTGGTTCA TTTCCTGCTC    360
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CACAAATATC GAGTCAAGGA GCCGGTCACA AAGGCAGAAA TGCTGGAGAG CGTCATCAAA   420
AATTACAAGC GCTACTTTCC TGTGATCTTC GGCAAAGCCT CCGAGTTCAT GCAGGTGATC   480
TTTGGCACTG ATGTGAAGGA GGTGGACCCC GCCGGCCACT CCTACATCCT TGTCACTGCT   540
CTTGGCCTCT CGTGCGATAG CATGCTGGGT GATGGTCATA GCATGCCCAA GGCCGCCCTC   600
CTGATCATTG TCCTGGGTGT GATCCTAACC AAAGACAACT GCGCCCCTGA AGAGGTTATC   660
TGGGAAGCGT TGAGTGTGAT GGGGGTGTAT GTTGGGAAGG AGCACATGTT CTACGGGGAG   720
CCCAGGAAGC TGCTCACCCA AGATTGGGTG CAGGAAAACT ACCTGGAGTA CCGGCAGGTG   780
CCCGGCAGTG ATCCTGCGCA CTACGAGTTC CTGTGGGGTT CCAAGGCCCA CGCTGAAACC   840
AGCTATGAGA AGGTCATAAA TTATTTGGTC ATGCTCAATG CAAGAGAGCC CATCTGCTAC   900
CCATCCCTTT ATGAAGAGGT TTTGGGAGAG GAGCAAGAGG GAGTCTGA
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Seq ID NO: 567 Protein sequence
Protein Accession #: NP_005356.1

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1          11         21         31         41         51
|          |          |          |          |          |
MSLEQRSPHC KPDEDLEAQG EDLGLMGAQE PTGEEEETTS SSDSKEEEVS AAGSSSPPQS    60
PQGGASSSIS VYYTLWSQFD EGSSSQEEEE PSSSVDPAQL EFMFQEALKL KVAELVHFLL   120
HKYRVKEPVT KAEMLESVIK NYKRYFPVIF GKASEFMQVI FGTDVKEVDP AGHSYILVTA   180
LGLSCDSMLG DGHSMPKAAL LIIVLGVILT KDNCAPEEVI WEALSVMGVY VGKEHMFYGE   240
PRKLLTQDWV QENYLEYRQV PGSDPAHYEF LWGSKAHAET SYEKVINYLV MLNAREPICY   300
PSLYEEVLGE EQEGV
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Seq ID NO: 568 DNA sequence
Nucleic Acid Accession #: NM_014400
Coding sequence: 86..1126

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1          11         21         31         41         51
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GACGCCAAGG GAGCAGGACG GAGCCATGGA CCCCGCCAGG AAAGCAGGTG CCCAGGCCAT   120
GATCTGGACT GCAGGCTGGC TGCTGCTGCT GCTGCTTCGC GGAGGAGCGC AGGCCCTGGA   180
GTGCTACAGC TGCGTGCAGA AAGCAGATGA CGGATGCTCC CCGAACAAGA TGAAGACAGT   240
GAAGTGCGCG CCGGGCGTGG ACGTCTGCAC CGAGGCCGTG GGGGCGGTGG AGACCATCCA   300
CGGACAATTC TCGCTGGCAG TGCSGGGTTG CGGTTCGGGA CTCCCCGGCA AGAATGACCG   360
CGGCCTGGAT CTTCACGGGC TTCTGGCGTT CATCCAGCTG CAGCAATGCG CTCAGGATCG   420
CTGCAACGCC AAGCTCAACC TCACCTCGCG GGCGCTCGAC CCGGCAGGTA ATGAGAGTGC   480
ATACCCGCCC AACGGCGTGG AGTGCTACAG CTGTGTGGGC CTGAGCCGGG AGGCGTGCCA   540
GGGTACATCG CCGCCGGTCG TGAGCTGCTA CAACGCCAGC GATCATGTCT ACAAGGGCTG   600
CTTCGACGGC AACGTCACCT TGACGGCAGC TAATGTGACT GTGTCCTTGC CTGTCCGGGG   660
CTGTGTCCAG GATGAATTCT GCACTCGGGA TGGAGTAACA GGCCCAGGGT TCACGCTCAG   720
TGGCTCCTGT TGCCAGGGGT CCCGCTGTAA CTCTGACCTC CGCAACAAGA CCTACTTCTC   780
CCCTCGAATC CCACCCCTTG TCCGGCTGCC CCCTCCAGAG CCCACGACTG TGGCCTCAAC   840
CACATCTGTC ACCACTTCTA CCTCGGCCCC AGTGAGACCC ACATCCACCA CCAAACCCAT   900
GCCAGCGCCA ACCAGTCAGA CTCCGAGACA GGGAGTAGAA CACGAGGCCT CCCGGGATGA   960
GGAGCCCAGG TTGACTGGAG GCGCCGCTGG CCACCAGGAC CGCAGCAATT CAGGGCAGTA  1020
TCCTGCAAAA GGGGGGCCCC AGCAGCCCCA TAATAAAGGC TGTGTGGCTC CCACAGCTGG  1080
ATTGGCAGCC CTTCTGTTGG CCGTGGCTGC TGGTGTCCTA CTGTGAGCTT CTCCACCTGG  1140
AAATTTCCCT CTCACCTACT TCTCTGGCCC TGGGTACCCC TCTTCTCATC ACTTCCTGTT  1200
CCCACCACTG GACTGGGCTG GCCCAGCCCC TGTTTTTCCA ACATTCCCCA GTATCCCCAG  1260
CTTCTGCTGC GCTGGTTTGC GGCTTTGGGA AATAAAATAC CGTTGTATAT ATTCTGGCAG  1320
GGGTGTTCTA GCTTTTTGAG GACAGCTCCT GTATCCTTCT CATCCTTGTC TCTCCGCTTG  1380
TCCTCTTGTG ATGTTAGGAC AGAGTGAGAG AAGTCAGCTG TCACGGGGAA GGTGAGAGAG  1440
AGGATGCTAA GCTTCCTACT CACTTTCTCC TAGCCAGCCT GGACTTTGGA GCGTGGGGTG  1500
GGTGGGACAA TGGCTCCCCA CTCTAAGCAC TGCCTCCCCT ACTCCCCGCA TCTTTGGGGA  1560
ATCGGTTCCC CATATGTCTT CCTTACTAGA CTGTGAGCTC CTCGAGGGCA GGGACCGTGC  1620
CTTATGTCTG TGTGTGATCA GTTTCTGGCA CATAAATGCC TCAATAAAGA TTTAATTACT  1680
TTGTATAGTG AAAAAAAA
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Seq ID NO: 569 Protein sequence
Protein Accession #: NP_055215

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SRALDPAGNE SAYPPNGVEC YSCVGLSREA CQGTSPPVVS CYNASDHVYK GCFDGNVTLT   180
AANVTVSLPV RGCVQDEFCT RDGVTGPGFT LSGSCCQGSR CNSDLRNKTY FSPRIPPLVR   240
LPPPEPTTVA STTSVTTSTS APVRPTSTTK PMPAPTSQTP RQGVEHEASR DEEPRLTGGA   300
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Seq ID NO: 570 DNA sequence
Nucleic Acid Accession #: NM_005329.1
Coding sequence: 1..1662

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CACTACCTGT CCTTCGGCCT GTACGGCGCC ATCCTGGGCC TGCACCTGCT CATTCAGAGC   180
CTTTTTGCCT TCCTGGAGCA CCGGCGCATG CGACGTGCCG GCCAGGCCCT GAAGCTGCCC   240
TCCCCGCGGC GGGGCTCGGT GGCACTGTGC ATTGCCGCGT ACCAGGAGGA CCCTGACTAC   300
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GGCGGCACCG AGCAGGCCGG CTTCTTTGTG TGGCGCAGCA ACTTCCATGA GGCAGGCGAG   480
GGTGAGACGG AGGCCAGCCT GCAGGAGGGC ATGGACCGTG TGCGGGATGT GGTGCGGGCC   540
AGCACCTTCT CGTGCATCAT GCAGAAGTGG GGAGGCAAGC GCGAGGTCAT GTACACGGCC   600
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ACAGAGACCC CCACTAAGTA CCTCCGGTGG CTCAACCAGC AAACCCGCTG GAGCAAGTCT   1080
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TGCCAGGACC TGTTCAGTGA GACAGAGCTA GCCTTCCTTG TCTCTGGGGC TATACTGTAT   1560
GGCTGCTACT GGGTGGCCCT CCTCATGCTA TATCTGGCCA TCATCGCCCG GCGATGTGGG   1620
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Seq ID NO: 571 Protein sequence
Protein Accession #: NP_005320.1

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STFSCIMQKW GGKREVMYTA FKALGDSVDY IQVCDSDTVL DPACTIEMLR VLEEDPQVGG    240
VGGDVQILNK YDSWISFLSS VRYWMAFNVE RACQSYFGCV QCISGPLGMY RNSLLQQFLE    300
DWYHQKFLGS KCSFGDDRHL TNRVLSLGYR TKYTARSKCL TETPTKYLRW LNQQTRWSKS    360
YFREWLYNSL WFHKHHLWMT YESVVTGFFP FFLIATVIQL FYRGRIWNIL LFLLTVQLVG    420
IIKATYACFL RGNAEMIFMS LYSLLYMSSL LPAKIFAIAT INKSGWGTSG RKTIVVNFIG    480
LIPVSIWVAV LLGGLAYTAY CQDLFSETEL AFLVSGAILY GCYWVALLML YLAIIARRCG    540
KKPEQYSLAF AEV
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Seq ID NO: 572 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 148-7095

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CAGCTCCTCT GTGTTTGCCG CCTGGATTGG GCTAATGGAT ACTACAGACA ACAGAGAAAA    240
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AAATATCCAA CATGTAATAG CCCAAAACAA TCTCCTATCA ATATTGATGA AGATCTTACA    360
CAAGTAAATG TGAATCTTAA GAAACTTAAA TTTCAGGGTT GGGATAAAAC ATCATTGGAA    420
AACACATTCA TTCATAACAC TGGGAAAACA GTGGAAATTA ATCTCACTAA TGACTACCGT    480
GTCAGCGGAG GAGTTTCAGA AATGGTGTTT AAAGCAAGCA AGATAACTTT TCACTGGGGA    540
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AGTTCAGAAC CAGAAAATGT TCAGGCTGAC CCAGAGAATT ATACCAGCCT TCTTGTTACA   1140
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Seq ID NO: 573 Protein sequence:
Protein Accession #: Eos sequence

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ILFEVGTEEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYYI YNGSLTSPPC    240
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Seq ID NO: 574 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 148-4518

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Nucleic Acid Accession #: EOS sequence
Coding sequence: 148-4494

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Seq ID NO: 579 Protein sequence:
Protein Accession #: EOS sequence

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Seq ID NO: 580 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 148-4632

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Seq ID NO: 581 Protein sequence:
Protein Accession #: EOS sequence

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Seq ID NO: 582 DNA sequence
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TGCTGGCCCA GGGACAGGTG GTGGAGTTTG ACACCCCATC GGTCCTTCTG TCCAACGACA 4380
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Seq ID NO: 585 Protein sequence
Protein Accession #: NP_005679.1

1 11 21 31 41 51
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VLTYIKFIKM YAWVKAFSQS VQKIREEERR ILEKAGYFQG ITVGVAPIVV VIASVVTFSV 420
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FNNLLLGETP PVEINSKKET SGSQKKSQDK GPKTGSVKKE KAVKPEEGQL VQLEEKGQGS 840

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LDDNQAPFFL FTCAMRWLAV RLDLISIALI TTTGLMIVLM HGQIPPAYAG LAISYAVQLT  1140
GLFQFTVRLA SETEARFTSV ERINHYIKTL SLEAPARIKN KAPSPDWPQE GEVTFENAEM  1200
RYRENLPLVL KKVSFTIKPK EKIGIVGRTG SGKSSLGMAL FRLVELSGGC IKIDGVRISD  1260
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SEVMENGDNF SVGERQLLCI ARALLRHCKI LILDEATAAM DTETDLLIQE TIREAFADCT  1380
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Seq ID NO: 586 DNA sequence
Nucleic Acid Accession #: NM_001327.1
Coding sequence: 89..631

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GACGGGCGAT GCTGATGGCC CAGGAGGCCC TGGCATTCCT GATGGCCCAG GGGCAATGC    180
TGGCGGCCCA GGAGAGGCGG GTGCCACGGG CGGCAGAGGT CCCCGGGGCG CAGGGGCAGC   240
AAGGGCCTCG GGGCCGGGAG GAGGCGCCCC GCGGGGTCCG CATGGCGGCG CGGCTTCAGG   300
GCTGAATGGA TGCTGCAGAT GCGGGGCCAG GGGGCCGGAG AGCCGCCTGC TTGAGTTCTA   360
CCTCGCCATG CCTTTCGCGA CACCCATGGA AGCAGAGCTG GCCCGCAGGA GCCTGGCCCA   420
GGATGCCCCA CCGCTTCCCG TGCCAGGGGT GCTTCTGAAG GAGTTCACTG TGTCCGGCAA   480
CATACTGACT ATCCGACTGA CTGCTGCAGA CCACCGCCAA CTGCAGCTCT CCATCAGCTC   540
CTGTCTCCAG CAGCTTTCCC TGTTGATGTG GATCACGCAG TGCTTTCTGC CCGTGTTTTT   600
GGCTCAGCCT CCCTCAGGGC AGAGGCGCTA AGCCCAGCCT GGCGCCCCTT CCTAGGTCAT   660
GCCTCCTCCC CTAGGGAATG GTCCCAGCAC GAGTGGCCAG TTCATTGTGG GGGCCTGATT   720
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Seq ID NO: 587 Protein sequence
Protein Accession #: NP_001318.1

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Seq ID NO: 588 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 52..459

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CCTGATGGCC CAGGGGGCAA TGCTGGCGGC CCAGGAGAGG CGGGTGCCAC GGGCGGCAGA   180
GGTCCCCGGG GCGCAGGGGC AGCAAGGGCC TCGGGGCCGA GAGGAGGCGC CCCGCGGGGT   240
CCGCATGGCG GTGCCGCTTC TGCGCAGGAT GGAAGGTGCC CCTGCGGGGC CAGGAGGCCG   300
GACAGCCGCC TGCTTCAGTT CCGACTGACT GCTGCAGACC ACCGCCAACT GCAGCTCTCC   360
ATCAGCTCCT GTCTCCAGCA GCTTTCCCTG TTGATGTGGA TCACGCAGTG CTTTCTGCCC   420
GTGTTTTTGG CTCAGGCTCC CTCAGGGCAG AGGCGCTAAG CCCAGCCTGG CGCCCCTTCC   480
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GCCTGATTGT TTGTCGCTGG AGGAGGACGG CTTACATGTT TGTTTCTGTA GAAAATAAAG   600
CTGAGCTA
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Seq ID NO: 589 Protein sequence
Protein Accession #: Eos sequence

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PRGPHGGAAS AQDGRCPCGA RRPDSRLLQF RLTAADHRQL QLSISSCLQQ LSLLMWITQC   120
FLPVFLAQAP SGQRR
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Seq ID NO: 590 DNA sequence
Nucleic Acid Accession #: NM_005562.1
Coding sequence: 90..3671

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GCTTCTCGCT CCTCCTGCCC GCAGCCCGGG CCACCTCCAG GAGGGAAGTC TGTGATTGCA   180
ATGGGAAGTC CAGGCAGTGT ATCTTTGATC GGGAACTTCA CAGACAAACT GGTAATGGAT   240
TCCGCTGCCT CAACTGCAAT GACAACACTG ATGGCATTCA CTGCGAGAAG TGCAAGAATG   300
GCTTTTACCG GCACAGAGAA AGGGACCGCT GTTTGCCCTG CAATTGTAAC TCCAAAGGTT   360
CTCTTAGTGC TCGATGTGAC AACTCTGGAC GGTGCAGCTG TAAACCAGGT GTGACAGGAG   420
CCAGATGCGA CCGATGTCTG CCAGGCTTCC ACATGCTCAC GGATGCGGGG TGCACCCAAG   480
ACCAGAGACT GCTAGACTCC AAGTGTGACT GTGACCCAGC TGGCATCGCA GGGCCCTGTG   540
ACGCGGGCCG CTGTGTCTGC AAGCCAGCTG TTACTGGAGA ACGCTGTGAT AGGTGTCGAT   600
CAGGTTACTA TAATCTGGAT GGGGGAACC CTGAGGGCTG TACCCAGTGT TTCTGCTATG    660
GGCATTCAGC CAGCTGCCGC AGCTCTGCAG AATACAGTGT CCATAAGATC ACCTCTACCT   720
TTCATCAAGA TGTTGATGGC TGGAAGGCTG TCCAACGAAA TGGGTCTCCT GCAAAGCTCC   780
AATGGTCACA GCGCCATCAA GATGTGTTTA GCTCAGCCCA ACGACTAGAC CCTGTCTATT   840
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CAATTGTTAG ATGCC

Seq ID NO: 591 Protein sequence
Protein Accession #: NP_005553.1

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PEGCTQCFCY GHSASCRSSA EYSVHKITST FHQDVDGWKA VQRNGSPAKL QWSQRHQDVF 240
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MPLGKTLPCG LTKTYTFRLN EHPSNNWSPQ LSYFEYRRLL RNLTALRIRA TYGEYSTGYI 360
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GGACDPDTGD CYSGDENPDI ECADCPIGFY NDPHDPRSCK PCPCHNGPSC SVMPETEEVV 480

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Seq ID NO: 592 DNA sequence
Nucleic Acid Accession #: AF101051.1
Coding sequence: 221.856

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GATAATCTGG TGACAAATAT TCTCTCTGTA GCTGTAAGCA AGTCACTTAA TCTTTCTACC   1980
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AATATTAATT AGTTTATATT ACTCTCATTC TTTGAACATG AACTATGCCT ATGTAGTGTC   2100
TTTATTTGCT CAGCTGGCTG AGACACTGAA GAAGTCACTG AACAAAACCT ACACACGTAC   2160
CTTCATGTGA TTCACTGCCT TCCTCTCTCT ACCAGTCTAT TTCCACTGAA CAAAACCTAC   2220
ACACATACCT TCATGTGGTT CAGTGCCTTC CTCTCTCTAC CAGTCTATTT CCACTGAACA   2280
AAACCTACGC ACATACCTTC ATGTGGCTCA GTGCCTTCCT CTCTCTACCA GTCTATTTCC   2340
ATTCTTTCAG CTGTGTCTGA CATGTTTGTG CTCTGTTCCA TTTTAACAAC TGCTCTTACT   2400
TTTCCAGTCT GTACAGAATG CTATTTCACT TGAGCAAGAT GATGTATGGA AAGGGTGTTG   2460
GCACTGGTGT CTGGAGACCT GGATTTGAGT CTTGGTGCTA TCAATCACCG TCTGTGTTTG   2520
AGCAAGGCAT TTGGCTGCTG TAAGCTTATT GCTTCATCTG TAAGCGGTGG TTTGTAATTC   2580
CTGATCTTCC CACCTCACAG TGATGTTGTG GGGATCCAGT GAGATAGAAT ACATGTAAGT   2640
GTGGTTTTGT AATTTGAAAA GTGCTATACT AAGGGAAAGA ATTGAGGAAT TAACTGCATA   2700
CGTTTTGGTG TTGCTTTTCA AATGTTTGAA AATAAAAAAA TGTTAAGAAA TGGGTTTCTT   2760
GCCTTAACCA GTCTCTCAAG TGATGAGACA GTGAAGTAAA ATTGAGTGCA CTAAACGAAT   2820
AAGATTCTGA GGAAGTCTTA TCTTCTGCAG TGAGTATGGC CCAATGCTTT CTGTGGCTAA   2880
ACAGATGTAA TGGGAAGAAA TAAAAGCCTA CGTGTTGGTA AATCCAACAG CAAGGGAGAT   2940
TTTTGAATCA TAATAACTCA TAAGGTGCTA TCTGTTCAGT GATGCCCTCA GAGCTCTTGC   3000
TGTTAGCTGG CAGCTGACGC TGCTAGGATA GTTAGTTTGG AAATGGTACT TCATAATAAA   3060
CTACACAAGG AAAGTCAGCC ACCGTGTCTT ATGAGGAATT GGACCTAATA AATTTTAGTG   3120
TGCCTTCCAA ACCTGAGAAT ATATGCTTTT GGAAGTTAAA ATTTAAATGG CTTTTGCCAC   3180
ATACATAGAT CTTCATGATG TGTGAGTGTA ATTCCATGTG GATATCAGTT ACCAAACATT   3240
ACAAAAAAAT TTTATGGCCC AAAATGACCA ACGAAATTGT TACAATAGAA TTTATCCAAT   3300
TTTGATCTTT TTATATTCTT CTACCACACC TGGAAACAGA CCAATAGACA TTTTGGGGTT   3360
TTATAATGGG AATTTGTATA AAGCATTACT CTTTTTCAAT AAATTGTTTT TTAATTTAAA   3420
AAAAGGAAAA AAAAAAAAAA AAA
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Seq ID NO: 593 Protein sequence
Protein Accession #: AAD16433.1

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QIQCKVFDSL LNLSSTLQAT RALMVVGILL GVIAIFVATV GMKCMKCLED DEVQKMRMAV    120
IGGAIFLLAG LAILVATAWY GNRIVQEFYD PMTPVNARYE FGQALFTGWA AASLCLLGGA    180
LLCCSCPRKT TSYPTPRPYP KPAPSSGKDY V
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Seq ID NO: 594 DNA sequence
Nucleic Acid Accession #: NM_006180.1
Coding sequence: 352..2820

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CCCCCTGTAA AGCGGTTCGC TATGCCGGGA CCACTGTGAA CCCTGCCGCC TGCCGGAACA  180
CTCTTCGCTC CGGACCAGCT CAGCCTCTGA TAAGCTGGAC TCGGCACGCC CGCAACAAGC  240
ACCGAGGAGT TAAGAGAGCC GCAAGCGCAG GGAAGGCCTC CCCGCACGGG TGGGGGAAAG  300
CGGCCGGTGC AGCGCGGGGA CAGGCACTCG GGCTGGCACT GGCTGCTAGG GATGTCGTCC  360
TGGATAAGGT GGCATGGACC CGCCATGGCG CGGCTCTGGG GCTTCTGCTG GCTGGTTGTG  420
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GATCCTGAGA ACATCACCGA AATTTTCATC GCAAACCAGA AAAGGTTAGA AATCATCAAC  600
GAAGATGATG TTGAAGCTTA TGTGGGACTG AGAAATCTGA CAATTGTGGA TTCTGGATTA  660
AAATTTGTGG CTCATAAAGC ATTTCTGAAA AACAGCAACC TGCAGCACAT CAATTTTACC  720
CGAAACAAAC TGACGAGTTT GTCTAGGAAA CATTTCCGTC ACCTTGACTT GTCTGAACTG  780
ATCCTGGTGG GCAATCCATT TACATGCTCC TGTGACATTA TGTGGATCAA GACTCTCCAA  840
GAGGCTAAAT CCAGTCCAGA CACTCAGGAT TTGTACTGCC TGAATGAAAG CAGCAAGAAT  900
ATTCCCCTGG CAAACCTGCA GATACCCAAT TGTGGTTTGC CATCTGCAAA TCTGGCCGCA  960
CCTAACCTCA CTGTGGAGGA AGGAAAGTCT ATCACATTAT CCTGTAGTGT GGCAGGTGAT 1020
CCGGTTCCTA ATATGTATTG GGATGTTGGT AACCTGGTTT CCAAACATAT GAATGAAACA 1080
AGCCACACAC AGGGCTCCTT AAGGATAACT AACATTTCAT CCGATGACAG TGGGAAGCAG 1140
ATCTCTTGTG TGGCGGAAAA TCTTGTAGGA GAAGATCAAG ATTCTGTCAA CCTCACTGTG 1200
CATTTTGCAC CAACTATCAC ATTTCTCGAA TCTCCAACCT CAGACCACCA CTGGTGCATT 1260
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GATAAAACCG GTCGGGAACA TCTCTCGGTC TATGCTGTGG TGGTGATTGC GTCTGTGGTG 1680
GGATTTTGCC TTTTGGTAAT GCTGTTTCTG CTTAAGTTGG CAAGACACTC CAAGTTTGGC 1740
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ATCTCCAATG GGAGTAACAC TCCATCTTCT TCGGAAGGTG GCCCAGATGC TGTCATTATT 1860
GGAATGACCA AGATCCCTGT CATTGAAAAT CCCCAGTACT TTGGCATCAC CAACAGTCAG 1920
CTCAAGCCAG ACACATTTGT TCAGCACATC AAGCGACATA ACATTGTTCT GAAAAGGGAG 1980
CTAGGCGAAG GAGCCTTTGG AAAAGTGTTC CTAGCTGAAT GCTATAACCT CTGTCCTGAG 2040
CAGGACAAGA TCTTGGTGGC AGTGAAGACC CTGAAGGATG CCAGTGACAA TGCACGCAAG 2100
GACTTCCACC GTGAGGCCGA GCTCCTGACC AACCTCCAGC ATGAGCACAT CGTCAAGTTC 2160
TATGGCGTCT GCGTGGAGGG CGACCCCCTC ATCATGGTCT TTGAGTACAT GAAGCATGGG 2220
GACCTCAACA AGTTCCTCAG GGCACACGGC CCTGATGCCG TGCTGATGGC TGAGGGCAAC 2280
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GTATTGACTT CTTTTTGGCA TTATCTCTTT CTCTCTTTCC ATCTCCCTTG GTTGTTCCTT 3060
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ACCCTTTCTT TTGAATCAAT CTGGCTTCTG CATTACTATT AACTCTGCAT AGACAAAGGC 3180
CTTAACAAAC GTAATTTGTT ATATCAGCAG ACACTCCAGT TTGCCCACCA CAACTAACAA 3240
TGCCTTGTTG TATTCCTGCC TTTGATGTGG ATGAAAAAAA GGGAAAACAA ATATTTCACT 3300
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AACTTGTGTT CAATCTGTGA AGCCTTTATC TATGGGAGAT TAAAACCAGA GAGAAAGAAG 3480
ATTTATTATG AACCGCAATA TGGGAGGAAC AAAGACAACC ACTGGGATCA GCTGGTGTCA 3540
GTCCCTACTT AGGAAATACT CAGCAACTGT TAGCTGGGAA GAATGTATTC GGCACCTTCC 3600
CCTGAGGACC TTTCTGAGGA GTAAAAAGAC TACTGGCCTC TGTGCCATGG ATGATTCTTT 3660
TCCCATCACC AGAAATGATA GCGTGCAGTA GAGAGCAAAG ATGGCTT
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Seq ID NO: 595 Protein sequence
Protein Accession #: NP_006171.1

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NFTRNKLTSL SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQEAKSSPD TQDLYCLNES  180
SKNIPLANLQ IPNCGLPSAN LAAPNLTVEE GKSITLSCSV AGDPVPNMYW DVGNLVSKHM  240
NETSHTQGSL RITNISSDDS GKQISCVAEN LVGEDQDSVN LTVHFAPTIT FLESPTSDHH  300
WCIPFTVKGN PKPALQWFYN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNNGDYT  360
LIAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST  420
DVTDKTGREH LSVYAVVVIA SVVGFCLLVM LFLLKLARHS KFGMKGPASV ISNDDDSASP  480
LHHISNGSNT PSSSEGGPDA VIIGMTKIPV IENPQYFGIT NSQLKPDTFV QHIKRHNIVL  540
KRELGEGAFG KVFLAECYNL CPEQDKILVA VKTLKDASDN ARKDFHREAE LLTNLQHEHI  600
VKFYGVCVEG DPLIMVFEYM KHGDLNKFLR AHGPDAVLMA EGNPPTELTQ SQMLHIAQQI  660
AAGMVYLASQ HFVHRDLATR NCLVGENLLV KIGDFGMSRD VYSTDYYRVG GHTMLPIRWM  720
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PPESIMYRKF TTESDVWSLG VVLWEIFTYG KQPWYQLSNN EVIECITQGR VLQRPRTCPQ   780
EVYELMLGCW QREPHMRKNI KGIHTLLQNL AKASPVYLDI LG
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Seq ID NO: 596 DNA sequence
Nucleic Acid Accession #: AF410899
Coding sequence: 483..2999

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TGCATACCGG ACCCCCATTC GCATCTAACA AGGAATCTGC GCCCCAGAGA GTCCCGGACG    180
CCGCCGGTCG GTGCCCGGCG CGCCGGGCCA TGCAGCGACG GCCGCCGCGG AGCTCCGAGC    240
AGCGGTAGCG CCCCCCTGTA AAGCGGTTCG CTATGCCGGG ACCACTGTGA ACCCTGCCGC    300
CTGCCGGAAC ACTCTTCGCT CCGGACCAGC TCAGCCTCTG ATAAGCTGGA CTCGGCACGC    360
CCGCAACAAG CACCGAGGAG TTAAGAGAGC CGCAAGCGCA GGGAAGGCCT CCCCGCACGG    420
GTGGGGGAAA GCGGCCGGTG CAGCGCGGGG ACAGGCACTC GGGCTGGCAC TGGCTGCTAG    480
GGATGTCGTC CTGGATAAGG TGGCATGGAC CCGCCATGGC GCGGCTCTGG GGCTTCTGCT    540
GGCTGGTTGT GGGCTTCTGG AGGGCCGCTT TCGCCTGTCC CACGTCCTGC AAATGCAGTG    600
CCTCTCGGAT CTGGTGCAGC GACCCTTCTC CTGGCATCGT GGCATTTCCG AGATTGGAGC    660
CTAACAGTGT AGATCCTGAG AACATCACCG AAATTTTCAT CGCAAACCAG AAAAGGTTAG    720
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AGACTCTCCA AGAGGCTAAA TCCAGTCCAG ACACTCAGGA TTTGTACTGC CTGAATGAAA   1020
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ATCTGGCCGC ACCTAACCTC ACTGTGGAGG AAGGAAAGTC TATCACATTA TCCTGTAGTG   1140
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TGAATGAAAC AAGCCACACA CAGGGCTCCT TAAGGATAAC TAACATTTCA TCCGATGACA   1260
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CTCTAATAGC CAAGAATGAG TATGGGAAGG ATGAGAAACA GATTTCTGCT CACTTCATGG   1620
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CAGACGTCAC TGATAAAACC GGTCGGGAAC ATCTCTCGGT CTATGCTGTG GTGGTGATTG   1800
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TAGGCGAAGG AGCCTTTGGA AAAGTGTTCC TAGCTGAATG CTATAACCTC TGTCCTGAGC   2220
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ACTTCCACCG TGAGGCCGAG CTCCTGACCA ACCTCCAGCA TGAGCACATC GTCAAGTTCT   2340
ATGGCGTCTG CGTGGAGGGC GACCCCCTCA TCATGGTCTT TGAGTACATG AAGCATGGGG   2400
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CGCCCACGGA ACTGACGCAG TCGCAGATGC TGCATATAGC CCAGCAGATC GCCGCGGGCA   2520
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TCAAAGACTC CGAGAAGCTC TCGAGGGAAG CAGTGTGTAC TTCTTCATCC ATAGACACAG   3180
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AAACTTTGTC ACTTCTGCTG TACAGATATC GAGAGTTTCT ATGGATTCAC TTCTATTTAT   3540
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Seq ID NO: 597 Protein sequence
Protein Accession #: AAL67965.1

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NSVDPENITE IFIANQKRLE IINEDDVEAY VGLRNLTIVD SGLKFVAHKA FLKNSNLQHI    120
NFTRNKLTSL SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQEAKSSPD TQDLYCLNES    180
SKNIPLANLQ IPNCGLPSAN LAAPNLTVEE GKSITLSCSV AGDPVPNMYW DVGNLVSKHM    240
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WCIPFTVKGN PKPALQWFYN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNNGDYT   360
LIAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST   420
DVTDKTGREH LSVYAVVVIA SVVGFCLLVM LFLLKLARHS KFGMKDPSWF GFGKVKSRQG   480
VGPASVISND DDSASPLHHI SNGSNTPSSS EGGPDAVIIG MTKIPVIENP QYFGITNSQL   540
KPDTFVQHIK RHNIVLKREL GEGAFGKVFL AECYNLCPEQ DKILVAVKTL KDASDNARKD   600
FHREAELLTN LQHEHIVKFY GVCVEGDPLI MVFEYMKHGD LNKFLRAHGP DAVLMAEGNP   660
PTELTQSQML HIAQQIAAGM VYLASQHFVH RDLATRNCLV GENLLVKIGD FGMSRDVYST   720
DYYRVGGHTM LPIRWMPPES IMYRKFTTES DVWSLGVVLW EIFTYGKQPW YQLSNNEVIE   780
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Seq ID NO: 598 DNA sequence
Nucleic Acid Accession #: AB052906
Coding sequence: 74..814

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GCTCCTGCTG TCCGGCTGGT CCCGGGCTGG GCGAGCCGAC CCTCACTCTC TTTGCTATGA    180
CATCACCGTC ATCCCTAAGT TCAGACCTGG ACCACGGTGG TGTGCGGTTC AAGGCCAGGT    240
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AATGTGGACA ACGGTTCATC CTGGAGCCAG AAAGATGAAA GAAAAGTGGG AGAATGACAA    600
GGTTGTGGCC ATGTCCTTCC ATTACTTCTC AATGGGAGAC TGTATAGGAT GGCTTGAGGA    660
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AAGCTGATAC CAAAAGGCTC CTGTGAGCAC GGTCTTGATC AAACTCGCCC TTCTGTCTGG    900
CCAGCTGCCC ACGACCTACG GTGTATGTCC AGTGGCCTCC AGCAGATCAT GATGACATCA    960
TGGACCCAAT AGCTCATTCA CTGCCTTGAT TCCTTTTGCC AACAATTTTA CCAGCAGTTA   1020
TACCTAACAT ATTATGCAAT TTTCTCTTGG TGCTACCTGA TGGAATTCCT GCACTTAAAG   1080
TTCTGGCTGA CTAAACAAGA TATATCATTT TCTTTCTTCT CTTTTTGTTT GGAAAATCAA   1140
GTACTTCTTT GAATGATGAT CTCTTTCTTG CAAATGATAT TGTCAGTAAA ATAATCACGT   1200
TAGACTTCAG ACCTCTGGGG ATTCTTTCCG TGTCCTGAAA GAGAATTTTT AAATTATTTA   1260
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TTTAAATAAA GAGTTCTATT TCCCAAAAAA AAAAAAAAAA AA
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Seq ID NO: 599 Protein sequence
Protein Accession #: BAB61048.1

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FLHYDCGNKT VTPVSPLGKK LNVTTAWKAQ NPVLREVVDI LTEQLRDIQL ENYTPKEPLT    120
LQARMSCEQK AEGHSSGSWQ FSFDGQIFLL FDSEKRMWTT VHPGARKMKE KWENDKVVAM    180
SFHYFSMGDC IGWLEDFLMG MDSTLEPSAG APLAMSSGTT QLRATATTLI LCCLLIILPC    240
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Seq ID NO: 600 DNA sequence
Nucleic Acid Accession #: NM_001898.1
Coding sequence: 57..482

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GCCCCAAGGA GGAGGATAGG ATAATCCCGG GTGGCATCTA TAACGCAGAC CTCAATGATG    180
AGTGGGTACA GCGTGCCCTT CACTTCGCCA TCAGCGAGTA TAACAAGGCC ACCAAAGATG    240
ACTACTACAG ACGTCCGCTG CGGGTACTAA GAGCCAGGCA ACAGACCGTT GGGGGGGTGA    300
ATTACTTCTT CGACGTAGAG GTGGGCCGCA CCATATGTAC CAAGTCCCAG CCCAACTTGG    360
ACACCTGTGC CTTCCATGAA CAGCCAGAAC TGCAGAAGAA ACAGTTGTGC TCTTTCGAGA    420
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AGGGATCTGT GCCAGGCCAT TCGCACCAGC CACCACCCAC TCCCACCCCC TGTAGTGCTC    540
CCACCCCTGG ACTGGTGGCC CCCACCCTGC GGGAGGCCTC CCCATGTGCC TGCGCCAAGA    600
GACAGACAGA GAAGGCTGCA GGAGTCCTTT GTTGCTCAGC AGGGCGCTCT GCCCTCCCTC    660
CTTCCTTCTT GCTTCTAATA GCCCTGGTAC ATGGTACACA CCCCCCCACC TCCTGCAATT    720
AAACAGTAGC ATCGCC
```

Seq ID NO: 601 Protein sequence
Protein Accession #: NP_001889.1

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1          11         21         31         41         51
|          |          |          |          |          |
MAQYLSTLLL LLATLAVALA WSPKEEDRII PGGIYNADLN DEWVQRALHF AISEYNKATK     60
DDYYRRPLRV LRARQQTVGG VNYFFDVEVG RTICTKSQPN LDTCAFHEQP ELQKKQLCSF    120
EIYEVPWENR RSLVKSRCQE S
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Seq ID NO: 602 DNA sequence
Nucleic Acid Accession #: NM_003976.2
Coding sequence: 299.961

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1          11         21         31         41         51
|          |          |          |          |          |
```

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CTCTGAGCTT CTCTGAGCCT TGTTTGCTCA TCTGGAAAAA GGGGATTAAA CCATTTACCT   60
CATGGAGTTG TGAAAGAATA GCTGCAAAGC ACCTAACACA TAGTAAGGTT CCCAGTGCAG  120
CTACTTCTGC TGGGTTGAGT CTAGCTGTGT AGGCCCCTTG TTCCTCACCT GGAGAAACTG  180
GGGTGGCAGG CCGGTCCCCC ACAAAAGATA ACTCATCTCT TAATTTGCAA GCTGCCTCAA  240
CAGGAGGGTG GGGGAACAGC TCAACAATGG CTGATGGGCG CTCCTGGTGT TGATAGAGAT  300
GGAACTTGGA CTTGGAGGCC TCTCCACGCT GTCCCACTGC CCCTGGCCTA GGCGGCAGCC  360
TGCCCTGTGG CCCACCCTGG CCGCTCTGGC TCTGCTGAGC AGCGTCGCAG AGGCCTCCCT  420
GGGCTCCGCG CCCCGCAGCC CTGCCCCCCG CGAAGGCCCC CCGCCTGTCC TGGCGTCCCC  480
CGCCGGCCAC CTGCCGGGGG GACGCACGGC CCGCTGGTGC AGTGGAAGAG CCCGGCGGCC  540
GCCGCCGCAG CCTTCTCGGC CCGCGCCCCC GCCGCCTGCA CCCCCATCTG CTCTTCCCCG  600
CGGGGGCCGC GCGGCGCGGG CTGGGGGCCC GGGCAGCCGC GCTCGGGCAG CGGGGGCGCG  660
GGGCTGCCGC CTGCGCTCGC AGCTGGTGCC GGTGCGCGCG CTCGGCCTGG GCCACCGCTC  720
CGACGAGCTG GTGCGTTTCC GCTTCTGCAG CGGCTCCTGC CGCCGCGCGC GCTCTCCACA  780
CGACCTCAGC CTGGCCAGCC TACTGGGCGC CGGGGCCCTG CGACCGCCCC CGGGCTCCCG  840
GCCCGTCAGC CAGCCCTGCT GCCGACCCAC GCGCTACGAA GCGGTCTCCT TCATGGACGT  900
CAACAGCACC TGGAGAACCG TGGACCGCCT CTCCGCCACC GCCTGCGGCT GCCTGGGCTG  960
AGGGCTCGCT CCAGGGCTTT GCAGACTGGA CCCTTACCGG TGGCTCTTCC TGCCTGGGAC 1020
CCTCCCGCAG AGTCCCACTA GCCAGCGGCC TCAGCCAGGG ACGAAGGCCT CAAAGCTGAG 1080
AGGCCCCTAC CGGTGGGTGA TGGATATCAT CCCCGAACAG GTGAAGGGAC AACTGACTAG 1140
CAGCCCCAGA GCCCTCACCC TGCGGATCCC AGCCTAAAAG ACACCAGAGA CCTCAGCTAT 1200
GGAGCCCTTC GGACCCACTT CTCACAGACT CTGGCACTGG CCAGGCCTCG AACCTGGGAC 1260
CCCTCCTCTG ATGAACACTA CAGTGGCTGA GGCATCAGCC CCCGCCCAGG CCCTGTAGGG 1320
ACAGCATTTG AAGGACACAT ATTGCAGTTG CTTGGTTGAA AGTGCCTGTG CTGGAACTGG 1380
CCTGTACTCA CTCATGGGAG CTGGCCCC
```

Seq ID NO: 603 Protein sequence
Protein Accession #: NP_003967.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MELGLGGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS   60
PAGHLPGGRT ARWCSGRARR PPPQPSRPAP PPPAPPSALP RGGRAARAGG PGSRARAAGA  120
RGCRLRSQLV PVRALGLGHR SDELVRFRFC SGSCRRARSP HDLSLASLLG AGALRPPPGS  180
RPVSQPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG
```

Seq ID NO: 604 DNA sequence
Nucleic Acid Accession #: NM_057091.1
Coding sequence: 783..1445

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1          11         21         31         41         51
|          |          |          |          |          |
ACTGGCCGCT GAGAGAAGAA TCGGGTGGAG CAGAGAGCAG CTGCTGCAGG GCAGACAGCC   60
GGACCCCCAA ATCTGCACGT ACCAGCAGTC AGCCGCCCCA CGCAGGGACC GGCTTACCCC  120
TCGCTCCCCG CCCTCACTCA CTTTCTCCCG CCCTCGGCCC GGCCTCCCAG CTCTCTACTT  180
CGCGTGTCTA CAAACTCAAC TCCCGGTTTC CGTGCCTCTC CACCGCTCGA GTTCTCTACT  240
CTCCATATCC GAGGGGCCCC TCCCAGCATC TACCCCCCTC CCAACCTCGG GGGACCTAGC  300
CAAGCTAGGG GGGACTGGAT CCGACGGGTG GAGCAGCCAG GTGAGCCCCG AAAGGTGGGG  360
CGGGGCAGGG GCGCTCCCAG CCCCACCCCG GGATCTGGTG ACGCTGGGGC TGGAATTTGA  420
CACCGGACGG CTGCGGCGGC GGGCAGGAGG CTGCTGAGGG ATGGAGTTGG GCCCGGCCCC  480
CAGACAAGGC CCGGGGGCTC CGCCAGCAGC AGGTCCCTCG GGCCCCAGCC CTCGCTGCCA  540
CCCGGGCCTG GAGCCCCACA CCCGAGGGTG CAGACTGGCT GCCAAGGCCA CACTTTTGGC  600
TAAAAGAGGC ACTGCCAGGT GTACAGTCCT GGGCATGCGC TGTTTGAGCT TCGGGGGAGA  660
GCCCAGCACT GGTCCCCGGA AAGGTGCCTA GAAGAACAAG GTGCAGGACC CCGTGCTGCC  720
TCAACAGGAG GGTGGGGGAA CAGCTCAACA ATGGCTGATG GGCGCTCCTG GTGTTGATAG  780
AGATGGAACT TGGACTTGGA GGCCTCTCCA CGCTGTCCCA CTGCCCCTGG CCTAGGCGGC  840
AGCCTGCCCT GTGGCCCACC CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCCT  900
CCCTGGGCTC CGCGCCCCGC AGCCCTGCCC CCCGCGAAGG CCCCCCGCCT GTCCTGGCGT  960
CCCCCGCCGG CCACCTGCCG GGGGGACGCA CGGCCCGCTG GTGCAGTGGA AGAGCCCGGC 1020
GGCCGCCGCC GCAGCCTTCT CGGCCCGCGC CCCCGCCGCC TGCACCCCCA TCTGCTCTTC 1080
CCCGCGGGGG CCGCGCGGCG CGGGCTGGGG GCCCGGGCAG CCGCGCTCGG GCAGCGGGGG 1140
CGCGGGGCTG CCGCCTGCGC TCGCAGCTGG TGCCGGTGCG CGCGCTCGGC CTGGGCCACC 1200
GCTCCGACGA GCTGGTGCGT TTCCGCTTCT GCAGCGGCTC CTGCCGCCGC GCGCGCTCTC 1260
CACACGACCT CAGCCTGGCC AGCCTACTGG GCGCCGGGGC CCTGCGACCG CCCCCGGGCT 1320
CCCGGCCCGT CAGCCAGCCC TGCTGCCGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG 1380
ACGTCAACAG CACCTGGAGA ACCGTGGACC GCCTCTCCGC CACCGCCTGC GGCTGCCTGG 1440
GCTGAGGGCT CGCTCCAGGG CTTTGCAGAC TGGACCCTTA CCGGTGGCTC TTCCTGCCTG 1500
GGACCCTCCC GCAGAGTCCC ACTAGCCAGC GGCCTCAGCC AGGGACGAAG GCCTCAAAGC 1560
TGAGAGGCCC CTACCGGTGG GTGATGGATA TCATCCCCGA ACAGGTGAAG GGACAACTGA 1620
CTAGCAGCCC CAGAGCCCTC ACCCTGCGGA TCCCAGCCTA AAAGACACCA GAGACCTCAG 1680
CTATGGAGCC CTTCGGACCC ACTTCTCACA GACTCTGGCA CTGGCCAGGC CTCGAACCTG 1740
GGACCCCTCC TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCCGCC CAGGCCCTGT 1800
AGGGACAGCA TTTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAAGTGCC TGTGCTGGAA 1860
CTGGCCTGTA CTCACTCATG GGAGCTGGCC CC
```

Seq ID NO: 605 Protein sequence
Protein Accession #: NP_003967.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MELGLGGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS   60
PAGHLPGGRT ARWCSGRARR PPPQPSRPAP PPPAPPSALP RGGRAARAGG PGSRARAAGA  120
RGCRLRSQLV PVRALGLGHR SDELVRFRFC SGSCRRARSP HDLSLASLLG AGALRPPPGS  180
RPVSQPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG
```

Seq ID NO: 606 DNA sequence
Nucleic Acid Accession #: NM_057160.1

Coding sequence: 1..714

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1          11         21         31         41         51
|          |          |          |          |          |
ATGCCCGGCC TGATCTCAGC CCGAGGACAG CCCCTCCTTG AGGTCCTTCC TCCCCAAGCC    60
CACCTGGGTG CCCTCTTTCT CCCTGAGGCT CCACTTGGTC TCTCCGCGCA GCCTGCCCTG   120
TGGCCCACCC TGGCCGCTCT GGCTCTGCTG AGCAGCGTCG CAGAGGCCTC CCTGGGCTCC   180
GCGCCCCGCA GCCCTGCCCC CCGCGAAGGC CCCCCGCCTG TCCTGGCGTC CCCCGCCGGC   240
CACCTGCCGG GGGGACGCAC GGCCCGCTGG TGCAGTGGAA GAGCCCGGCG GCCGCCGCCG   300
CAGCCTTCTC GGCCCGCGCC CCCGCCGCCT GCACCCCCAT CTGCTCTTCC CCGCGGGGGC   360
CGCGCGGCGC GGGCTGGGGG CCCGGGCAGC CGCGCTCGGG CAGCGGGGGC GCGGGGCTGC   420
CGCCTGCGCT CGCAGCTGGT GCCGGTGCGC GCGCTCGGCC TGGGCCACCG CTCCGACGAG   480
CTGGTGCGTT TCCGCTTCTG CAGCGGCTCC TGCCGCCGCG CGCGCTCTCC ACACGACCTC   540
AGCCTGGCCA GCCTACTGGG CGCCGGGGCC CTGCGACCGC CCCCGGGCTC CCGGCCCGTC   600
AGCCAGCCCT GCTGCCGACC CACGCGCTAC GAAGCGGTCT CCTTCATGGA CGTCAACAGC   660
ACCTGGAGAA CCGTGGACCG CCTCTCCGCC ACCGCCTGCG GCTGCCTGGG CTGAGGGCTC   720
GCTCCAGGGC TTTGCAGACT GGACCCTTAC CGGTGGCTCT TCCTGCCTGG GACCCTCCCG   780
CAGAGTCCCA CTAGCCAGCG GCCTCAGCCA GGGACGAAGG CCTCAAAGCT GAGAGGCCCC   840
TACCGGTGGG TGATGGATAT CATCCCCGAA CAGGTGAAGG GACAACTGAC TAGCAGCCCC   900
AGAGCCCTCA CCCTGCGGAT CCCAGCCTAA AAGACACCAG AGACCTCAGC TATGGAGCCC   960
TTCGGACCCA CTTCTCACAG ACTCTGGCAC TGGCCAGGCC TCGAACCTGG GACCCCTCCT  1020
CTGATGAACA CTACAGTGGC TGAGGCATCA GCCCCCGCCC AGGCCCTGTA GGGACAGCAT  1080
TTGAAGGACA CATATTGCAG TTGCTTGGTT GAAAGTGCCT GTGCTGGAAC TGGCCTGTAC  1140
TCACTCATGG GAGCTGGCCC C
```

Seq ID NO: 607 Protein sequence
Protein Accession #: NP_476501.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MPGLISARGQ PLLEVLPPQA HLGALFLPEA PLGLSAQPAL WPTLAALALL SSVAEASLGS    60
APRSPAPREG PPPVLASPAG HLPGGRTARW CSGRARRPPP QPSRPAPPPP APPSALPRGG   120
RAARAGGPGS RARAAGARGC RLRSQLVPVR ALGLGHRSDE LVRFRFCSGS CRRARSPHDL   180
SLASLLGAGA LRPPPGSRPV SQPCCRPTRY EAVSFMDVNS TWRTVDRLSA TACGCLG
```

Seq ID NO: 608 DNA sequence
Nucleic Acid Accession #: NM_057090.1
Coding sequence: 29..715

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1          11         21         31         41         51
|          |          |          |          |          |
CTGATGGGCG CTCCTGGTGT TGATAGAGAT GGAACTTGGA CTTGGAGGCC TCTCCACGCT    60
GTCCCACTGC CCCTGGCCTA GGCGGCAGGC TCCACTTGGT CTCTCCGCGC AGCCTGCCCT   120
GTGGCCCACC CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCCT CCCTGGGCTC   180
CGCGCCCCGC AGCCCTGCCC CCCGCGAAGG CCCCCCGCCT GTCCTGGCGT CCCCCGCCGG   240
CCACCTGCCG GGGGGACGCA CGGCCCGCTG GTGCAGTGGA AGAGCCCGGC GGCCGCCGCC   300
GCAGCCTTCT CGGCCCGCGC CCCCGCCGCC TGCACCCCCA TCTGCTCTTC CCCGCGGGGG   360
CCGCGCGGCG CGGGCTGGGG GCCCGGGCAG CCGCGCTCGG GCAGCGGGGG CGCGGGGCTG   420
CCGCCTGCGC TCGCAGCTGG TGCCGGTGCG CGCGCTCGGC CTGGGCCACC GCTCCGACGA   480
GCTGGTGCGT TTCCGCTTCT GCAGCGGCTC CTGCCGCCGC GCGCGCTCTC CACACGACCT   540
CAGCCTGGCC AGCCTACTGG GCGCCGGGGC CCTGCGACCG CCCCCGGGCT CCCGGCCCGT   600
CAGCCAGCCC TGCTGCCGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG ACGTCAACAG   660
CACCTGGAGA ACCGTGGACC GCCTCTCCGC CACCGCCTGC GGCTGCCTGG GCTGAGGGCT   720
CGCTCCAGGG CTTTGCAGAC TGGACCCTTA CCGGTGGCTC TTCCTGCCTG GGACCCTCCC   780
GCAGAGTCCC ACTAGCCAGC GGCCTCAGCC AGGGACGAAG GCCTCAAAGC TGAGAGGCCC   840
CTACCGGTGG GTGATGGATA TCATCCCCGA ACAGGTGAAG GGACAACTGA CTAGCAGCCC   900
CAGAGCCCTC ACCCTGCGGA TCCCAGCCTA AAAGACACCA GAGACCTCAG CTATGGAGCC   960
CTTCGGACCC ACTTCTCACA GACTCTGGCA CTGGCCAGGC CTCGAACCTG GGACCCCTCC  1020
TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCCGCC CAGGCCCTGT AGGGACAGCA  1080
TTTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAAGTGCC TGTGCTGGAA CTGGCCTGTA  1140
CTCACTCATG GGAGCTGGCC CC
```

Seq ID NO: 609 Protein sequence
Protein Accession #: NP_476431.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MELGLGGLST LSHCPWPRRQ APLGLSAQPA LWPTLAALAL LSSVAEASLG SAPRSPAPRE    60
GPPPVLASPA GHLPGGRTAR WCSGRARRPP PQPSRPAPPP PAPPSALPRG GRAARAGGPG   120
SRARAAGARG CRLRSQLVPV RALGLGHRSD ELVRFRFCSG SCRRARSPHD LSLASLLGAG   180
ALRPPPGSRP VSQPCCRPTR YEAVSFMDVN STWRTVDRLS ATACGCLG
```

Seq ID NO: 610 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1746

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1          11         21         31         41         51
|          |          |          |          |          |
ATGCCACTGA AGCATTATCT CCTTTTGCTG GTGGGCTGCC AAGCCTGGGG TGCAGGGTTG    60
GCCTACCATG GCTGCCCTAG CGAGTGTACC TGCTCCAGGG CCTCCCAGGT GGAGTGCACC   120
GGGGCACGCA TTGTGGCGGT GCCCACCCCT CTGCCCTGGA ACGCCATGAG CCTGCAGATC   180
CTCAACACGC ACATCACTGA ACTCAATGAG TCCCCGTTCC TCAATATCTC AGCCCTCATC   240
GCCCTGAGGA TTGAGAAGAA TGAGCTGTCG CGCATCACGC CTGGGGCCTT CCGAAACCTG   300
GGCTCGCTGC GCTATCTCAG CCTCGCCAAC AACAAGCTGC AGGTTCTGCC CATCGGCCTC   360
TTCCAGGGCC TGGACAGCCT TGAGTCTCTC CTTCTGTCCA GTAACCAGCT GTTGCAGATC   420
CAGCCGGCCC ACTTCTCCCA GTGCAGCAAC CTCAAGGAGC TGCAGTTGCA CGGCAACCAC   480
CTGGAATACA TCCCTGACGG AGCCTTCGAC CACCTGGTAG GACTCACGAA GCTCAATCTG   540
```

GGCAAGAATA GCCTCACCCA CATCTCACCC AGGGTCTTCC AGCACCTGGG CAATCTCCAG 600
GTCCTCCGGC TGTATGAGAA CAGGCTCACG GATATCCCCA TGGGCACTTT TGATGGGCTT 660
GTTAACCTGC AGGAACTGGC TCTACAGCAG AACCAGATTG GACTGCTCTC CCCTGGTCTC 720
TTCCACAACA ACCACAACCT CCAGAGACTC TACCTGTCCA ACAACCACAT CTCCCAGCTG 780
CCACCCAGCA TCTTCATGCA GCTGCCCCAG CTCAACCGTC TTACTCTCTT TGGGAATTCC 840
CTGAAGGAGC TCTCTCTGGG GATCTTCGGG CCCATGCCCA ACCTGCGGGA GCTTTGGCTC 900
TATGACAACC ACATCTCTTC TCTACCCGAC AATGTCTTCA GCAACCTCCG CCAGTTGCAG 960
GTCCTGATTC TTAGCCGCAA TCAGATCAGC TTCATCTCCC CGGGTGCCTT CAACGGGCTA 1020
ACGGAGCTTC GGGAGCTGTC CCTCCACACC AACGCACTGC AGGACCTGGA CGGGAATGTC 1080
TTCCGCATGT TGGCCAACCT GCAGAACATC TCCCTGCAGA ACAATCGCCT CAGACAGCTC 1140
CCAGGGAATA TCTTCGCCAA CGTCAATGGC CTCATGGCCA TCCAGCTGCA GAACAACCAG 1200
CTGGAGAACT TGCCCCTCGG CATCTTCGAT CACCTGGGGA AACTGTGTGA GCTGCGGCTG 1260
TATGACAATC CCTGGAGGTG TGACTCAGAC ATCCTTCCGC TCCGCAACTG GCTCCTGCTC 1320
AACCAGCCTA GGTTAGGGAC GGACACTGTA CCTGTGTGTT TCAGCCCAGC CAATGTCCGA 1380
GGCCAGTCCC TCATTATCAT CAATGTCAAC GTTGCTGTTC CAAGCGTCCA TGTCCCTGAG 1440
GTGCCTAGTT ACCCAGAAAC ACCATGGTAC CCAGACACAC CCAGTTACCC TGACACCACA 1500
TCCGTCTCTT CTACCACTGA GCTAACCAGC CCTGTGGAAG ACTACACTGA TCTGACTACC 1560
ATTCAGGTCA CTGATGACCG CAGCGTTTGG GGCATGACCC AGGCCCAGAG CGGGCTGGCC 1620
ATTGCCGCCA TTGTAATTGG CATTGTCGCC CTGGCCTGCT CCCTGGCTGC CTGCGTCGGC 1680
TGTTGCTGCT GCAAGAAGAG GAGCCAAGCT GTCCTGATGC AGATGAAGGC ACCCAATGAG 1740
TGTTAAAGAG GCAGGCTGGA GCAGGGCTGG GGAATGATGG GACTGGAGGA CCTGGGAATT 1800
TCATCTTTCT GCCTCCACCC CTGGGTCCAT GGAGCTTTCC CGTGATTGCT CTTTCTGGCC 1860
CTAGATAAAG GTGTGCCTAC CTCTTCCTGA CTTGCCTGAT TCTCCCGTAG AGAAGCAGGT 1920
CGTGCCGGAC CTTCCTACAA TCAGGAAGAT AGATCCAACT GGCCATGGCA AAAGCCCTGG 1980
GGATTTCCGA TTCATACCCC TGGGCTTCCT TCGAGAGGGC TCTTCCTCCA AATCCTCCCC 2040
ACCTGTCCTC CAAGAACAGC CTTCCCTGCG CCCAGGCCCC CTCCGGGCCT CTGTAGACTC 2100
AGTTAGTCCA CAGCCTGCTC ACTTCGTGGG AATAGTTCTC CGCTGAGATA GCCCCTCTCG 2160
CCTAAGTATT ATGTAAGTTG ATTTCCCTTC TTTTGTTTCT CTTGTTTGTG CTATGGCTTG 2220
ACCCAGCATG TCCCCTCAAA TGAAAGTTCT CCCCTTGATT TTCTGCTCCT GAAGGCAGGG 2280
TGAGTTCTCT CCTCAAAGAA GACTTCAAAC CATTTAACTG GTTTCTTAAG AGCCGTCAAT 2340
CAGCCTGGTT TTGGGGATGC TATGAAAGAG AGAAGGAAAA TCATGCCGCT CAGTTCCTGG 2400
AGACAGAAGA GCCGTCATCA GTGTCTCACT TGTGATTTTT ATCTGGAAAA GGAAGAAACA 2460
CCCCAGCACA GCAAGCTCAG CCTTTTAGAG AAGGATATTT CCAAACTGCA AACTTTGCTT 2520
TGAAAAGTTT AGCCCTTTAA GGAATGAAAT CATGTAGAAT TTTGGACTTC TAAAAACATT 2580
AAAATCAGCT TATTAATACG GGATAGAGAA AGAAATCTGG TGCCTGGGGG TCCCTGTGTT 2640
CACCCCTAGA GTTTGTTTTA AAATTTTTAA TTGAAGCATG TGAAGTGTAC STGCAGAAAA 2700
GTGGGAACAT GATAGTGTAT GGCTTGGTGG ATTTTCACAA ACTGAACATA CCTGTGTAAT 2760
CAGCATCTAG ACCCAGACCC AGAGCATCAC AAATATCCCC CATCCTGGGC TTTTCCCAGA 2820
GGAGATGGGG GCTTCTGAAG ATGGACTTAC CTGGGACCTG CCCCCCATGA GCCAGGACGG 2880
TCCCCCCACA GTCAGCCTGT GCAAAGGCCC CGTGGCCAGG GGTGGAGGAG AATATGTGGG 2940
TGTGGACAGG ATGGGAGACT GTGGCCTGAA CAGGAGATTT TATTATATCT GGAGACCCTG 3000
AGAGACCCTG AGACCTGGGG CACCATGGCT GGCCAGGTCA GAAGCATCCT GACTGCAGAG 3060
GTCCGTGCAG CCACACCCTC TTCCCTGCCA GCAAGTTGTC TGCGGCTCAT CGGAGGCCCC 3120
TCCGCCTGGA GCCTTCTATG GACGTGATAT GCCTGTATCT GTTTTTAATT TTCATTCTTC 3180
ACTTAGGGGA AGTGAAATCG CTCAGAGATG AGATCCTTTA ATTGAAAACG AAGTGTAACG 3240
GAATCTAGTG TCTTTCTAAT GTGGTAAAAT TCTCCATCAA CATCACAGTC AGCTGGCAGC 3300
TGAACTTCAG AATCTCACTT ACAGCAGGCG ACACGGGGGT ACACCGATGG GTCACACTGG 3360
GTCTGGGGGC TCCCTGGAGC TCCTCCTGCG TGTGGTCTGG TTAGGAGTTG AGTTGTTTGC 3420
TCCAGGGTTA TTCTCCTCCT CGAGTCACAG TCACACGAAT ACCTGCCTTC TCTGGCTTTC 3480
CTGCTATACA CATATTCACA TGGCGCTCAA GAAGTTAGGC TCATGGCAAC GTGTGTCTTT 3540
CTCTGGACAA CTGGCCCAGT TTACAGTGAA ATGGAGAATT TCAGGTCTCC ACGTCTGCCC 3600
AGGAAAGAAC TTCAGCTGAC TCCACGGGGA TCTGGAAATC CACGACCAAT CCCGATCGGC 3660
TCTTATTAGC TCCCCGCTCC ACAAGACACC TGTGCTTTGG AAATCCACCA CCAATCCCGA 3720
TCGGCTCTTA TTAGCTCCCC GCTCCACAAG ACACCTGTGA TCTGGAAATC TACCACCAAT 3780
CCCGATCGGC TCTTATTAGC TCCCCGCTCC ACAAGACACC TGTGACATCC TCCAGGGCCA 3840
CAGGAGCACG TGCTGACCAG TTTTCCCTTC CAGTTCCTGC ACAAAAAGTG TCCAGAGGGC 3900
TGTTTGCAAA CACTAGTGCA CTTTGTAGCT TTTCACCCTC TGTCCCAGGG AATCTAGGAG 3960
AGATGAGGCC CGTCAGAGTC AAGAGATGTC ATCCCCCCAG GGTCTCCAAG GCATTTCCAC 4020
ACTATTGGTG GCACCTGGAG GACATGCACC AAGGCTTGCC AGAGCCAACA GGAAGTGAGC 4080
CCAGAGCATG GCACATGAGC ATCACCCGCT GATGGTGGCC TGCTGTGCCT GGTGCCAACA 4140
GGGGCATCCC GGCCCGTACC CCTCCAGACA GGAAGCATGG GTTTGCCCAC AGACCTGTCG 4200
GGTGCTCCTG TGAGTGGCCT CCAGATGTCT TTGTGCATAG GCACAAGTGG GCCAGGGCTG 4260
GAGGGAGGTG GGAAACCTCA TCATCCGGTG GGCCCTGCCA ATCTTAACCC AGAACCCTTA 4320
GGTATTCCTG GCAGTAGCCA TGACATTGGA GCACCTTCCT CTCCAGCCAG AGGCTGACCT 4380
GAGGGCCACT GTCCTCAGAT GACACCACCC AGGAGCACCC TAGGTGAGGG GTGAGGGCCC 4440
CCTTATGTGA ACCTCTTGCC TCTTCCTTTC TCCCATCAGA GTGGTTGGAT GGAGCCATTG 4500
GCCTCCTTTT CTTCAGCGGG CCCTTCAACC TCTCTGCACC ATGTTGTCTG GCTGAGGAGC 4560
TACTAGAAAA GCTGAGTGGA GTCTCCTTTC CAACAGGATG ATGCATTTGC TCAATTCTCA 4620
GGGCTGGAAT GAGCCGGCTG GTCCCCCAGA AAGCTGGAGT GGGGTACAGA GTTCAGTTTT 4680
CCTCTCTGTT TACAGCTCCT TGACAGTCCC ACGCCCATCT GGAGTGGGAG CTGGGAGTTA 4740
GTGTTGGAGA AGAAACAACA AAAGCCAATT AGAACCACTA TTTTTAAAAA GTGCTTACTG 4800
TGCACAGATA CTCTTCAAGC ACTGGACGTG GATTCTCTCT CTAGCCCTCA GCACCCCTGC 4860
GGTAGGAGTG CCGCCTCTAC CCACTTGTGA TGGGGTACAG AGGCACTTGC TCTTCTGCAT 4920
GGTGTTCAAT AGGCTGGGAG TTTTATTTAT CTCTTCAAAC TTTGTACAAG AGCTCATGGC 4980
TTGTCTTGGG CTTTCGTCAT TAAACCAAAG GAAATGGAAG CCATTCCCCT GTTGCTCTCC 5040
TTAGTCTTGG TCATCAGAAC CTCACTTGGT ACCATATAGA TCAAAAGCTT TGTAACCACA 5100
GGAAAAAATA AACTCTTCCA TCCCTTAAAG AATAGAATAG TTTGTCCCTC TCATGGGAAT 5160
TGGGCTGTAT GTATATTGTT CTTCCTCCTT AGAATTTAGA GATACAAGAG TTCTACTTAG 5220
AACTTTTCAT GGACACAATT TCCACAACCT TTCAGATGCT GATGTAGAGC TATTGGGAAA 5280
GAACTTCCAA ACTCAGGAAG TTTGCAGAGA GCAGACAGCT AGAGATAACT CGGGACCCAG 5340
AGTTGGTCGA CAGATGTTAG ATGTATCCTA GCTTTTAGCC ATAAACCACT CAAAGATTCA 5400
GCCCCCAGAT CCCACAGTCA GAACTGAATC TGCGTTGTTG GGAAGCCAGC AGTGGCCTTG 5460
GGAAGGAAGC CATGGCTGTG GTTCAGAGAG GGTGGGCTGG CAAGCCACTT CCGGGGAAAA 5520
CTCCTTCCGC CCCAGGTTTC TTCTTCTCTT AAGGAGAGAT TGTTCTCACC AACCCGCTGC 5580
CTTCATGCTG CCTTCAAAGC TAGATCATGT TTGCCTTGCT TAGAGAATTA CTGCAAATCA 5640
GCCCCAGTGC TTGGCGATGC ATTTACAGAT TTCTAGGCCC TCAGGGTTTT GTAGAGTGTG 5700
AGCCCTGGTG GGCAGGGTTG GGGGGTCTGT CTTCTGCTGG ATGCTGCTTG TAATCCATTT 5760

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GGTGTACAGA ATCAACAATA AATAATATAC ATGTAT
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Seq ID NO: 611 Protein sequence
Protein Accession #: BAB84587.1

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1          11         21         31         41         51
|          |          |          |          |          |
MPLKHYLLLL VGCQAWGAGL AYHGCPSECT CSRASQVECT GARIVAVPTP LPWNAMSLQI    60
LNTHITELNE SPFLNISALI ALRIEKNELS RITPGAFRNL GSLRYLSLAN NKLQVLPIGL   120
FQGLDSLESL LLSSNQLLQI QPAHFSQCSN LKELQLHGNH LEYIPDGAFD HLVGLTKLNL   180
GKNSLTHISP RVFQHLGNLQ VLRLYENRLT DIPMGTFDGL VNLQELALQQ NQIGLLSPGL   240
FHNNHNLQRL YLSNNHISQL PPSIFMQLPQ LNRLTLFGNS LKELSLGIFG PMPNLRELWL   300
YDNHISSLPD NVFSNLRQLQ VLILSRNQIS FISPGAFNGL TELRELSLHT NALQDLDGNV   360
FRMLANLQNI SLQNNRLRQL PGNIFANVNG LMAIQLQNNQ LENLPLGIFD HLGKLCELRL   420
YDNPWRCDSD ILPLRNWLLL NQPRLGTDTV PVCFSPANVR GQSLIIINVN VAVPSVHVPE   480
VPSYPETPWY PDTPSYPDTT SVSSTTELTS PVEDYTDLTT IQVTDDRSVW GMTQAQSGLA   540
IAAIVIGIVA LACSLAACVG CCCCKKRSQA VLMQMKAPNE C
```

Seq ID NO: 612 DNA sequence
Nucleic Acid Accession #: XM_098151
Coding sequence: 1..447

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1          11         21         31         41         51
|          |          |          |          |          |
ATGATGCATT TGCTCAATTC TCAGGGCTGG AATGAGCCGG CTGGTCCCCC AGAAAGCTGG    60
AGTGGGGTAC AGAGTTCAGT TTTCCTCTCT GTTTACAGCT CCTTGACAGT CCCACGCCCA   120
TCTGGAGTGG GAGCTGGGAG TCAGTGTTGG AGAAGAAACA ACAAAAGCCA ATTAGAACCA   180
CTATTTTTAA AAAGTGCTTA CTGTGCACAG ATACTCTTCA AGCACTGGAC GTGGATTCTC   240
TCTCTAGCCC TCAGCACCCC TGCGGTAGGA GTGCCGCCTC TACCCACTTG TGATGGGGTA   300
CAGAGGCACT TGCTCTTCTG CATGGTGTTC AATAGGCTGG GAGTTTTATT TATCTCTTCA   360
AACTTTGTAC AAGAGCTCAT GGCTTGTCTT GGGCTTTCGT CATTAAACCA AAGGAAATGG   420
AAGCCATTCC CCTGTTGCTC TCCTTAG
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Seq ID NO: 613 Protein sequence
Protein Accession #: XP_098151

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LFLKSAYCAQ ILFKHWTWIL SLALSTPAVG VPPLPTCDGV QRHLLFCMVF NRLGVLFISS   120
NFVQELMACL GLSSLNQRKW KPFPCCSP
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Seq ID NO: 614 DNA sequence
Nucleic Acid Accession #: NM_002658.1
Coding sequence: 77..1372

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GAGCGACTCC AAAGGCAGCA ATGAACTTCA TCAAGTTCCA TCGAACTGTG ACTGTCTAAA   180
TGGAGGAACA TGTGTGTCCA ACAAGTACTT CTCCAACATT CACTGGTGCA ACTGCCCAAA   240
GAAATTCGGA GGGCAGCACT GTGAAATAGA TAAGTCAAAA ACCTGCTATG AGGGGAATGG   300
TCACTTTTAC CGAGGAAAGG CCAGCACTGA CACCATGGGC CGGCCCTGCC TGCCCTGGAA   360
CTCTGCCACT GTCCTTCAGC AAACGTACCA TGCCCACAGA TCTGATGCTC TTCAGCTGGG   420
CCTGGGGAAA CATAATTACT GCAGGAACCC AGACAACCGG AGGCGACCCT GGTGCTATGT   480
GCAGGTGGGC CTAAAGCCGC TTGTCCAAGA GTGCATGGTG CATGACTGCG CAGATGGAAA   540
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CCGCTTTAAG ATTATTGGGG GAGAATTCAC CACCATCGAG AACCAGCCCT GGTTTGCGGC   660
CATCTACAGG AGGCACCGGG GGGGCTCTGT CACCTACGTG TGTGGAGGCA GCCTCATCAG   720
CCCTTGCTGG GTGATCAGCG CCACACACTG CTTCATTGAT TACCCAAAGA AGGAGGACTA   780
CATCGTCTAC CTGGGTCGCT CAAGGCTTAA CTCCAACACG CAAGGGGAGA TGAAGTTTGA   840
GGTGGAAAAC CTCATCCTAC ACAAGGACTA CAGCGCTGAC ACGCTTGCTC ACCACAACGA   900
CATTGCCTTG CTGAAGATCC GTTCCAAGGA GGGCAGGTGT GCGCAGCCAT CCCGGACTAT   960
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CACTGGCTTT GGAAAAGAGA ATTCTACCGA CTATCTCTAT CCGGAGCAGC TGAAAATGAC  1080
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CTCAGGGGGA CCCCTCGTCT GTTCCCTCCA AGGCCGCATG ACTTTGACTG GAATTGTGAG  1260
CTGGGGCCGT GGATGTGCCC TGAAGGACAA GCCAGGCGTC TACACGAGAG TCTCACACTT  1320
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GCTGTGAGTG TAAGTGTGAG TAAGAGCTGG TGTCTGATTG TTAAGTCTAA ATATTTCCTT  1980
AAACTGTGTG GACTGTGATG CCACACAGAG TGGTCTTTCT GGAGAGGTTA TAGGTCACTC  2040
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ACCTGTGACC AGCACTGTCT CAGTTTCACT TTCACATAGA TGTCCCTTTC TTGGCCAGTT  2160
ATCCCTTCCT TTTAGCCTAG TTCATCCAAT CCTCACTGGG TGGGGTGAGG ACCACTCCTT  2220
ACACTGAATA TTTATATTTC ACTATTTTTA TTTATATTTT TGTAATTTTA AATAAAAGTG  2280
ATCAATAAAA TGTGATTTTT CTGA
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Seq ID NO: 615 Protein sequence
Protein Accession #: NP_002649.1

1 11 21 31 41 51
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HCEIDKSKTC YEGNGHFYRG KASTDTMGRP CLPWNSATVL QQTYHAHRSD ALQLGLGKHN 120
YCRNPDNRRR PWCYVQVGLK PLVQECMVHD CADGKKPSSP PEELKFQCGQ KTLRPRFKII 180
GGEFTTIENQ PWFAAIYRRH RGGSVTYVCG GSLISPCWVI SATHCFIDYP KKEDYIVYLG 240
RSRLNSNTQG EMKFEVENLI LHKDYSADTL AHHNDIALLK IRSKEGRCAQ PSRTIQTICL 300
PSMYNDPQFG TSCEITGFGK ENSTDYLYPE QLKMTVVKLI SHRECQQPHY YGSEVTTKML 360
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Seq ID NO: 616 DNA sequence
Nucleic Acid Accession #: NM_024422.1
Coding sequence: 202..2907

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GCTCCGGCCG CGGCCCTCGC CCCGCGGAGC CCTCCTACCC CGGCCCGACG CTCGGCCCGC 180
GACCTGCCCC GAGCCCTCTC CATGGAGGCA GCCCGCCCCT CCGGCTCCTG GAACGGAGCC 240
CTCTGCCGGC TGCTCCTGCT GACCCTCGCG ATCTTAATAT TTGCCAGTGA TGCCTGCAAA 300
AATGTGACAT TACATGTTCC CTCCAAACTA GATGCCGAGA AACTTGTTGG TAGAGTTAAC 360
CTGAAAGAGT GCTTTACAGC TGCAAATCTA ATTCATTCAA GTGATCCTGA CTTCCAAATT 420
TTGGAGGATG GTTCAGTCTA TACAACAAAT ACTATTCTAT TGTCCTCGGA GAAGAGAAGT 480
TTTACCATAT TACTTTCCAA CACTGAGAAC CAAGAAAAGA AGAAAATATT TGTCTTTTTG 540
GAGCATCAAA CAAAGGTCCT AAAGAAAAGA CATACTAAAG AAAAAGTTCT AAGGCGCGCC 600
AAGAGAAGAT GGGCTCCAAT TCCTTGTTCG ATGCTAGAAA ACTCCTTGGG TCCTTTTCCA 660
CTTTTCCTTC AACAGGTTCA ATCTGACACG GCCCAAAACT ATACCATATA CTATTCCATA 720
AGAGGTCCTG GAGTTGACCA AGAACCTCGG AATTTATTTT ATGTGGAGAG AGACACTGGA 780
AACTTGTATT GTACTCGTCC TGTAGATCGT GAGCAGTATG AATCTTTTGA GATAATTGCC 840
TTTGCAACAA CTCCAGATGG GTATACTCCA GAACTTCCAC TGCCCCTAAT AATCAAAATA 900
GAGGATGAAA ATGATAACTA CCCAATTTTT ACAGAAGAAA CTTATACTTT TACAATTTTT 960
GAAAATTGCA GAGTGGGCAC TACTGTGGGA CAAGTGTGTG CTACTGACAA AGATGAGCCT 1020
GACACGATGC ACACACGCCT GAAGTACTCC ATCATTGGGC AGGTGCCACC ATCACCCACC 1080
CTATTTTCTA TGCATCCAAC TACAGGCGTG ATCACCACAA CATCATCTCA GCTAGACAGA 1140
GAGTTAATTG ACAAGTACCA GTTGAAAATA AAAGTACAAG ACATGGATGG TCAGTATTTT 1200
GGTCTACAGA CAACTTCAAC TTGTATCATT AACATTGATG ATGTAAATGA CCACTTGCCA 1260
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TTACGAGTTA CTGTTGAGGA TAAGGACTTA GTGAATACTG CTAACTGGAG AGCTAATTAT 1380
ACCATTTTAA AGGGCAATGA AAATGGCAAT TTTAAAATTG TAACAGATGC CAAAACCAAT 1440
GAAGGAGTTC TTTGTGTAGT TAAGCCTTTG AATTATGAAG AAAAGCAACA GATGATCTTG 1500
CAAATTGGTG TAGTTAATGA AGCTCCATTT TCCAGAGAGG CTAGTCCAAG ATCAGCCATG 1560
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AAAGCATATG ACCCAGAAAC AAGAAGTAGC AGTGGCATAA GGTATAAGAA ATTAACTGAT 1740
CCAACAGGGT GGGTCACCAT TGATGAAAAT ACAGGATCAA TCAAAGTTTT CAGAAGCCTG 1800
GATAGAGAGG CAGAGACCAT CAAAAATGGC ATATATAATA TTACAGTCCT TGCATCAGAC 1860
CAAGGAGGGA GAACATGTAC GGGGACACTG GGCATTATAC TTCAAGACGT GAATGATAAC 1920
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CGTCTTTCCT ATCAGAATGA TCCTCCATTT GGCTCATATG TAGTACCTAT AACAGTGAGA 2160
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CAGCAGAACC TAATTGTATC AAACACAGAA GCTCCTGGAG ATGACAAAGT GTATTCTGCG 2460
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CTAGCAGAAG CATGCATGAA GAGATGAGTG TGTTCTAATA AGTCTCTGAA AGCCAGTGGC 2940
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TGGGGGTTTT TCTCTCATTA TTTGGATGGA ATCTCTTTGG TCAAATGCAC ATTTACAGAG 3060
AGACACTATA AACAAGTACA CAAATTTTTC AATTTTTACA TATTTTTAAA TTACTTATCT 3120
TCTATCCAAG GAGGTCTACA GAGAAATTAA AGTCTGCCTT ATTTGTTACA TTTGGGTATA 3180
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TATTTGAAGC ACAACCTAAT GGAAAATTGT AGAGACCTTG CTTTAACATT ATCTCCAGTT 3300
AATTAAGTGT TCATGTGGTG CTTGGAAACT GTTGTTTTCC TGAACATCTA AAGTGTGTAG 3360
ACTGCATTCT TGCTATTATT TTATTCTTGT AATGTGACCT TTTCACTGTG CAAAGGGAGA 3420
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Seq ID NO: 617 Protein sequence
Protein Accession #: NP_077740.1

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ANLIHSSDPD FQILEDGSVY TTNTILLSSE KRSFTILLSN TENQEKKKIF VFLEHQTKVL 120

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KKRHTKEKVL RRAKRRWAPI PCSMLENSLG PFPLFLQQVQ SDTAQNYTIY YSIRGPGVDQ   180
EPRNLFYVER DTGNLYCTRP VDREQYESFE IIAFATTPDG YTPELPLPLI IKIEDENDNY   240
PIFTEETYTF TIFENCRVGT TVGQVCATDK DEPDTMHTRL KYSIIGQVPP SPTLFSMHPT   300
TGVITTTSSQ LDRELIDKYQ LKIKVQDMDG QYFGLQTTST CIINIDDVND HLPTFTRTSY   360
VTSVEENTVD VEILRVTVED KDLVNTANWR ANYTILKGNE NGNFKIVTDA KTNEGVLCVV   420
KPLNYEEKQQ MILQIGVVNE APFSREASPR SAMSTATVTV NVEDQDEGPE CNPPIQTVRM   480
KENAEVGTTS NGYKAYDPET RSSSGIRYKK LTDPTGWVTI DENTGSIKVF RSLDREAETI   540
KNGIYNITVL ASDQGGRTCT GTLGIILQDV NDNSPFIPKK TVIICKPTMS SAEIVAVDPD   600
EPIHGPPFDF SLESSTSEVQ RMWRLKAIND TAARLSYQND PPFGSYVVPI TVRDRLGMSS   660
VTSLDVTLCD CITENDCTHR VDPRIGGGGV QLGKWAILAI LLGIALLFCI LFTLVCGASG   720
TSKQPKVIPD DLAQQNLIVS NTEAPGDDKV YSANGFTTQT VGASAQGVCG TVGSGIKNGG   780
QETIEMVKGG HQTSESCRGA GHHHTLDSCR GGHTEVDNCR YTYSEWHSFT QPRLGEKVYL   840
CNQDENHKHA QDYVLTYNYE GRGSVAGSVG CCSERQEEDG LEFLDNLEPK FRTLAEACMK   900
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Seq ID NO: 618 DNA sequence
Nucleic Acid Accession #: NM_004949.1
Coding sequence: 202..2745

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GACCTGCCCC GAGCCCTCTC CATGGAGGCA GCCCGCCCCT CCGGCTCCTG GAACGGAGCC    240
CTCTGCCGGC TGCTCCTGCT GACCCTCGCG ATCTTAATAT TTGCCAGTGA TGCCTGCAAA    300
AATGTGACAT TACATGTTCC CTCCAAACTA GATGCCGAGA AACTTGTTGG TAGAGTTAAC    360
CTGAAAGAGT GCTTTACAGC TGCAAATCTA ATTCATTCAA GTGATCCTGA CTTCCAAATT    420
TTGGAGGATG GTTCAGTCTA TACAACAAAT ACTATTCTAT TGTCCTCGGA GAAGAGAAGT    480
TTTACCATAT TACTTTCCAA CACTGAGAAC CAAGAAAAGA AGAAAATATT TGTCTTTTTG    540
GAGCATCAAA CAAAGGTCCT AAAGAAAAGA CATACTAAAG AAAAAGTTCT AAGGCGCGCC    600
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AACTTGTATT GTACTCGTCC TGTAGATCGT GAGCAGTATG AATCTTTTGA GATAATTGCC    840
TTTGCAACAA CTCCAGATGG GTATACTCCA GAACTTCCAC TGCCCCTAAT AATCAAAATA    900
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GAAAATTGCA GAGTGGGCAC TACTGTGGGA CAAGTGTGTG CTACTGACAA AGATGAGCCT   1020
GACACGATGC ACACACGCCT GAAGTACTCC ATCATTGGGC AGGTGCCACC ATCACCCACC   1080
CTATTTTCTA TGCATCCAAC TACAGGCGTG ATCACCACAA CATCATCTCA GCTAGACAGA   1140
GAGTTAATTG ACAAGTACCA GTTGAAAATA AAAGTACAAG ACATGGATGG TCAGTATTTT   1200
GGTCTACAGA CAACTTCAAC TTGTATCATT AACATTGATG ATGTAAATGA CCACTTGCCA   1260
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GAAGGAGTTC TTTGTGTAGT TAAGCCTTTG AATTATGAAG AAAAGCAACA GATGATCTTG   1500
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GTGGTGCTTG GAAACTGTTG TTTTCCTGAA CATCTAAAGT GTGTAGACTG CATTCTTGCT   3420
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Seq ID NO: 619 Protein sequence
Protein Accession #: NP_004940.1

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PIFTEETYTF TIFENCRVGT TVGQVCATDK DEPDTMHTRL KYSIIGQVPP SPTLFSMHPT   300
TGVITTTSSQ LDRELIDKYQ LKIKVQDMDG QYFGLQTTST CIINIDDVND HLPTFTRTSY   360
VTSVEENTVD VEILRVTVED KDLVNTANWR ANYTILKGNE NGNFKIVTDA KTNEGVLCVV   420
KPLNYEEKQQ MILQIGVVNE APFSREASPR SAMSTATVTV NVEDQDEGPE CNPPIQTVRM   480
KENAEVGTTS NGYKAYDPET RSSSGIRYKK LTDPTGWVTI DENTGSIKVF RSLDREAETI   540
KNGIYNITVL ASDQGGRTCT GTLGIILQDV NDNSPFIPKK TVIICKPTMS SAEIVAVDPD   600
EPIHGPPFDF SLESSTSEVQ RMWRLKAIND TAARLSYQND PPFGSYVVPI TVRDRLGMSS   660
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TSKQPKVIPD DLAQQNLIVS NTEAPGDDKV YSANGFTTQT VGASAQGVCG TVGSGIKNGG   780
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Seq ID NO: 620 DNA sequence
Nucleic Acid Accession #: NM_032545.1
Coding sequence: 46..718

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GCACCGACAG TCACCGCTCA ACTGGACCTC CAGTCATTTC GGAGAGGTGA CTGGGAGCGC   240
CGAGGGCTGG GGGCCGGAGG AGCCGCTCCC CTACTCCCGG GCTTTCGGAG AGGGTGCGTC   300
CGCGCGGCCG CGCTGCTGCA GGAACGGCGG TACCTGCGTG CTGGGCAGCT TCTGCGTGTG   360
CCCGGCCCAC TTCACCGGCC GCTACTGCGA GCATGACCAG AGGCGCAGTG AATGCGGCGC   420
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CCTGCACTGC CTCCCCCTCC AGACGCCTGA CCGCTGTGAC CCGAAAGACT TCCTGGCCTC   540
CCACGCTCAC GGGCCGAGCG CCGGGGGCGC GCCCAGCCTG CTACTCTTGC TGCCCTGCGC   600
ACTCCTGCAC CGCCTCCTGC GCCCGGATGC GCCCGCGCAC CCTCGGTCCC TGGTCCCTTC   660
CGTCCTCCAG CGGGAGCGGC GCCCCTGCGG AAGGCCGGGA CTTGGGCATC GCCTTTAATT   720
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Seq ID NO: 621 Protein sequence
Protein Accession #: NP_115934.1

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VTGSAEGWGP EEPLPYSRAF GEGASARPRC CRNGGTCVLG SFCVCPAHFT GRYCEHDQRR   120
SECGALEHGA WTLRACHLCR CIFGALHCLP LQTPDRCDPK DFLASHAHGP SAGGAPSLLL   180
LLPCALLHRL LRPDAPAHPR SLVPSVLQRE RRPCGRPGLG HRL
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Seq ID NO: 622 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..390

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ATGAGGTTCA GTGTCTCAGG CATGAGGACC GACTACCCCA GGAGTGTGCT GGCTCCTGCT    60
TATGTGTCAG TCTGTCTCCT CCTCTTGTGT CCAAGGGAAG TCATCGCTCC CGCTGGCTCA   120
GAACCATGGC TGTGCCAGCC GGCACCCAGG TGTGGAGACA AGATCTACAA CCCCTTGGAG   180
CAGTGCTGTT ACAATGACGC CATCGTGTCC CTGAGCGAGA CCCGCCAATG TGGTCCCCCC   240
TGCACCTTCT GGCCCTGCTT TGAGCTCTGC TGTCTTGATT CCTTTGGCCT CACAAACGAT   300
TTTGTTGTGA AGCTGAAGGT TCAGGGTGTG AATTCCCAGT GCCACTCATC TCCCATCTCC   360
AGTAAATGTG AAAGAGGCCG GATATGTTAG
```

Seq ID NO: 623 Protein sequence
Protein Accession #: FGENESH predicted

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1          11         21         31         41         51
|          |          |          |          |          |
MRFSVSGMRT DYPRSVLAPA YVSVCLLLLC PREVIAPAGS EPWLCQPAPR CGDKIYNPLE    60
QCCYNDAIVS LSETRQCGPP CTFWPCFELC CLDSFGLTND FVVKLKVQGV NSQCHSSPIS   120
SKCERGRIC
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Seq ID NO: 624 DNA sequence
Nucleic Acid Accession #: M18728.1
Coding sequence: 51..1085

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1          11         21         31         41         51
|          |          |          |          |          |
GGAGCTCAAG CTCCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC    60
CCTCAGCCCC TCCCTGCAGA TTGCATGTCC CCTGGAAGGA GGTCCTGCTC ACAGCCTCAC   120
TTCTAACCTT CTGGAACCCA CCCACCACTG CCAAGCTCAC TATTGAATCC ACGCCATTCA   180
ATGTCGCAGA GGGGAAGGAG GTTCTTCTAC TCGCCCACAA CCTGCCCCAG AATCGTATTG   240
GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA   300
TAGGAACTCA ACAAGCTACC CCAGGGCCCG CATACAGTGG TCGAGAGACA ATATACCCCA   360
ATGCATCCCT GCTGATCCAG AACGTCACCC AGAATGACAC AGGATTCTAT ACCCTACAAG   420
TCATAAAGTC AGATCTTGTG AATGAAGAAG CAACCGGACA GTTCCATGTA TACCCGGAGC   480
TGCCCAAGCC CTCCATCTCC AGCAACAACT CCAACCCCGT GGAGGACAAG GATGCTGTGG   540
CCTTCACCTG TGAACCTGAG GTTCAGAACA CAACCTACCT GTGGTGGGTA AATGGTCAGA   600
GCCTCCCGGT CAGTCCCAGG CTGCAGCTGT CCAATGGCAA CATGACCCTC ACTCTACTCA   660
```

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GCGTCAAAAG GAACGATGCA GGATCCTATG AATGTGAAAT ACAGAACCCA GCGAGTGCCA   720
ACCGCAGTGA CCCAGTCACC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCCC   780
CCTCAAAGGC CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCCTGCCAC GCAGCCTCTA   840
ACCCACCTGC ACAGTACTCT TGGTTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC   900
TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCATAACT   960
CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGCTCCTG  1020
TCCTCTCAGC TGTGGCCACC GTCGGCATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA  1080
TATAGCAGCC CTGGTGTATT TTCGATATTT CAGGAAGACT GGCAGATTGG ACCAGACCCT  1140
GAATTCTTCT AGCTCCTCCA ATCCCATTTT ATCCCATGGA ACCACTAAAA ACAAGGTCTG  1200
CTCTGCTCCT GAAGCCCTAT ATGCTGGAGA TGGACAACTC AATGAAAATT TAAAGGGAAA  1260
ACCCTCAGGC CTGAGGTGTG TGCCACTCAG AGACTTCACC TAACTAGAGA CAGTCAAACT  1320
GCAAACCATG GTGAGAAATT GACGACTTCA CACTATGGAC AGCTTTTCCC AAGATGTCAA  1380
AACAAGACTC CTCATCATGA TAAGGCTCTT ACCCCCTTTT AATTTGTCCT TGCTTATGCC  1440
TGCCTCTTTC GCTTGGCAGG ATGATGCTGT CATTAGTATT TCACAAGAAG TAGCTTCAGA  1500
GGGTAACTTA ACAGAGTGTC AGATCTATCT TGTCAATCCC AACGTTTTAC ATAAAATAAG  1560
AGATCCTTTA GTGCACCCAG TGACTGACAT TAGCAGCATC TTTAACACAG CCGTGTGTTC  1620
AAATGTACAG TGGTCCTTTT CAGAGTTGGA CTTCTAGACT CACCTGTTCT CACTCCCTGT  1680
TTTAATTCAA CCCAGCCATG CAATGCCAAA TAATAGAATT GCTCCCTACC AGCTGAACAG  1740
GGAGGAGTCT GTGCAGTTTC TGACACTTGT TGTTGAACAT GGCTAAATAC AATGGGTATC  1800
GCTGAGACTA AGTTGTAGAA ATTAACAAAT GTGCTGCTTG GTTAAAATGG CTACACTCAT  1860
CTGACTCATT CTTTATTCTA TTTTAGTTGG TTTGTATCTT GCCTAAGGTG CGTAGTCCAA  1920
CTCTTGGTAT TACCCTCCTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT  1980
CTCTAAAAGC TTTAAATGTC TGCATGCAGC CAGCCATCAA ATAGTGAATG GTCTCTCTTT  2040
GGCTGGAATT ACAAAACTCA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG  2100
ATAAAAGCCC CAAATGGTGG TAACTGATAA TAGCACTAAT GCTTTAAGAT TTGGTCACAC  2160
TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT  2220
GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTAAAAC CAATTTAAAA AAAAAAAAGA  2280
ACACAGGAGA TTCCAGTCTA CTTGAGTTAG CATAATACAG AAGTCCCCTC TACTTTAACT  2340
TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTTAACCAA TGTATTTATT TCTGTGGTTC  2400
TGTTTCCTTG TTCCAATTTG ACAAAACCCA CTGTTCTTGT ATTGTATTGC CCAGGGGGAG  2460
CTATCACTGT ACTTGTAGAG TGGTGCTGCT TTAATTCATA AATCACAAAT AAAAGCCAAT  2520
TAGCTCTATA ACT
```

Seq ID NO: 625 Protein sequence
Protein Accession #: AAA59907.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MGPPSAPPCR LHVPWKEVLL TASLLTFWNP PTTAKLTIES TPFNVAEGKE VLLLAHNLPQ    60
NRIGYSWYKG ERVDGNSLIV GYVIGTQQAT PGPAYSGRET IYPNASLLIQ NVTQNDTGFY   120
TLQVIKSDLV NEEATGQFHV YPELPKPSIS SNNSNPVEDK DAVAFTCEPE VQNTTYLWWV   180
NGQSLPVSPR LQLSNGNMTL TLLSVKRNDA GSYECEIQNP ASANRSDPVT LNVLYGPDVP   240
TISPSKANYR PGENLNLSCH AASNPPAQYS WFINGTFQQS TQELFIPNIT VNNSGSYMCQ   300
AHNSATGLNR TTVTMITVSG SAPVLSAVAT VGITIGVLAR VALI
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Seq ID NO: 626 DNA sequence
Nucleic Acid Accession #: M18728.1
Coding sequence: 1355..1657

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1          11         21         31         41         51
|          |          |          |          |          |
GGAGCTCAAG CTCCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC    60
CCTCAGCCCC TCCCTGCAGA TTGCATGTCC CCTGGAAGGA GGTCCTGCTC ACAGCCTCAC   120
TTCTAACCTT CTGGAACCCA CCCACCACTG CCAAGCTCAC TATTGAATCC ACGCCATTCA   180
ATGTCGCAGA GGGGAAGGAG GTTCTTCTAC TCGCCCACAA CCTGCCCCAG AATCGTATTG   240
GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA   300
TAGGAACTCA ACAAGCTACC CCAGGGCCCG CATACAGTGG TCGAGAGACA ATATACCCCA   360
ATGCATCCCT GCTGATCCAG AACGTCACCC AGAATGACAC AGGATTCTAT ACCCTACAAG   420
TCATAAAGTC AGATCTTGTG AATGAAGAAG CAACCGGACA GTTCCATGTA TACCCGGAGC   480
TGCCCAAGCC CTCCATCTCC AGCAACAACT CCAACCCCGT GGAGGACAAG GATGCTGTGG   540
CCTTCACCTG TGAACCTGAG GTTCAGAACA CAACCTACCT GTGGTGGGTA AATGGTCAGA   600
GCCTCCCGGT CAGTCCCAGG CTGCAGCTGT CCAATGGCAA CATGACCCTC ACTCTACTCA   660
GCGTCAAAAG GAACGATGCA GGATCCTATG AATGTGAAAT ACAGAACCCA GCGAGTGCCA   720
ACCGCAGTGA CCCAGTCACC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCCC   780
CCTCAAAGGC CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCCTGCCAC GCAGCCTCTA   840
ACCCACCTGC ACAGTACTCT TGGTTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC   900
TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCATAACT   960
CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGCTCCTG  1020
TCCTCTCAGC TGTGGCCACC GTCGGCATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA  1080
TATAGCAGCC CTGGTGTATT TTCGATATTT CAGGAAGACT GGCAGATTGG ACCAGACCCT  1140
GAATTCTTCT AGCTCCTCCA ATCCCATTTT ATCCCATGGA ACCACTAAAA ACAAGGTCTG  1200
CTCTGCTCCT GAAGCCCTAT ATGCTGGAGA TGGACAACTC AATGAAAATT TAAAGGGAAA  1260
ACCCTCAGGC CTGAGGTGTG TGCCACTCAG AGACTTCACC TAACTAGAGA CAGTCAAACT  1320
GCAAACCATG GTGAGAAATT GACGACTTCA CACTATGGAC AGCTTTTCCC AAGATGTCAA  1380
AACAAGACTC CTCATCATGA TAAGGCTCTT ACCCCCTTTT AATTTGTCCT TGCTTATGCC  1440
TGCCTCTTTC GCTTGGCAGG ATGATGCTGT CATTAGTATT TCACAAGAAG TAGCTTCAGA  1500
GGGTAACTTA ACAGAGTGTC AGATCTATCT TGTCAATCCC AACGTTTTAC ATAAAATAAG  1560
AGATCCTTTA GTGCACCCAG TGACTGACAT TAGCAGCATC TTTAACACAG CCGTGTGTTC  1620
AAATGTACAG TGGTCCTTTT CAGAGTTGGA CTTCTAGACT CACCTGTTCT CACTCCCTGT  1680
TTTAATTCAA CCCAGCCATG CAATGCCAAA TAATAGAATT GCTCCCTACC AGCTGAACAG  1740
GGAGGAGTCT GTGCAGTTTC TGACACTTGT TGTTGAACAT GGCTAAATAC AATGGGTATC  1800
GCTGAGACTA AGTTGTAGAA ATTAACAAAT GTGCTGCTTG GTTAAAATGG CTACACTCAT  1860
CTGACTCATT CTTTATTCTA TTTTAGTTGG TTTGTATCTT GCCTAAGGTG CGTAGTCCAA  1920
CTCTTGGTAT TACCCTCCTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT  1980
CTCTAAAAGC TTTAAATGTC TGCATGCAGC CAGCCATCAA ATAGTGAATG GTCTCTCTTT  2040
GGCTGGAATT ACAAAACTCA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG  2100
ATAAAAGCCC CAAATGGTGG TAACTGATAA TAGCACTAAT GCTTTAAGAT TTGGTCACAC  2160
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TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT 2220
GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTAAAAC CAATTTAAAA AAAAAAAAGA 2280
ACACAGGAGA TTCCAGTCTA CTTGAGTTAG CATAATACAG AAGTCCCCTC TACTTTAACT 2340
TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTTAACCAA TGTATTTATT TCTGTGGTTC 2400
TGTTTCCTTG TTCCAATTTG ACAAAACCCA CTGTTCTTGT ATTGTATTGC CCAGGGGGAG 2460
CTATCACTGT ACTTGTAGAG TGGTGCTGCT TTAATTCATA AATCACAAAT AAAAGCCAAT 2520
TAGCTCTATA ACT
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Seq ID NO: 627 Protein sequence
Protein Accession #: AAA59908.1

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1          11         21         31         41         51
|          |          |          |          |          |
MDSFSQDVKT RLLIMIRLLP PFNLSLLMPA SPAWQDDAVI SISQEVASEG NLTECQIYLV   60
NPNVLHKIRD PLVHPVTDIS SIFNTAVCSN VQWSFSELDP
```

Seq ID NO: 628 DNA sequence
Nucleic Acid Accession #: M18728.1
Coding sequence: 2370..2501

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1          11         21         31         41         51
|          |          |          |          |          |
GGAGCTCAAG CTCCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC   60
CCTCAGCCCC TCCCTGCAGA TTGCATGTCC CCTGGAAGGA GGTCCTGCTC ACAGCCTCAC  120
TTCTAACCTT CTGGAACCCA CCCACCACTG CCAAGCTCAC TATTGAATCC ACGCCATTCA  180
ATGTCGCAGA GGGGAAGGAG GTTCTTCTAC TCGCCCACAA CCTGCCCCAG AATCGTATTG  240
GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA  300
TAGGAACTCA ACAAGCTACC CCAGGGCCCG CATACAGTGG TCGAGAGACA ATATACCCCA  360
ATGCATCCCT GCTGATCCAG AACGTCACCC AGAATGACAC AGGATTCTAT ACCCTACAAG  420
TCATAAAGTC AGATCTTGTG AATGAAGAAG CAACCGGACA GTTCCATGTA TACCCGGAGC  480
TGCCCAAGCC CTCCATCTCC AGCAACAACT CCAACCCCGT GGAGGACAAG GATGCTGTGG  540
CCTTCACCTG TGAACCTGAG GTTCAGAACA CAACCTACCT GTGGTGGGTA AATGGTCAGA  600
GCCTCCCGGT CAGTCCCAGG CTGCAGCTGT CCAATGGCAA CATGACCCTC ACTCTACTCA  660
GCGTCAAAAG GAACGATGCA GGATCCTATG AATGTGAAAT ACAGAACCCA GCGAGTGCCA  720
ACCGCAGTGA CCCAGTCACC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCCC  780
CCTCAAAGGC CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCCTGCCAC GCAGCCTCTA  840
ACCCACCTGC ACAGTACTCT TGGTTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC  900
TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCATAACT  960
CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGCTCCTG 1020
TCCTCTCAGC TGTGGCCACC GTCGGCATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA 1080
TATAGCAGCC CTGGTGTATT TTCGATATTT CAGGAAGACT GGCAGATTGG ACCAGACCCT 1140
GAATTCTTCT AGCTCCTCCA ATCCCATTTT ATCCCATGGA ACCACTAAAA ACAAGGTCTG 1200
CTCTGCTCCT GAAGCCCTAT ATGCTGGAGA TGGACAACTC AATGAAAATT TAAAGGGAAA 1260
ACCCTCAGGC CTGAGGTGTG TGCCACTCAG AGACTTCACC TAACTAGAGA CAGTCAAACT 1320
GCAAACCATG GTGAGAAATT GACGACTTCA CACTATGGAC AGCTTTTCCC AAGATGTCAA 1380
AACAAGACTC CTCATCATGA TAAGGCTCTT ACCCCCTTTT AATTTGTCCT TGCTTATGCC 1440
TGCCTCTTTC GCTTGGCAGG ATGATGCTGT CATTAGTATT TCACAAGAAG TAGCTTCAGA 1500
GGGTAACTTA ACAGAGTGTC AGATCTATCT TGTCAATCCC AACGTTTTAC ATAAAATAAG 1560
AGATCCTTTA GTGCACCCAG TGACTGACAT TAGCAGCATC TTTAACACAG CCGTGTGTTC 1620
AAATGTACAG TGGTCCTTTT CAGAGTTGGA CTTCTAGACT CACCTGTTCT CACTCCCTGT 1680
TTTAATTCAA CCCAGCCATG CAATGCCAAA TAATAGAATT GCTCCCTACC AGCTGAACAG 1740
GGAGGAGTCT GTGCAGTTTC TGACACTTGT TGTTGAACAT GGCTAAATAC AATGGGTATC 1800
GCTGAGACTA AGTTGTAGAA ATTAACAAAT GTGCTGCTTG GTTAAAATGG CTACACTCAT 1860
CTGACTCATT CTTTATTCTA TTTTAGTTGG TTTGTATCTT GCCTAAGGTG CGTAGTCCAA 1920
CTCTTGGTAT TACCCTCCTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT 1980
CTCTAAAAGC TTTAAATGTC TGCATGCAGC CAGCCATCAA ATAGTGAATG GTCTCTCTTT 2040
GGCTGGAATT ACAAAACTCA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG 2100
ATAAAAGCCC CAAATGGTGG TAACTGATAA TAGCACTAAT GCTTTAAGAT TTGGTCACAC 2160
TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT 2220
GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTAAAAC CAATTTAAAA AAAAAAAAGA 2280
ACACAGGAGA TTCCAGTCTA CTTGAGTTAG CATAATACAG AAGTCCCCTC TACTTTAACT 2340
TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTTAACCAA TGTATTTATT TCTGTGGTTC 2400
TGTTTCCTTG TTCCAATTTG ACAAAACCCA CTGTTCTTGT ATTGTATTGC CCAGGGGGAG 2460
CTATCACTGT ACTTGTAGAG TGGTGCTGCT TTAATTCATA AATCACAAAT AAAAGCCAAT 2520
TAGCTCTATA ACT
```

Seq ID NO: 629 Protein sequence
Protein Accession #: AAA59909.1

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1          11         21         31         41         51
|          |          |          |          |          |
MLTNVFISVV LFPCSNLTKP TVLVLYCPGG AITVLVEWCC FNS
```

Seq ID NO: 630 DNA sequence
Nucleic Acid Accession #: NM_016639.1
Coding sequence: 40..429

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1          11         21         31         41         51
|          |          |          |          |          |
GCGGCGGGCG CAGACAGCGG CGGGCGCAGG ACGTGCACTA TGGCTCGGGG CTCGCTGCGC   60
CGGTTGCTGC GGCTCCTCGT GCTGGGGCTC TGGCTGGCGT TGCTGCGCTC CGTGGCCGGG  120
GAGCAAGCGC CAGGCACCGC CCCCTGCTCC CGCGGCAGCT CCTGGAGCGC GGACCTGGAC  180
AAGTGCATGG ACTGCGCGTC TTGCAGGGCG CGACCGCACA GCGACTTCTG CCTGGGCTGC  240
GCTGCAGCAC CTCCTGCCCC CTTCCGGCTG CTTTGGCCCA TCCTTGGGGG CGCTCTGAGC  300
CTGACCTTCG TGCTGGGGCT GCTTTCTGGC TTTTTGGTCT GGAGACGATG CCGCAGGAGA  360
GAGAAGTTCA CCACCCCCAT AGAGGAGACC GGCGGAGAGG GCTGCCCAGC TGTGGCGCTG  420
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ATCCAGTGAC AATGTGCCCC CTGCCAGCCG GGGCTCGCCC ACTCATCATT CATTCATCCA    480
TTCTAGAGCC AGTCTCTGCC TCCCAGACGC GGCGGGAGCC AAGCTCCTCC AACCACAAGG    540
GGGGTGGGGG GCGGTGAATC ACCTCTGAGG CCTGGGCCCA GGGTTCAGGG GAACCTTCCA    600
AGGTGTCTGG TTGCCCTGCC TCTGGCTCCA GAACAGAAAG GGAGCCTCAC GCTGGCTCAC    660
ACAAAACAGC TGACACTGAC TAAGGAACTG CAGCATTTGC ACAGGGGAGG GGGGTGCCCT    720
CCTTCCTTAG GACCTGGGGG CCAGGCTGAC TTGGGGGGCA GACTTGACAC TAGGCCCCAC    780
TCACTCAGAT GTCCTGAAAT TCCACCACGG GGGTCACCCT GGGGGGTTAG GGACCTATTT    840
TTAACACTAG GGGCTGGCCC ACTAGGAGGG CTGGCCCTAA GATACAGACC CCCCCAACTC    900
CCCAAAGCGG GGAGGAGATA TTTATTTTGG GGAGAGTTTG GAGGGGAGGG AGAATTTATT    960
AATAAAAGAA TCTTTAACTT TAAAAAAAAA AAAAAAAA
```

Seq ID NO: 631 Protein sequence
Protein Accession #: NP_057723.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MARGSLRRLL RLLVLGLWLA LLRSVAGEQA PGTAPCSRGS SWSADLDKCM DCASCRARPH     60
SDFCLGCAAA PPAPFRLLWP ILGGALSLTF VLGLLSGFLV WRRCRRREKF TTPIEETGGE    120
GCPAVALIQ
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Seq ID NO: 632 DNA sequence
Nucleic Acid Accession #: NM_003816.1
Coding sequence: 79..2538

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1          11         21         31         41         51
|          |          |          |          |          |
CGGCAGGGTT GGAAAATGAT GGAAGAGGCG GAGGTGGAGG CGACCGAGTG CTGAGAGGAA     60
CCTGCGGAAT CGGCCGAGAT GGGGTCTGGC GCGCGCTTTC CCTCGGGGAC CCTTCGTGTC    120
CGGTGGTTGC TGTTGCTTGG CCTGGTGGGC CCAGTCCTCG GTGCGGCGCG GCCAGGCTTT    180
CAACAGACCT CACATCTTTC TTCTTATGAA ATTATAACTC CTTGGAGATT AACTAGAGAA    240
AGAAGAGAAG CCCCTAGGCC CTATTCAAAA CAAGTATCTT ATGTTATTCA GGCTGAAGGA    300
AAAGAGCATA TTATTCACTT GGAAAGGAAC AAAGACCTTT TGCCTGAAGA TTTTGTGGTT    360
TATACTTACA ACAAGGAAGG GACTTTAATC ACTGACCATC CCAATATACA GAATCATTGT    420
CATTATCGGG GCTATGTGGA GGGAGTTCAT AATTCATCCA TTGCTCTTAG CGACTGTTTT    480
GGACTCAGAG GATTGCTGCA TTTAGAGAAT GCGAGTTATG GGATTGAACC CCTGCAGAAC    540
AGCTCTCATT TTGAGCACAT CATTTATCGA ATGGATGATG TCTACAAAGA GCCTCTGAAA    600
TGTGGAGTTT CCAACAAGGA TATAGAGAAA GAAACTGCAA AGGATGAAGA GGAAGAGCCT    660
CCCAGCATGA CTCAGCTACT TCGAAGAAGA AGAGCTGTCT TGCCACAGAC CCGGTATGTG    720
GAGCTGTTCA TTGTCGTAGA CAAGGAAAGG TATGACATGA TGGGAAGAAA TCAGACTGCT    780
GTGAGAGAAG AGATGATTCT CCTGGCAAAC TACTTGGATA GTATGTATAT TATGTTAAAT    840
ATTCGAATTG TGCTAGTTGG ACTGGAGATT TGGACCAATG GAAACCTGAT CAACATAGTT    900
GGGGGTGCTG GTGATGTGCT GGGGAACTTC GTGCAGTGGC GGGAAAAGTT TCTTATCACA    960
CGTCGGAGAC ATGACAGTGC ACAGCTAGTT CTAAAGAAAG GTTTTGGTGG AACTGCAGGA   1020
ATGGCATTTG TGGGAACAGT GTGTTCAAGG AGCCACGCAG GCGGGATTAA TGTGTTTGGA   1080
CAAATCACTG TGGAGACATT TGCTTCCATT GTTGCTCATG AATTGGGTCA TAATCTTGGA   1140
ATGAATCACG ATGATGGGAG AGATTGTTCC TGTGGAGCAA AGAGCTGCAT CATGAATTCA   1200
GGAGCATCGG GTTCCAGAAA CTTTAGCAGT TGCAGTGCAG AGGACTTTGA GAAGTTAACT   1260
TTAAATAAAG GAGGAAACTG CCTTCTTAAT ATTCCAAAGC CTGATGAAGC CTATAGTGCT   1320
CCCTCCTGTG GTAATAAGTT GGTGGACGCT GGGGAAGAGT GTGACTGTGG TACTCCAAAG   1380
GAATGTGAAT TGGACCCTTG CTGCGAAGGA AGTACCTGTA AGCTTAAATC ATTTGCTGAG   1440
TGTGCATATG GTGACTGTTG TAAAGACTGT CGGTTCCTTC CAGGAGGTAC TTTATGCCGA   1500
GGAAAAACCA GTGAGTGTGA TGTTCCAGAG TACTGCAATG GTTCTTCTCA GTTCTGTCAG   1560
CCAGATGTTT TTATTCAGAA TGGATATCCT TGCCAGAATA ACAAAGCCTA TTGCTACAAC   1620
GGCATGTGCC AGTATTATGA TGCTCAATGT CAAGTCATCT TTGGCTCAAA AGCCAAGGCT   1680
GCCCCCAAAG ATTGTTTCAT TGAAGTGAAT TCTAAAGGTG ACAGATTTGG CAATTGTGGT   1740
TTCTCTGGCA ATGAATACAA GAAGTGTGCC ACTGGGAATG CTTTGTGTGG AAAGCTTCAG   1800
TGTGAGAATG TACAAGAGAT ACCTGTATTT GGAATTGTGC CTGCTATTAT TCAAACGCCT   1860
AGTCGAGGCA CCAAATGTTG GGGTGTGGAT TTCCAGCTAG GATCAGATGT TCCAGATCCT   1920
GGGATGGTTA ACGAAGGCAC AAAATGTGGT GCTGGAAAGA TCTGTAGAAA CTTCCAGTGT   1980
GTAGATGCTT CTGTTCTGAA TTATGACTGT GATGTTCAGA AAAAGTGTCA TGGACATGGG   2040
GTATGTAATA GCAATAAGAA TTGTCACTGT GAAAATGGCT GGGCTCCCCC AAATTGTGAG   2100
ACTAAAGGAT ACGGAGGAAG TGTGGACAGT GGACCTACAT ACAATGAAAT GAATACTGCA   2160
TTGAGGGACG GACTTCTGGT CTTCTTCTTC CTAATTGTTC CCCTTATTGT CTGTGCTATT   2220
TTTATCTTCA TCAAGAGGGA TCAACTGTGG AGAAGCTACT TCAGAAAGAA GAGATCACAA   2280
ACATATGAGT CAGATGGCAA AAATCAAGCA AACCCTTCTA GACAGCCGGG GAGTGTTCCT   2340
CGACATGTTT CTCCAGTGAC ACCTCCCAGA GAAGTTCCTA TATATGCAAA CAGATTTGCA   2400
GTACCAACCT ATGCAGCCAA GCAACCTCAG CAGTTCCCAT CAAGGCCACC TCCACCACAA   2460
CCGAAAGTAT CATCTCAGGG AAACTTAATT CCTGCCCGTC CTGCTCCTGC ACCTCCTTTA   2520
TATAGTTCCC TCACTTGATT TTTTTAACCT TCTTTTTGCA AATGTCTTCA GGGAACTGAG   2580
CTAATACTTT TTTTTTTTCT TGATGTTTTC TTGAAAAGCC TTTCTGTTGC AACTATGAAT   2640
GAAAACAAAA CACCACAAAA CAGACTTCAC TAACACAGAA AAACAGAAAC TGAGTGTGAG   2700
AGTTGTGAAA TACAAGGAAA TGCAGTAAAG CCAGGGAATT TACAATAACA TTTCCGTTTC   2760
CATCATTGAA TAAGTCTTAT TCAGTCATCG GTGAGGTTAA TGCACTAATC ATGGATTTTT   2820
TGAACATGTT ATTGCAGTGA TTCTCAAATT AACTGTATTG GTGTAAGATT TTTGTCATTA   2880
AGTGTTTAAG TGTTATTCTG AATTTTCTAC CTTAGTTATC ATTAATGTAG TTCCTCATTG   2940
AACATGTGAT AATCTAATAC CTGTGAAAAC TGACTAATCA GCTGCCAATA ATATCTAATA   3000
TTTTTCATCA TGCACGAATT AATAATCATC ATACTCTAGA ATCTTGTCTG TCACTCACTA   3060
CATGAATAAG CAAATATTGT CTTCAAAAGA ATGCACAAGA ACCACAATTA AGATGTCATA   3120
TTATTTTGAA AGTACAAAAT ATACTAAAAG AGTGTGTGTG TATTCACGCA GTTACTCGCT   3180
TCCATTTTTA TGACCTTTCA ACTATAGGTA ATAACTCTTA GAGAAATTAA TTTAATATTA   3240
GAATTTCTAT TATGAATCAT GTGAAAGCAT GACATTCGTT CACAATAGCA CTATTTTAAA   3300
TAAATTATAA GCTTTAAGGT ACGAAGTATT TAATAGATCT AATCAAATAT GTTGATTCAT   3360
GGCTATAATA AAGCAGGAGC AATTATAAAA TCTTCAATCA ATTGAACTTT TACAAAACCA   3420
CTTGAGAATT TCATGAGCAC TTTAAAATCT GAACTTTCAA AGCTTGCTAT TAAATCATTT   3480
AGAATGTTTA CATTTACTAA GGTGTGCTGG GTCATGTAAA ATATTAGACA CTAATATTTT   3540
CATAGAAATT AGGCTGGAGA AAGAAGGAAG AAATGGTTTT CTTAAATACC TACAAAAAAG   3600
TTACTGTGGT ATCTATGAGT TATCATCTTA GCTGTGTTAA AAATGAATTT TTACTATGGC   3660
```

AGATATGGTA TGGATCGTAA AATTTTAAGC ACTAAAAATT TTTTCATAAC CTTTCATAAT 3720
AAAGTTTAAT AATAGGTTTA TTAACTGAAT TTCATTAGTT TTTTAAAAGT GTTTTTGGTT 3780
TGTGTATATA TACATATACA AATACAACAT TTACAATAAA TAAAATACTT GAAATTCTCA 3840
AAAAAAAAAA AAAAAAAAAA AAAAA

Seq ID NO: 633 Protein sequence
Protein Accession #: NP_003807.1

1 11 21 31 41 51
| | | | | |
MGSGARFPSG TLRVRWLLLL GLVGPVLGAA RPGFQQTSHL SSYEIITPWR LTRERREAPR 60
PYSKQVSYVI QAEGKEHIIH LERNKDLLPE DFVVYTYNKE GTLITDHPNI QNHCHYRGYV 120
EGVHNSSIAL SDCFGLRGLL HLENASYGIE PLQNSSHFEH IIYRMDDVYK EPLKCGVSNK 180
DIEKETAKDE EEEPPSMTQL LRRRRAVLPQ TRYVELFIVV DKERYDMMGR NQTAVREEMI 240
LLANYLDSMY IMLNIRIVLV GLEIWTNGNL INIVGGAGDV LGNFVQWREK FLITRRRHDS 300
AQLVLKKGFG GTAGMAFVGT VCSRSHAGGI NVFGQITVET FASIVAHELG HNLGMNHDDG 360
RDCSCGAKSC IMNSGASGSR NFSSCSAEDF EKLTLNKGGN CLLNIPKPDE AYSAPSCGNK 420
LVDAGEECDC GTPKECELDP CCEGSTCKLK SFAECAYGDC CKDCRFLPGG TLCRGKTSEC 480
DVPEYCNGSS QFCQPDVFIQ NGYPCQNNKA YCYNGMCQYY DAQCQVIFGS KAKAAPKDCF 540
IEVNSKGDRF GNCGPSGNEY KKCATGNALC GKLQCENVQE IPVFGIVPAI IQTPSRGTKC 600
WGVDFQLGSD VPDPGMVNEG TKCGAGKICR NFQCVDASVL NYDCDVQKKC HGHGVCNSNK 660
NCHCENGWAP PNCETKGYGG SVDSGPTYNE MNTALRDGLL VFFFLIVPLI VCAIFIFIKR 720
DQLWRSYFRK KRSQTYESDG KNQANPSRQP GSVPRHVSPV TPPREVPIYA NRFAVPTYAA 780
KQPQQFPSRP PPPQPKVSSQ GNLIPARPAP APPLYSSLT

Seq ID NO: 634 DNA sequence
Nucleic Acid Accession #: NM_002091.1
Coding sequence: 56..503

1 11 21 31 41 51
| | | | | |
AGTCTCTGCT CTTCCCAGCC TCTCCGGCGC GCTCCAAGGG CTTCCCGTCG GGACCATGCG 60
CGGCAGTGAG CTCCCGCTGG TCCTGCTGGC GCTGGTCCTC TGCCTAGCGC CCCGGGGGCG 120
AGCGGTCCCG CTGCCTGCGG GCGGAGGGAC CGTGCTGACC AAGATGTACC CGCGCGGCAA 180
CCACTGGGCG GTGGGGCACT TAATGGGGAA AAAGAGCACA GGGGAGTCTT CTTCTGTTTC 240
TGAGAGAGGG AGCCTGAAGC AGCAGCTGAG AGAGTACATC AGGTGGGAAG AAGCTGCAAG 300
GAATTTGCTG GGTCTCATAG AAGCAAAGGA GAACAGAAAC CACCAGCCAC CTCAACCCAA 360
GGCCTTGGGC AATCAGCAGC CTTCGTGGGA TTCAGAGGAT AGCAGCAACT TCAAAGATGT 420
AGGTTCAAAA GGCAAAGTTG GTAGACTCTC TGCTCCAGGT TCTCAACGTG AAGGAAGGAA 480
CCCCCAGCTG AACCAGCAAT GATAATGATG GCCTCTCTCA AAAGAGAAAA ACAAAACCCC 540
TAAGAGACTG AGTTCTGCAA GCATCAGTTC TACGGATCAT CAACAAGATT TCCTTGTGCA 600
AAATATTTGA CTATTCTGTA TCTTTCATCC TTGACTAAAT TCGTGATTTT CAAGCAGCAT 660
CTTCTGGTTT AAACTTGTTT GCTGTGAACA ATTGTCGAAA AGAGTCTTCC AATTAATGCT 720
TTTTTATATC TAGGCTACCT GTTGGTTAGA TTCAAGGCCC CGAGCTGTTA CCATTCACAA 780
TAAAAGCTTA AACACAT

Seq ID NO: 635 Protein sequence
Protein Accession #: NP_002082.1

1 11 21 31 41 51
| | | | | |
MRGSELPLVL LALVLCLAPR GRAVPLPAGG GTVLTKMYPR GNHWAVGHLM GKKSTGESSS 60
VSERGSLKQQ LREYIRWEEA ARNLLGLIEA KENRNHQPPQ PKALGNQQPS WDSEDSSNFK 120
DVGSKGKVGR LSAPGSQREG RNPQLNQQ

Seq ID NO: 636 DNA sequence
Nucleic Acid Accession #: NM_016522.1
Coding sequence: 265..1299

1 11 21 31 41 51
| | | | | |
GCGGAAGCAG CGAGGAGGGA GCCCCCTTTG GCCGTCCTCC GTGGAACCGG TTTTCCGAGG 60
CTGGCAAAAG CCGAGGCTGG ATTTGGGGGA GGAATATTAG ACTCGGAGGA GTCTGCGCGC 120
TTTTCTCCTC CCCGCGCCTC CCGGTCGCCG CGGGTTCACC GCTCAGTCCC CGCGCTCGCT 180
CCGCACCCCA CCCACTTCCT GTGCTCGCCC GGGGGGCGTG TGCCGTGCGG CTGCCGGAGT 240
TCGGGGAAGT TGTGGCTGTC GAGAATGGGG GTCTGTGGGT ACCTGTTCCT GCCCTGGAAG 300
TGCCTCGTGG TCGTGTCTCT CAGGCTGCTG TTCCTTGTAC CCACAGGAGT GCCCGTGCGC 360
AGCGGAGATG CCACCTTCCC CAAAGCTATG GACAACGTGA CGGTCCGGCA GGGGGAGAGC 420
GCCACCCTCA GGTGCACTAT TGACAACCGG GTCACCCGGG TGGCCTGGCT AAACCGCAGC 480
ACCATCCTCT ATGCTGGGAA TGACAAGTGG TGCCTGGATC CTCGCGTGGT CCTTCTGAGC 540
AACACCCAAA CGCAGTACAG CATCGAGATC CAGAACGTGG ATGTGTATGA CGAGGGCCCT 600
TACACCTGCT CGGTGCAGAC AGACAACCAC CCAAAGACCT CTAGGGTCCA CCTCATTGTG 660
CAAGTATCTC CCAAAATTGT AGAGATTTCT TCAGATATCT CCATTAATGA AGGGAACAAT 720
ATTAGCCTCA CCTGCATAGC AACTGGTAGA CCAGAGCCTA CGGTTACTTG GAGACACATC 780
TCTCCCAAAG CGGTTGGCTT TGTGAGTGAA GACGAATACT TGGAAATTCA GGGCATCACC 840
CGGGAACAGT CAGGGGACTA CGAGTGCAGT GCCTCCAATG ACGTGGCCGC GCCCGTGGTA 900
CGGAGAGTAA AGGTCACCGT GAACTATCCA CCATACATTT CAGAAGCCAA GGGTACAGGT 960
GTCCCCGTGG GACAAAAGGG GACACTGCAG TGTGAAGCCT CAGCAGTCCC CTCAGCAGAA 1020
TTCCAGTGGT ACAAGGATGA CAAAAGACTG ATTGAAGGAA AGAAAGGGGT GAAAGTGGAA 1080
AACAGACCTT TCCTCTCAAA ACTCATCTTC TTCAATGTCT CTGAACATGA CTATGGGAAC 1140
TACACTTGCG TGGCCTCCAA CAAGCTGGGC CACACCAATG CCAGCATCAT GCTATTTGGT 1200
CCAGGCGCCG TCAGCGAGGT GAGCAACGGC ACGTCGAGGA GGGCAGGCTG CGTCTGGCTG 1260
CTGCCTCTTC TGGTCTTGCA CCTGCTTCTC AAATTTTGAT GTGAGTGCCA CTTCCCCACC 1320
CGGGAAAGGC TGCCGCCACC ACCACCACCA ACACAACAGC AATGGCAACA CCGACAGCAA 1380
CCAATCAGAT ATATACAAAT GAAATTAGAA GAAACACAGC CTCATGGGAC AGAAATTTGA 1440
GGGAGGGGAA CAAAGAATAC TTTGGGGGGA AAAGAGTTTT AAAAAAGAAA TTGAAAATTG 1500
CCTTGCAGAT ATTTAGGTAC AATGGAGTTT TCTTTTCCCA AACGGGAAGA ACACAGCACA 1560

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CCCGGCTTGG ACCCACTGCA AGCTGCATCG TGCAACCTCT TTGGTGCCAG TGTGGGCAAG  1620
GGCTCAGCCT CTCTGCCCAC AGACTGCCCC CACGTGGAAC ATTCTGGAGC TGGCCATCCC  1680
AAATTCAATC AGTCCATAGA GACGAACAGA ATGAGACCTT CCGGCCCAAG CGTGGCGCTT  1740
CCGGCCCAAG CGTGGCGCTG CGGGCACTTT GGTAGACTGT GCCACCACGG CGTGTGTTGT  1800
GAAACGTGAA ATAAAAAGAG CAAAAAAAAA AAAAAAAAA
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Seq ID NO: 637 Protein sequence
Protein Accession #: NP_057606.1

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1          11         21         31         41         51
|          |          |          |          |          |
MGVCGYLFLP WKCLVVVSLR LLFLVPTGVP VRSGDATFPK AMDNVTVRQG ESATLRCTID    60
NRVTRVAWLN RSTILYAGND KWCLDPRVVL LSNTQTQYSI EIQNVDVYDE GPYTCSVQTD   120
NHPKTSRVHL IVQVSPKIVE ISSDISINEG NNISLTCIAT GRPEPTVTWR HISPKAVGFV   180
SEDEYLEIQG ITREQSGDYE CSASNDVAAP VVRRVKVTVN YPPYISEAKG TGVPVGQKGT   240
LQCEASAVPS AEFQWYKDDK RLIEGKKGVK VENRPFLSKL IFFNVSEHDY GNYTCVASNK   300
LGHTNASIML FGPGAVSEVS NGTSRRAGCV WLLPLLVLHL LLKF
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Seq ID NO: 638 DNA sequence
Nucleic Acid Accession #: NM_012261.1
Coding sequence: 203..1045

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1          11         21         31         41         51
|          |          |          |          |          |
GATTTGCTCT GCCAGCAGCT GTCGGTGCCG CGCTCGACAC CGAGTCCTAG CTAGGCGCTC    60
ACAGAATACG CGCTCCCTCC CTCCCCCTTC TCTGTCCCCC GCCTCTCGCT CACCCCGGCC   120
CACTCCAGCG GCGACTTTGA GGGATTCCCT CTCTGGCGGC CTCTGCAGCA GCACAGCCGG   180
CCTCATTCGG GGCACTGCGA GTATGGATCT CCAAGGAAGA GGGGTCCCCA GCATCGACAG   240
ACTTCGAGTT CTCCTGATGT TGTTCCATAC AATGGCTCAA ATCATGGCAG AACAAGAAGT   300
GGAAAATCTC TCAGGCCTTT CCACTAACCC TGAAAAAGAT ATATTTGTGG TGCGGGAAAA   360
TGGGACGACG TGTCTCATGG CAGAGTTTGC AGCCAAATTT ATTGTACCTT ATGATGTGTG   420
GGCCAGCAAC TACGTAGATC TGATCACAGA ACAGGCCGAT ATCGCATTGA CCCGGGGAGC   480
TGAGGTGAAG GGCCGCTGTG GCCACAGCCA GTCGGAGCTG CAAGTGTTCT GGGTGGATCG   540
CGCATATGCA CTCAAAATGC TCTTTGTAAA GGAAAGCCAC AACATGTCCA AGGGACCTGA   600
GGCGACTTGG AGGCTGAGCA AAGTGCAGTT TGTCTACGAC TCCTCGGAGA AAACCCACTT   660
CAAAGACGCA GTCAGTGCTG GGAAGCACAC AGCCAACTCG CACCACCTCT CTGCCTTGGT   720
CACCCCCGCT GGGAAGTCCT ATGAGTGTCA AGCTCAACAA ACCATTTCAC TGGCCTCTAG   780
TGATCCGCAG AAGACGGTCA CCATGATCCT GTCTGCGGTC CACATCCAAC CTTTTGACAT   840
TATCTCAGAT TTTGTCTTCA GTGAAGAGCA TAAATGCCCA GTGGATGAGC GGGAGCAACT   900
GGAAGAAACC TTGCCCCTGA TTTTGGGGCT CATCTTGGGC CTCGTCATCA TGGTAACACT   960
CGCGATTTAC CACGTCCACC ACAAAATGAC TGCCAACCAG GTGCAGATCC CTCGGGACAG  1020
ATCCCAGTAT AAGCACATGG GCTAGAGGCC GTTAGGCAGG CACCCCCTAT TCCTGCTCCC  1080
CCAACTGGAT CAGGTAGAAC AACAAAAGCA CTTTTCCATC TTGTACACGA GATACACCAA  1140
CATAGCTACA ATCAAACAGG CCTGGGTATC TGAGGCTTGC TTGGCTTGTG TCCATGCTTA  1200
AACCCACGGA AGGGGGAGAC TCTTTCGGAT TTGTAGGGTG AAATGGCAAT TATTCTCTCC  1260
ATGCTGGGGA GGAGGGGAGG AGGGTCTCAG ACAGCTTTCG TGCTCATGGT GGCTTGGCTT  1320
TGACTCTCCA AAGAGCAATA AATGCCACTT GGAGCTGTAT CTGGCCCCAA AGTTTAGGGA  1380
TTGAAAACAT GCTTCTTTGA GGAGGAAACC CCTTTAGGTT CAGAAGAATA TGGGGTGCTT  1440
TGCTCCCTTG GACACAGCTG GCTTATCCTA TACAGTTGTC AATGCACACA GAATACAACC  1500
TCATGCTCCC TGCAGCAAGA CCCCTGAAAG TGATTCATGC TTCTGGCTGG CATTCTGCAT  1560
GTTTAGTGAT TGTCTTGGGA ATGTTTCACT GCTACCCGCA TCCAGCGACT GCAGCACCAG  1620
AAAACGACTA ATGTAACTAT GCAGAGTTGT TTGGACTTCT TCCTGTGCCA GGTCCAAGTC  1680
GGGGGACCTG AAGAATCAAT CTGTGTGAGT CTGTTTTTCA AAATGAAATA AAACACACTA  1740
TTCTCTGGC
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Seq ID NO: 639 Protein sequence
Protein Accession #: NP_036393.1

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1          11         21         31         41         51
|          |          |          |          |          |
MDLQGRGVPS IDRLRVLLML FHTMAQIMAE QEVENLSGLS TNPEKDIFVV RENGTTCLMA    60
EFAAKFIVPY DVWASNYVDL ITEQADIALT RGAEVKGRCG HSQSELQVFW VDRAYALKML   120
FVKESHNMSK GPEATWRLSK VQFVYDSSEK THFKDAVSAG KHTANSHHLS ALVTPAGKSY   180
ECQAQQTISL ASSDPQKTVT MILSAVHIQP FDIISDFVFS EEHKCPVDER EQLEETLPLI   240
LGLILGLVIM VTLAIYHVHH KMTANQVQIP RDRSQYKHMG
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Seq ID NO: 640 DNA sequence
Nucleic Acid Accession #: NM_002993.1
Coding sequence: 64..408

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1          11         21         31         41         51
|          |          |          |          |          |
GGCACGAGCC AGTCTCCGCG CCTCCACCCA GCTCAGGAAC CCGCGAACCC TCTCTTGACC    60
ACTATGAGCC TCCCGTCCAG CCGCGCGGCC CGTGTCCCGG GTCCTTCGGG CTCCTTGTGC   120
GCGCTGCTCG CGCTGCTGCT CCTGCTGACG CCGCCGGGGC CCCTCGCCAG CGCTGGTCCT   180
GTCTCTGCTG TGCTGACAGA GCTGCGTTGC ACTTGTTTAC GCGTTACGCT GAGAGTAAAC   240
CCCAAAACGA TTGGTAAACT GCAGGTGTTC CCCGCAGGCC CGCAGTGCTC CAAGGTGGAA   300
GTGGTAGCCT CCCTGAAGAA CGGGAAGCAA GTTTGTCTGG ACCCGGAAGC CCCTTTTCTA   360
AAGAAAGTCA TCCAGAAAAT TTTGGACAGT GGAAACAAGA AAAACTGAGT AACAAAAAAG   420
ACCATGCATC ATAAAATTGC CCAGTCTTCA GCGGAGCAGT TTTCTGGAGA TCCCTGGACC   480
CAGTAAGAAT AAGAAGGAAG GGTTGGTTTT TTTCCATTTT CTACATGGAT TCCCTACTTT   540
GAAGAGTGTG GGGGAAAGCC TACGCTTCTC CCTGAAGTTT ACAGCTCAGC TAATGAAGTA   600
CTAATATAGT ATTTCCACTA TTTACTGTTA TTTTACCTGA TAAGTTATTG AACCCTTTGG   660
CAATTGACCA TATTGTGAGC AAAGAATCAC TGGTTATTAG TCTTTCAATG AATATTGAAT   720
TGAAGATAAC TATTGTATTT CTATCATACA TTCCTTAAAG TCTTACCGAA AAGGCTGTGG   780
ATTTCGTATG GAAATAATGT TTTATTAGTG TGCTGTTGAG GGAGGTATCC TGTTGTTCTT   840
ACTCACTCTT CTCATAAAAT AGGAAATATT TTAGTTCTGT TTTCTTGGGG AATATGTTAC   900
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TCTTTACCCT AGGATGCTAT TTAAGTTGTA CTGTATTAGA ACACTGGGTG TGTCATACCG    960
TTATCTGTGC AGAATATATT TCCTTATTCA GAATTTCTAA AAATTTAAGT TCTGTAAGGG   1020
CTAATATATT CTCTTCCTAT GGTTTTAGAT GTTTGATGTC TTCTTAGTAT GGCATAATGT   1080
CATGATTTAC TCATTAAACT TTGATTTTGT ATGCTATTTT TTCACTATAG GATGACTATA   1140
ATTCTGGTCA CTAAATATAC ACTTTAGATA GATGAAGAAG CCCAAAAACA GATAAATTCC   1200
TGATTGCTAA TTTACATAGA AATGTATTCT CTTGGTTTTT TAAATAAAAG CAAAATTAAC   1260
AATGATCTGT GCTCTGCAAA GTTTTGAAAA TATATTTGAA CAATTTGAAT ATAAATTCAT   1320
CATTTAGTCC TCAAAATATA TACAGCATTG CTAAGATTTT CAGATATCTA TTGTGGATCT   1380
TTTAAAGGTT TTGACCATTT TGTTATGAGG AATTATACAT GTATCACATT CACTATATTA   1440
AAATTGCACT TTTATTTTTT CCTGTGTGTC ATGTTGGTTT TTGGTACTTG TATTGTCATT   1500
TGGAGAAACA ATAAAAGATT TCTAAACCAA AAAAAAAAAA AAAAAAA
```

Seq ID NO: 641 Protein sequence
Protein Accession #: NP_002984.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MSLPSSRAAR VPGPSGSLCA LLALLLLLTP PGPLASAGPV SAVLTELRCT CLRVTLRVNP     60
KTIGKLQVFP AGPQCSKVEV VASLKNGKQV CLDPEAPFLK KVIQKILDSG NKKN
```

Seq ID NO: 642 DNA sequence
Nucleic Acid Accession #: NM_013271.1
Coding sequence: 27..809

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1          11         21         31         41         51
|          |          |          |          |          |
TCCGGAGCCA GGCTCGCTGG GGCAGCATGG CGGGGTCGCC GCTGCTCTGG GGGCCGCGGG     60
CCGGGGGCGT CGGCCTTTTG GTGCTGCTGC TGCTCGGCCT GTTTCGGCCG CCCCCCGCGC    120
TCTGCGCGCG GCCGGTAAAG GAACCCCGCG GCCTAAGCGC AGCGTCTCCG CCCTTGGCTG    180
AGACTGGCGC TCCTCGCCGC TTCCGGCGGT CAGTGCCCCG AGGTGAGGCG GCGGGGGCGG    240
TGCAGGAGCT GGCGCGGGCG CTGGCGCATC TGCTGGAGGC CGAACGTCAG GAGCGGGCGC    300
GGGCCGAGGC GCAGGAGGCT GAGGATCAGC AGGCGCGCGT CCTGGCGCAG CTGCTGCGCG    360
TCTGGGGCGC CCCCCGCAAC TCTGATCCGG CTCTGGGCCT GGACGACGAC CCCGACGCGC    420
CTGCAGCGCA GCTCGCTCGC GCTCTGCTCC GCGCCCGCCT TGACCCTGCC GCCCTAGCAG    480
CCCAGCTTGT CCCCGCGCCC GTCCCCGCCG CGGCGCTCCG ACCCCGGCCC CCGGTCTACG    540
ACGACGGCCC CGCGGGCCCG GATGCTGAGG AGGCAGGCGA CGAGACACCC GACGTGGACC    600
CCGAGCTGTT GAGGTACTTG CTGGGACGGA TTCTTGCGGG AAGCGCGGAC TCCGAGGGGG    660
TGGCAGCCCC GCGCCGCCTC CGCCGTGCCG CCGACCACGA TGTGGGCTCT GAGCTGCCCC    720
CTGAGGGCGT GCTGGGGGCG CTGCTGCGTG TGAAACGCCT AGAGACCCCG GCGCCCCAGG    780
TGCCTGCACG CCGCCTCTTG CCACCCTGAG CACTGCCCGG ATCCCGTGCA CCCTGGGACC    840
CAGAAGTGCC CCCGCCATCC CGCCACCAGG ACTTCTCCCC GCCAGCACGT CCAGAGCAAC    900
TTACCCCGGC CAGCCAGCCC TCTCACCCGA GGATCCCTAC CCCCTGGCCC ACAATAACAT    960
GATCTGAGC
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Seq ID NO: 643 Protein sequence
Protein Accession #: NP_037403.1

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1          11         21         31         41         51
|          |          |          |          |          |
MAGSPLLWGP RAGGVGLLVL LLLGLFRPPP ALCARPVKEP RGLSAASPPL AETGAPRRFR     60
RSVPRGEAAG AVQELARALA HLLEAERQER ARAEAQEAED QQARVLAQLL RVWGAPRNSD    120
PALGLDDDPD APAAQLARAL LRARLDPAAL AAQLVPAPVP AAALRPRPPV YDDGPAGPDA    180
EEAGDETPDV DPELLRYLLG RILAGSADSE GVAAPRRLRR AADHDVGSEL PPEGVLGALL    240
RVKRLETPAP QVPARRLLPP
```

Seq ID NO: 644 DNA sequence
Nucleic Acid Accession #: NM_002214
Coding sequence: 681..2990

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1          11         21         31         41         51
|          |          |          |          |          |
CCCAGAGCCG CCTCCCCCTG TTGCTGGCAT CCCGAGCTTC CTCCCTTGCC AGCCAGGACG     60
CTGCCGACTT GTCTTTGCCC GCTGCTCCGC AGACGGGGCT GCAAAGCTGC AACTAATGGT    120
GTTGGCCTCC CTGCCCACCT GTGGAAGCAA CTGCGCTGAT TGATGCGCCA CAGACTTTTT    180
TCCCCTCGAC CTCGCCGGCG TACCCTCCCA CAGATCCAGC ATCACCCAGT GAATGTACAT    240
TAGGGTGGTT TCCCCCCCAG CTTCGGGCTT TGTTTGGGTT TGATTGTGTT TGGCTCTTCG    300
CTAAGCTGAT TTATGCAGCA GAAGCCCCAC CGGCTGGAGA GAAACAAAAG CTCTTTTCTT    360
TGTCCCGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTCGCC GCCGGGCCCT    420
TGGCCGTCGA AGGAGGTGCT TCTCGCGGAG ACCGCGGGAC CCGCCGTGCC GAGCCGGGAG    480
GGCCGTAGGG GCCCTGAGAT GCCGAGCGGT GCCCGGGCCC GCTTACCTGC ACCGCTTGCT    540
CCGAGCCGCG GGGTCCGCCT GCTAGGCCTG CGGAAAACGT CCTAGCGACA CTCGCCCGCG    600
GGCCCCGAGG TCGCCCGGGA GGCCGAGCCC GCGTCCGGAA GGCAGCCAGG CGGCGGGCGC    660
GGGGCGGGCT GTTTTGCATT ATGTGCGGCT CGGCCCTGGC TTTTTTTACC GCTGCATTTG    720
TCTGCCTGCA AAACGACCGG CGAGGTCCCG CCTCGTTCCT CTGGGCAGCC TGGGTGTTTT    780
CACTTGTTCT TGGACTGGGC CAAGGTGAAG ACAATAGATG TGCATCTTCA AATGCAGCAT    840
CCTGTGCCAG GTGCCTTGCG CTGGGTCCAG AATGTGGATG GTGTGTTCAA GAGGATTTCA    900
TTTCAGGTGG ATCAAGAAGT GAACGTTGTG ATATTGTTTC CAATTTAATA AGCAAAGGCT    960
GCTCAGTTGA TTCAATAGAA TACCCATCTG TGCATGTTAT AATACCCACT GAAAATGAAA   1020
TTAATACCCA GGTGACACCA GGAGAAGTGT CTATCCAGCT GCGTCCAGGA GCCGAAGCTA   1080
ATTTTATGCT GAAAGTTCAT CCTCTGAAGA AATATCCTGT GGATCTTTAT TATCTTGTTG   1140
ATGTCTCAGC ATCAATGCAC AATAATATAG AAAAATTAAA TTCCGTTGGA AACGATTTAT   1200
CTAGAAAAAT GGCATTTTTC TCCCGTGACT TTCGTCTTGG ATTTGGCTCA TACGTTGATA   1260
AAACAGTTTC ACCATACATT AGCATCCACC CCGAAAGGAT TCATAATCAA TGCAGTGACT   1320
ACAATTTAGA CTGCATGCCT CCCCATGGAT ACATCCATGT GCTGTCTTTG ACAGAGAACA   1380
TCACTGAGTT TGAGAAAGCA GTTCATAGAC AGAAGATCTC TGGAAACATA GATACACCAG   1440
AAGGAGGTTT TGACGCCATG CTTCAGGCAG CTGTCTGTGA AAGTCATATC GGATGGCGAA   1500
AAGAGGCTAA AAGATTGCTG CTGGTGATGA CAGATCAGAC GTCTCATCTC GCTCTTGATA   1560
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GCAAATTGGC AGGCATAGTG GTGCCCAATG ACGGAAACTG TCATCTGAAA AACAACGTCT  1620
ACGTCAAATC GACAACCATG GAACACCCCT CACTAGGCCA ACTTTCAGAG AAATTAATAG  1680
ACAACAACAT TAATGTCATC TTTGCAGTTC AAGGAAAACA ATTTCATTGG TATAAGGATC  1740
TTCTACCCCT CTTGCCAGGC ACCATTGCTG GTGAAATAGA ATCAAAGGCT GCAAACCTCA  1800
ATAATTTGGT AGTGGAAGCC TATCAGAAGC TCATTTCAGA AGTGAAAGTT CAGGTGGAAA  1860
ACCAGGTACA AGGCATCTAT TTTAACATTA CCGCCATCTG TCCAGATGGG TCCAGAAAGC  1920
CAGGCATGGA AGGATGCAGA AACGTGACGA GCAATGATGA AGTTCTTTTC AATGTAACAG  1980
TTACAATGAA AAAATGTGAT GTCACAGGAG GAAAAAACTA TGCAATAATC AAACCTATTG  2040
GTTTTAATGA AACCGCTAAA ATTCATATAC ACAGAAACTG CAGCTGTCAG TGTGAGGACA  2100
ACAGAGGACC TAAAGGAAAG TGTGTAGATG AAACTTTTCT AGATTCCAAG TGTTTCCAGT  2160
GTGATGAGAA TAAATGTCAT TTTGATGAAG ATCAGTTTTC TTCTGAGAGT TGCAAGTCAC  2220
ACAAGGATCA GCCTGTTTGC AGTGGTCGAG GAGTTTGTGT TTGTGGGAAA TGTTCATGTC  2280
ACAAAATTAA GCTTGGAAAA GTGTATGGAA AATACTGTGA AAAGGATGAC TTTTCTTGTC  2340
CATATCACCA TGGAAATCTG TGTGCTGGGC ATGGAGAGTG TGAAGCAGGC AGATGCCAAT  2400
GCTTCAGTGG CTGGGAAGGT GATCGATGCC AGTGCCCTTC AGCAGCAGCC CAGCACTGTG  2460
TCAATTCAAA GGGCCAAGTG TGCAGTGGAA GAGGCACGTG TGTGTGTGGA AGGTGTGAGT  2520
GCACCGATCC CAGGAGCATC GGCCGCTTCT GTGAACACTG CCCCACCTGT TATACAGCCT  2580
GCAAGGAAAA CTGGAATTGT ATGCAATGCC TTCACCCTCA CAATTTGTCT CAGGCTATAC  2640
TTGATCAGTG CAAAACCTCA TGTGCTCTCA TGGAACAACA GCATTATGTC GACCAAACTT  2700
CAGAATGTTT CTCCAGCCCA AGCTACTTGA GAATATTTTT CATCATTTTC ATAGTTACAT  2760
TCTTGATTGG GTTGCTTAAA GTCCTGATCA TTAGACAGGT GATACTACAA TGGAATAGTA  2820
ATAAAATTAA GTCCTCATCA GATTACAGAG TGTCAGCCTC AAAAAAGGAT AAGTTGATTC  2880
TGCAAAGTGT TTGCACAAGA GCAGTCACCT ACCGACGTGA GAAGCCTGAA GAAATAAAAA  2940
TGGATATCAG CAAATTAAAT GCTCATGAAA CTTTCAGGTG CAACTTCTAA AAAAAGATTT  3000
TTAAACACTT AATGGGAAAC TGGAATTGTT AATAATTGCT CCTAAAGATT ATAATTTTAA  3060
AAGTCACAGG AGGAGACAAA TTGCTCACGG TCATGCCAGT TGCTGGTTGT ACACTCGAAC  3120
GAAGACTGAC AAGTATCCTC ATCATGATGT GACTCACATA GCTGCTGACT TTTTCAGAGA  3180
AAAATGTGTC TTACTACTGT TTGAGACTAG TGTCGTTGTA GCACTTTACT GTAATATATA  3240
ACTTATTTAG ATCAGCATAG AATGTAGATC CTCTGAAGAG CACTGATTAC ACTTTACAGG  3300
TACCTGTTAT CCCTACGCTT CCCAGAGAGA ACAATGCTGT GAGAGAGTTT AGCATTGTGT  3360
CACTACAAGG GTACAGTAAT CCCTGCACTG GACATGTGAG GAAAAAAATA ATCTGGCAAG  3420
TATATTCTAA GGTTGCCAAA CACTTCAACA GTTGGTGGTT GAATAGACAA GAACAGCTAG  3480
ATGAATAAAT GATTCGTGTT TCACTCTTTC AAGAGGTGAA CAGATACAAC CTTAATCTTA  3540
AAAGATTATT GCTTTTTAAA GTGTGTAGTT TTATGCATGT GTGTTTATGG TTTGCTTATT  3600
TTTGCAAGAT GGATACTAAT TCCAGCATTC TCTCCTCTTT GCCTTTATGT TTTGTTTTCT  3660
TTTTTACAGG ATAAGTTTAT GTATGTCACA GATGACTGGA TTAATTAAGT GCTAAGTTAC  3720
TACTGCCATA AAAAACTAAT AATACAATGT CACTTTATCA GAATACTAGT TTTAAAAGCT  3780
GAATGTTAA
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Seq ID NO: 645 Protein sequence
Protein Accession #: NP_002205

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1          11         21         31         41         51
|          |          |          |          |          |
MCGSALAFFT AAFVCLQNDR RGPASFLWAA WVFSLVLGLG QGEDNRCASS NAASCARCLA    60
LGPECGWCVQ EDFISGGSRS ERCDIVSNLI SKGCSVDSIE YPSVHVIIPT ENEINTQVTP   120
GEVSIQLRPG AEANFMLKVH PLKKYPVDLY YLVDVSASMH NNIEKLNSVG NDLSRKMAFF   180
SRDFRLGFGS YVDKTVSPYI SIHPERIHNQ CSDYNLDCMP PHGYIHVLSL TENITEFEKA   240
VHRQKISGNI DTPEGGFDAM LQAAVCESHI GWRKEAKRLL LVMTDQTSHL ALDSKLAGIV   300
VPNDGNCHLK NNVYVKSTTM EHPSLGQLSE KLIDNNINVI FAVQGKQFHW YKDLLPLLPG   360
TIAGEIESKA ANLNNLVVEA YQKLISEVKV QVENQVQGIY FNITAICPDG SRKPGMEGCR   420
NVTSNDEVLF NVTVTMKKCD VTGGKNYAII KPIGFNETAK IHIHRNCSCQ CEDNRGPKGK   480
CVDETFLDSK CFQCDENKCH FDEDQFSSES CKSHKDQPVC SGRGVCVCGK CSCHKIKLGK   540
VYGKYCEKDD FSCPYHHGNL CAGHGECEAG RCQCFSGWEG DRCQCPSAAA QHCVNSKGQV   600
CSGRGTCVCG RCECTDPRSI GRFCEHCPTC YTACKENWNC MQCLHPHNLS QAILDQCKTS   660
CALMEQQHYV DQTSECFSSP SYLRIFFIIF IVTFLIGLLK VLIIRQVILQ WNSNKIKSSS   720
DYRVSASKKD KLILQSVCTR AVTYRREKPE EIKMDISKLN AHETFRCNF
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Seq ID NO: 646 DNA sequence
Nucleic Acid Accession #: NM_003318.1
Coding sequence: 1..2574

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AGAGACATTA AAAATAAGTT TAAAAATGAA GACCTTACTG ATGAACTAAG CTTGAATAAA   120
ATTTCTGCTG ATACTACAGA TAACTCGGGA ACTGTTAACC AAATTATGAT GATGGCAAAC   180
AACCCAGAGG ACTGGTTGAG TTTGTTGCTC AAACTAGAGA AAAACAGTGT TCCGCTAAGT   240
GATGCTCTTT TAAATAAATT GATTGGTCGT TACAGTCAAG CAATTGAAGC GCTTCCCCCA   300
GATAAATATG GCCAAAATGA GAGTTTTGCT AGAATTCAAG TGAGATTTGC TGAATTAAAA   360
GCTATTCAAG AGCCAGATGA TGCACGTGAC TACTTTCAAA TGGCCAGAGC AAACTGCAAG   420
AAATTTGCTT TTGTTCATAT ATCTTTTGCA CAATTTGAAC TGTCACAAGG TAATGTCAAA   480
AAAAGTAAAC AACTTCTTCA AAAAGCTGTA GAACGTGGAG CAGTACCACT AGAAATGCTG   540
GAAATTGCCC TGCGGAATTT AAACCTCCAA AAAAAGCAGC TGCTTTCAGA GGAGGAAAAG   600
AAGAATTTAT CAGCATCTAC GGTATTAACT GCCCAAGAAT CATTTTCCGG TTCACTTGGG   660
CATTTACAGA ATAGGAACAA CAGTTGTGAT TCCAGAGGAC AGACTACTAA AGCCAGGTTT   720
TTATATGGAG AGAACATGCC ACCACAAGAT GCAGAAATAG GTTACCGGAA TTCATTGAGA   780
CAAACTAACA AAACTAAACA GTCATGCCCA TTTGGAAGAG TCCCAGTTAA CCTTCTAAAT   840
AGCCCAGATT GTGATGTGAA GACAGATGAT TCAGTTGTAC CTTGTTTTAT GAAAAGACAA   900
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TCCTGTGAAT TAAGAAATTT AAAGTCTGTT CAAAATAGTC ATTTCAAGGA ACCTCTGGTG  1020
TCAGATGAAA AGAGTTCTGA ACTTATTATT ACTGATTCAA TAACCCTGAA GAATAAAACG  1080
GAATCAAGTC TTCTAGCTAA ATTAGAAGAA ACTAAAGAGT ATCAAGAACC AGAGGTTCCA  1140
GAGAGTAACC AGAAACAGTG GCAATCTAAG AGAAAGTCAG AGTGTATTAA CCAGAATCCT  1200
GCTGCATCTT CAAATCACTG GCAGATTCCG GAGTTAGCCC GAAAAGTTAA TACAGAGCAG  1260
AAACATACCA CTTTTGAGCA ACCTGTCTTT TCAGTTTCAA AACAGTCACC ACCAATATCA  1320
ACATCTAAAT GGTTTGACCC AAAAATCTATT TGTAAGACAC CAAGCAGCAA TACCTTGGAT  1380
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GATTACATGA GCTGTTTTAG AACTCCAGTT GTAAAGAATG ACTTTCCACC TGCTTGTCAG  1440
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CAGGTGTTAA ATGAAAAGAA ACAGATATAT GCTATAAAAT ATGTGAACTT AGAAGAAGCA  1680
GATAACCAAA CTCTTGATAG TTACCGGAAC GAAATAGCTT ATTTGAATAA ACTACAACAA  1740
CACAGTGATA AGATCATCCG ACTTTATGAT TATGAAATCA CGGACCAGTA CATCTACATG  1800
GTAATGGAGT GTGGAAATAT TGATCTTAAT AGTTGGCTTA AAAAGAAAAA ATCCATTGAT  1860
CCATGGGAAC GCAAGAGTTA CTGGAAAAAT ATGTTAGAGG CAGTTCACAC AATCCATCAA  1920
CATGGCATTG TTCACAGTGA TCTTAAACCA GCTAACTTTC TGATAGTTGA TGGAATGCTA  1980
AAGCTAATTG ATTTTGGGAT TGCAAACCAA ATGCAACCAG ATACAACAAG TGTTGTTAAA  2040
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TCCAGAGAGA ATGGGAAATC TAAGTCAAAG ATAAGCCCCA AAAGTGATGT TTGGTCCTTA  2160
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GAGAAAGATC TTCAAGATGT GTTAAAGTGT TGTTTAAAAA GGGACCCAAA ACAGAGGATA  2340
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ATGGCCAAGG GAACCACTGA AGAAATGAAA TATGTTCTGG GCCAACTTGT TGGTCTGAAT  2460
TCTCCTAACT CCATTTTGAA AGCTGCTAAA ACTTTATATG AACACTATAG TGGTGGTGAA  2520
AGTCATAATT CTTCATCCTC CAAGACTTTT GAAAAAAAAA GGGGAAAAAA ATGA
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Seq ID NO: 647 Protein sequence
Protein Accession #: NP_003309.1

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NPEDWLSLLL KLEKNSVPLS DALLNKLIGR YSQAIEALPP DKYGQNESFA RIQVRFAELK   120
AIQEPDDARD YFQMARANCK KFAFVHISFA QFELSQGNVK KSKQLLQKAV ERGAVPLEML   180
EIALRNLNLQ KKQLLSEEEK KNLSASTVLT AQESFSGSLG HLQNRNNSCD SRGQTTKARF   240
LYGENMPPQD AEIGYRNSLR QTNKTKQSCP FGRVPVNLLN SPDCDVKTDD SVVPCFMKRQ   300
TSRSECRDLV VPGSKPSGND SCELRNLKSV QNSHFKEPLV SDEKSSELII TDSITLKNKT   360
ESSLLAKLEE TKEYQEPEVP ESNQKQWQSK RKSECINQNP AASSNHWQIP ELARKVNTEQ   420
KHTTFEQPVF SVSKQSPPIS TSKWFDPKSI CKTPSSNTLD DYMSCFRTPV VKNDFPPACQ   480
LSTPYGQPAC FQQQQHQILA TPLQNLQVLA SSSANECISV KGRIYSILKQ IGSGGSSKVF   540
QVLNEKKQIY AIKYVNLEEA DNQTLDSYRN EIAYLNKLQQ HSDKIIRLYD YEITDQYIYM   600
VMECGNIDLN SWLKKKKSID PWERKSYWKN MLEAVHTIHQ HGIVHSDLKP ANFLIVDGML   660
KLIDFGIANQ MQPDTTSVVK DSQVGTVNYM PPEAIKDMSS SRENGKSKSK ISPKSDVWSL   720
GCILYYMTYG KTPFQQIINQ ISKLHAIIDP NHEIEFPDIP EKDLQDVLKC CLKRDPKQRI   780
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SHNSSSSKTF EKKRGKK
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Seq ID NO: 648 DNA sequence
Nucleic Acid Accession #: NM_015507
Coding sequence: 241..1902

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CGCCCCTGCC GCGGTGCCTG GCCTCCCCTC CCAGACTGCA GGGACAGCAC CCGGTAACTG   120
CGAGTGGAGC GGAGGACCCG AGCGGCTGAG GAGAGAGGAG GCGGCGGCTT AGCTGCTACG   180
GGGTCCGGCC GGCGCCCTCC CGAGGGGGGC TCAGGAGGAG GAAGGAGGAC CCGTGCGAGA   240
ATGCCTCTGC CCTGGAGCCT TGCGCTCCCG CTGCTGCTCT CCTGGGTGGC AGGTGGTTTC   300
GGGAACGCGG CCAGTGCAAG GCATCACGGG TTGTTAGCAT CGGCACGTCA GCCTGGGGTC   360
TGTCACTATG GAACTAAACT GGCCTGCTGC TACGGCTGGA GAAGAAACAG CAAGGGAGTC   420
TGTGAAGCTA CATGCGAACC TGGATGTAAG TTTGGTGAGT GCGTGGGACC AAACAAATGC   480
AGATGCTTTC CAGGATACAC CGGGAAAACC TGCAGTCAAG ATGTGAATGA GTGTGGAATG   540
AAACCCCGGC CATGCCAACA CAGATGTGTG AATACACACG GAAGCTACAA GTGCTTTTGC   600
CTCAGTGGCC ACATGCTCAT GCCAGATGCT ACGTGTGTGA ACTCTAGGAC ATGTGCCATG   660
ATAAACTGTC AGTACAGCTG TGAAGACACA GAAGAAGGGC CACAGTGCCT GTGTCCATCC   720
TCAGGACTCC GCCTGGCCCC AAATGGAAGA GACTGTCTAG ATATTGATGA ATGTGCCTCT   780
GGTAAAGTCA TCTGTCCCTA CAATCGAAGA TGTGTGAACA CATTTGGAAG CTACTACTGC   840
AAATGTCACA TTGGTTTCGA ACTGCAATAT ATCAGTGGAC GATATGACTG TATAGATATA   900
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ATCCCTGAAA ATTCTGTGAA GGAAGTCCTC AGAGCACCTG GTACCATCAA AGACAGAATC  1080
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TCAGGCTTAT GTCCAGATAG CCTTTTATCT GTGGATGACT GAATGTTACT ATCTTTATAT  1920
TTGACTTTGT ATGTCAGTTC CCTGGTTTTT TTGATATTGC ATCATAGGAC CTCTGGCATT  1980
TTAGAATTAC TAGCTGAAAA ATTGTAATGT ACCAACAGAA ATATTATTGT AAGATGCCTT  2040
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TTTCTGAATC TTTCCACATT ATATTATAAA ATATGGAAAT GTCAGTTTAT CTCCCCTCCT  2160
CAGTATATCT GATTTGTATA AGTAAGTTGA TGAGCTTCTC TCTACAACAT TTCTAGAAAA  2220
TAGAAAAAAA AGCACAGAGA AATGTTTAAC TGTTTGACTC TTATGATACT TCTTGGAAAC  2280
TATGACATCA AAGATAGACT TTTGCCTAAG TGGCTTAGCT GGGTCTTTCA TAGCCAAACT  2340
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TGTATATTTA AATTCTTTGT AATAATAATA TCCAAATCAT CAAAAAAAAA AAAAAAA
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Seq ID NO: 649 Protein sequence
Protein Accession #: NP_056322

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MPLPWSLALP LLLSWVAGGF GNAASARHHG LLASARQPGV CHYGTKLACC YGWRRNSKGV    60
CEATCEPGCK FGECVGPNKC RCFPGYTGKT CSQDVNECGM KPRPCQHRCV NTHGSYKCFC   120
LSGHMLMPDA TCVNSRTCAM INCQYSCEDT EEGPQCLCPS SGLRLAPNGR DCLDIDECAS   180
GKVICPYNRR CVNTFGSYYC KCHIGFELQY ISGRYDCIDI NECTMDSHTC SHHANCFNTQ   240
GSFKCKCKQG YKGNGLRCSA IPENSVKEVL RAPGTIKDRI KKLLAHKNSM KKKAKIKNVT   300
PEPTRTPTPK VNLQPFNYEE IVSRGGNSHG GKKGNEEKMK EGLEDEKREE KALKNDIEER   360
SLRGDVFFPK VNEAGEFGLI LVQRKALTSK LEHKDLNISV DCSFNHGICD WKQDREDDFD   420
WNPADRDNAI GFYMAVPALA GHKKDIGRLK LLLPDLQPQS NFCLLFDYRL AGDKVGKLRV   480
FVKNSNNALA WEKTTSEDEK WKTGKIQLYQ GTDATKSIIF EAERGKGKTG EIAVDGVLLV   540
SGLCPDSLLS VDD
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Seq ID NO: 650 DNA sequence
Nucleic Acid Accession #: NM_003506.1
Coding sequence: 259..2379

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CTCATTTTCA GGAAAGCCTG AAAATGAGTA AAATAGTGAA ATGAGGAATT TGAACATTTT   180
ATCTTTGGAT GGGGATCTTC TGAGGATGCA AAGAGTGATT CATCCAAGCC ATGTGGTAAA   240
ATCAGGAATT TGAAGAAAAT GGAGATGTTT ACATTTTTGT TGACGTGTAT TTTTCTACCC   300
CTCCTAAGAG GGCACAGTCT CTTCACCTGT GAACCAATTA CTGTTCCCAG ATGTATGAAA   360
ATGGCCTACA ACATGACGTT TTTCCCTAAT CTGATGGGTC ATTATGACCA GAGTATTGCC   420
GCGGTGGAAA TGGAGCATTT TCTTCCTCTC GCAAATCTGG AATGTTCACC AAACATTGAA   480
ACTTTCCTCT GCAAAGCATT TGTACCAACC TGCATAGAAC AAATTCATGT GGTTCCACCT   540
TGTCGTAAAC TTTGTGAGAA AGTATATTCT GATTGCAAAA AATTAATTGA CACTTTTGGG   600
ATCCGATGGC CTGAGGAGCT TGAATGTGAC AGATTACAAT ACTGTGATGA GACTGTTCCT   660
GTAACTTTTG ATCCACACAC AGAATTTCTT GGTCCTCAGA AGAAAACAGA ACAAGTCCAA   720
AGAGACATTG GATTTTGGTG TCCAAGGCAT CTTAAGACTT CTGGGGGACA AGGATATAAG   780
TTTCTGGGAA TTGACCAGTG TGCGCCTCCA TGCCCCAACA TGTATTTTAA AAGTGATGAG   840
CTAGAGTTTG CAAAAAGTTT TATTGGAACA GTTTCAATAT TTTGTCTTTG TGCAACTCTG   900
TTCACATTCC TTACTTTTTT AATTGATGTT AGAAGATTCA GATACCCAGA GAGACCAATT   960
ATATATTACT CTGTCTGTTA CAGCATTGTA TCTCTTATGT ACTTCATTGG ATTTTTGCTG  1020
GGCGATAGCA CAGCCTGCAA TAAGGCAGAT GAGAAGCTAG AACTTGGTGA CACTGTTGTC  1080
CTAGGCTCTC AAAATAAGGC TTGCACCGTT TTGTTCATGC TTTTGTATTT TTTCACAATG  1140
GCTGGCACTG TGTGGTGGGT GATTCTTACC ATTACTTGGT TCTTAGCTGC AGGAAGAAAA  1200
TGGAGTTGTG AAGCCATCGA GCAAAAAGCA GTGTGGTTTC ATGCTGTTGC ATGGGGAACA  1260
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CTGTGCCTTT GTGTGTTTGT TGGGCTCTCT CTTCTTTTAG CTGGCATTAT TTCCTTAAAT  1440
CATGTTCGAC AAGTCATACA ACATGATGGC CGGAACCAAG AAAAACTAAA GAAATTTATG  1500
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CGTCAGTACC ATATCCCATG TCCTTATCAG GCAAAAGCAA AAGCTCGACC AGAATTGGCT  1680
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GGAAGCAAAA AGACATGCAC AGAATGGGCT GGGTTTTTTA AACGAAATCG CAAGAGAGAT  1800
CCAATCAGTG AAAGTCGAAG AGTACTACAG GAATCATGTG AGTTTTTCTT AAAGCACAAT  1860
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TCAAGAATAA TATGACTCAT TTCACACAAA GGTTAATGAC AACAATATAC CTGAAAACAG  2580
AAATGTGCAG GTTAATAATA TTTTTTTAAT AGTGTGGGAG GACAGAGTTA GAGGAATCTT  2640
CCTTTTCTAT TTATGAAGAT TCTACTCTTG GTAAGAGTAT TTTAAGATGT ACTATGCTAT  2700
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GTATCTTTTT ATACATATTT GAAAATAAGC TTATATGTAT TTGAACTTTT TTGAAATCCT  2820
ATTCAAGTAT TTTTATCATG CTATTGTGAT ATTTTAGCAC TTTGGTAGCT TTTACACTGA  2880
ATTTCTAAGA AAATTGTAAA ATAGTCTTCT TTTATACTGT AAAAAAAGAT ATACCAAAAA  2940
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TGTGATTTTT ATAGTCTCGT TTTAGGAATT TCACAGATCT AAATTATGTA ACTGAAATAA  3060
GGTGCTTACT CAAAGAGTGT CCACTATTGA TTGTATTATG CTGCTCACTG ATCCTTCTGC  3120
ATATTTAAAA TAAAATGTCC TAAAGGGTTA GTAGACAAAA TGTTAGTCTT TTGTATATTA  3180
GGCCAAGTGC AATTGACTTC CCTTTTTTAA TGTTTCATGA CCACCCATTG ATTGTATTAT  3240
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TACATTTTGT ATTATACAGT ACCTTTCTCA GACATTTTGT AG
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Seq ID NO: 651 Protein sequence
Protein Accession #: NP_003497.1

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LECDRLQYCD ETVPVTFDPH TEFLGPQKKT EQVQRDIGFW CPRHLKTSGG QGYKFLGIDQ   180
CAPPCPNMYF KSDELEFAKS FIGTVSIFCL CATLFTFLTF LIDVRRFRYP ERPIIYYSVC   240
YSIVSLMYFI GFLLGDSTAC NKADEKLELG DTVVLGSQNK ACTVLFMLLY FFTMAGTVWW   300
VILTITWFLA AGRKWSCEAI EQKAVWFHAV AWGTPGFLTV MLLALNKVEG DNISGVCFVG   360
LYDLDASRYF VLLPLCLCVF VGLSLLLAGI ISLNHVRQVI QHDGRNQEKL KKFMIRIGVF   420
SGLYLVPLVT LLGCYVYEQV NRITWEITWV SDHCRQYHIP CPYQAKAKAR PELALFMIKY   480
LMTLIVGISA VFWVGSKKTC TEWAGFFKRN RKRDPISESR RVLQESCEFF LKHNSKVKHK   540
KKHYKPSSHK LKVISKSMGT STGATANHGT SAVAITSHDY LGQETLTEIQ TSPETSMREV   600
KADGASTPRL REQDCGEPAS PAASISRLSG EQVDGKGQAG SVSESARSEG RISPKSDITD   660
TGLAQSNNLQ VPSSSEPSSL KGSTSLLVHP VSGVRKEQGG GCHSDT
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Seq ID NO: 652 DNA sequence
Nucleic Acid Accession #: NM_014791.1
Coding sequence: 171..2126

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TCCGCCCCTC AGGTTCTTTT TCTAATTCCA AATAAACTTG CAAGAGGACT ATGAAAGATT   180
ATGATGAACT TCTCAAATAT TATGAATTAC ATGAAACTAT TGGGACAGGT GGCTTTGCAA   240
AGGTCAAACT TGCCTGCCAT ATCCTTACTG GAGAGATGGT AGCTATAAAA ATCATGGATA   300
AAAACACACT AGGGAGTGAT TTGCCCCGGA TCAAAACGGA GATTGAGGCC TTGAAGAACC   360
TGAGACATCA GCATATATGT CAACTCTACC ATGTGCTAGA GACAGCCAAC AAAATATTCA   420
TGGTTCTTGA GTACTGCCCT GGAGGAGAGC TGTTTGACTA TATAATTTCC CAGGATCGCC   480
TGTCAGAAGA GGAGACCCGG GTTGTCTTCC GTCAGATAGT ATCTGCTGTT GCTTATGTGC   540
ACAGCCAGGG CTATGCTCAC AGGGACCTCA AGCCAGAAAA TTTGCTGTTT GATGAATATC   600
ATAAATTAAA GCTGATTGAC TTTGGTCTCT GTGCAAAACC CAAGGGTAAC AAGGATTACC   660
ATCTACAGAC ATGCTGTGGG AGTCTGGCTT ATGCAGCACC TGAGTTAATA CAAGGCAAAT   720
CATATCTTGG ATCAGAGGCA GATGTTTGGA GCATGGGCAT ACTGTTATAT GTTCTTATGT   780
GTGGATTTCT ACCATTTGAT GATGATAATG TAATGGCTTT ATACAAGAAG ATTATGAGAG   840
GAAAATATGA TGTTCCCAAG TGGCTCTCTC CCAGTAGCAT TCTGCTTCTT CAACAAATGC   900
TGCAGGTGGA CCCAAAGAAA CGGATTTCTA TGAAAAATCT ATTGAACCAT CCCTGGATCA   960
TGCAAGATTA CAACTATCCT GTTGAGTGGC AAAGCAAGAA TCCTTTTATT CACCTCGATG  1020
ATGATTGCGT AACAGAACTT TCTGTACATC ACAGAAACAA CAGGCAAACA ATGGAGGATT  1080
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AGGCTCGGGG AAAACCAGTT CGTTTAAGGC TTTCTTCTTT CTCCTGTGGA CAAGCCAGTG  1200
CTACCCCATT CACAGACATC AAGTCAAATA ATTGGAGTCT GGAAGATGTG ACCGCAAGTG  1260
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GTGCTGCTAC TCCCCGAACA TCACAGTTTA CCAAGTACTG GACAGAATCA AATGGGGTGG  1380
AATCTAAATC ATTAACTCCA GCCTTATGCA GAACACCTGC AAATAAATTA AAGAACAAAG  1440
AAAATGTATA TACTCCTAAG TCTGCTGTAA AGAATGAAGA GTACTTTATG TTTCCTGAGC  1500
CAAAGACTCC AGTTAATAAG AACCAGCATA AGAGAGAAAT ACTCACTACG CCAAATCGTT  1560
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TAAATTCAAC AGGAACAGAC AAGTTAATGA CAGGTGTCAT TAGCCCTGAG AGGCGGTGCC  1680
GCTCAGTGGA ATTGGATCTC AACCAAGCAC ATATGGAGGA GACTCCAAAA AGAAAGGGAG  1740
CCAAAGTGTT TGGGAGCCTT GAAAGGGGGT TGGATAAGGT TATCACTGTG CTCACCAGGA  1800
GCAAAAGGAA GGGTTCTGCC AGAGACGGGC CCAGAAGACT AAAGCTTCAC TATAATGTGA  1860
CTACAACTAG ATTAGTGAAT CCAGATCAAC TGTTGAATGA AATAATGTCT ATTCTTCCAA  1920
AGAAGCATGT TGACTTTGTA CAAAAGGGTT ATACACTGAA GTGTCAAACA CAGTCAGATT  1980
TTGGGAAAGT GACAATGCAA TTTGAATTAG AAGTGTGCCA GCTTCAAAAA CCCGATGTGG  2040
TGGGTATCAG GAGGCAGCGG CTTAAGGGCG ATGCCTGGGT TTACAAAAGA TTAGTGGAAG  2100
ACATCCTATC TAGCTGCAAG GTATAATTGA TGGATTCTTC CATCCTGCCG GATGAGTGTG  2160
GGTGTGATAC AGCCTACATA AAGACTGTTA TGATCGCTTT GATTTTAAAG TTCATTGGAA  2220
CTACCAACTT GTTTCTAAAG AGCTATCTTA AGACCAATAT CTCTTTGTTT TTAAACAAAA  2280
GATATTATTT TGTGTATGAA TCTAAATCAA GCCCATCTGT CATTATGTTA CTGTCTTTTT  2340
TAATCATGTG GTTTTGTATA TTAATAATTG TTGACTTTCT TAGATTCACT TCCATATGTG  2400
AATGTAAGCT CTTAACTATG TCTCTTTGTA ATGTGTAATT TCTTTCTGAA ATAAAACCAT  2460
TTGTGAATAT
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Seq ID NO: 653 Protein sequence
Protein Accession #: NP_055606.1

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1          11         21         31         41         51
|          |          |          |          |          |
MKDYDELLKY YELHETIGTG GFAKVKLACH ILTGEMVAIK IMDKNTLGSD LPRIKTEIEA    60
LKNLRHQHIC QLYHVLETAN KIFMVLEYCP GGELFDYIIS QDRLSEEETR VVFRQIVSAV   120
AYVHSQGYAH RDLKPENLLF DEYHKLKLID FGLCAKPKGN KDYHLQTCCG SLAYAAPELI   180
QGKSYLGSEA DVWSMGILLY VLMCGFLPFD DDNVMALYKK IMRGKYDVPK WLSPSSILLL   240
QQMLQVDPKK RISMKNLLNH PWIMQDYNYP VEWQSKNPFI HLDDDCVTEL SVHHRNNRQT   300
MEDLISLWQY DHLTATYLLL LAKKARGKPV RLRLSSFSCG QASATPFTDI KSNNWSLEDV   360
TASDKNYVAG LIDYDWCEDD LSTGAATPRT SQFTKYWTES NGVESKSLTP ALCRTPANKL   420
KNKENVYTPK SAVKNEEYFM FPEPKTPVNK NQHKREILTT PNRYTTPSKA RNQCLKETPI   480
KIPVNSTGTD KLMTGVISPE RRCRSVELDL NQAHMEETPK RKGAKVFGSL ERGLDKVITV   540
LTRSKRKGSA RDGPRRLKLH YNVTTTRLVN PDQLLNEIMS ILPKKHVDFV QKGYTLKCQT   600
QSDFGKVTMQ FELEVCQLQK PDVVGIRRQR LKGDAWVYKR LVEDILSSCK V
```

Seq ID NO: 654 DNA sequence
Nucleic Acid Accession #: NM_000582
Coding sequence: 88..990

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1          11         21         31         41         51
|          |          |          |          |          |
GCAGAGCACA GCATCGTCGG GACCAGACTC GTCTCAGGCC AGTTGCAGCC TTCTCAGCCA    60
AACGCCGACC AAGGAAAACT CACTACCATG AGAATTGCAG TGATTTGCTT TTGCCTCCTA   120
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GGCATCACCT GTGCCATACC AGTTAAACAG GCTGATTCTG GAAGTTCTGA GGAAAAGCAG   180
CTTTACAACA AATACCCAGA TGCTGTGGCC ACATGGCTAA ACCCTGACCC ATCTCAGAAG   240
CAGAATCTCC TAGCCCCACA GACCCTTCCA AGTAAGTCCA ACGAAAGCCA TGACCACATG   300
GATGATATGG ATGATGAAGA TGATGATGAC CATGTGGACA GCCAGGACTC CATTGACTCG   360
AACGACTCTG ATGATGTAGA TGACACTGAT GATTCTCACC AGTCTGATGA GTCTCACCAT   420
TCTGATGAAT CTGATGAACT GGTCACTGAT TTTCCCACGG ACCTGCCAGC AACCGAAGTT   480
TTCACTCCAG TTGTCCCCAC AGTAGACACA TATGATGGCC GAGGTGATAG TGTGGTTTAT   540
GGACTGAGGT CAAAATCTAA GAAGTTTCGC AGACCTGACA TCCAGTACCC TGATGCTACA   600
GACGAGGACA TCACCTCACA CATGGAAAGC GAGGAGTTGA ATGGTGCATA CAAGGCCATC   660
CCCGTTGCCC AGGACCTGAA CGCGCCTTCT GATTGGGACA GCCGTGGGAA GGACAGTTAT   720
GAAACGAGTC AGCTGGATGA CCAGAGTGCT GAAACCCACA GCCACAAGCA GTCCAGATTA   780
TATAAGCGGA AAGCCAATGA TGAGAGCAAT GAGCATTCCG ATGTGATTGA TAGTCAGGAA   840
CTTTCCAAAG TCAGCCGTGA ATTCCACAGC CATGAATTTC ACAGCCATGA AGATATGCTG   900
GTTGTAGACC CCAAAAGTAA GGAAGAAGAT AAACACCTGA AATTTCGTAT TTCTCATGAA   960
TTAGATAGTG CATCTTCTGA GGTCAATTAA AAGGAGAAAA AATACAATTT CTCACTTTGC  1020
ATTTAGTCAA AAGAAAAAAT GCTTTATAGC AAAATGAAAG AGAACATGAA ATGCTTCTTT  1080
CTCAGTTTAT TGGTTGAATG TGTATCTATT TGAGTCTGGA AATAACTAAT GTGTTTGATA  1140
ATTAGTTTAG TTTGTGGCTT CATGGAAACT CCCTGTAAAC TAAAAGCTTC AGGGTTATGT  1200
CTATGTTCAT TCTATAGAAG AAATGCAAAC TATCACTGTA TTTTAATATT TGTTATTCTC  1260
TCATGAATAG AAATTTATGT AGAAGCAAAC AAAATACTTT TACCCACTTA AAAAGAGAAT  1320
ATAACATTTT ATGTCACTAT AATCTTTTGT TTTTTAAGTT AGTGTATATT TTGTTGTGAT  1380
TATCTTTTTG TGGTGTGAAT AAATCTTTTA TCTTGAATGT AATAAGAATT TGGTGGTGTC  1440
AATTGCTTAT TTGTTTTCCC ACGGTTGTCC AGCAATTAAT AAAACATAAC CTTTTTTACT  1500
GCCTAAAAAA AAAAAAAAAA AAAA
```

Seq ID NO: 655 Protein sequence
Protein Accession #: NP_000573

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1          11         21         31         41         51
|          |          |          |          |          |
MRIAVICFCL LGITCAIPVK QADSGSSEEK QLYNKYPDAV ATWLNPDPSQ KQNLLAPQTL    60
PSKSNESHDH MDDMDDEDDD DHVDSQDSID SNDSDDVDDT DDSHQSDESH HSDESDELVT   120
DFPTDLPATE VFTPVVPTVD TYDGRGDSVV YGLRSKSKKF RRPDIQYPDA TDEDITSHME   180
SEELNGAYKA IPVAQDLNAP SDWDSRGKDS YETSQLDDQS AETHSHKQSR LYKRKANDES   240
NEHSDVIDSQ ELSKVSREFH SHEFHSHEDM LVVDPKSKEE DKHLKFRISH ELDSASSEVN
```

Seq ID NO: 656 DNA sequence
Nucleic Acid Accession #: NM_003108.1
Coding sequence: 76..1401

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1          11         21         31         41         51
|          |          |          |          |          |
GGGGTGGGAG GGGGAGGGGG ACCTCCGCAC GAGACCCAGC GGCCCGGGTT GGAGCGTCCA    60
GCCCTGCAAC GGATCATGGT GCAGCAGGCG GAGAGCTTGG AAGCGGAGAG CAACCTGCCC   120
CGGGAGGCGC TGGACACGGA GGAGGGCGAA TTCATGGCTT GCAGCCCGGT GGCCCTGGAC   180
GAGAGCGACC CAGACTGGTG CAAGACGGCG TCGGGCCACA TCAAGCGGCC GATGAACGCG   240
TTCATGGTAT GGTCCAAGAT CGAACGCAGG AAGATCATGG AGCAGTCTCC GGACATGCAC   300
AACGCCGAGA TCTCCAAGAG GCTGGGCAAG CGCTGGAAAA TGCTGAAGGA CAGCGAGAAG   360
ATCCCGTTCA TCCGGGAGGC GGAGCGGCTG CGGCTCAAGC ACATGGCCGA CTACCCCGAC   420
TACAAGTACC GGCCCCGGAA AAAGCCCAAA ATGGACCCCT CGGCCAAGCC CAGCGCCAGC   480
CAGAGCCCAG AGAAGAGCGC GGCCGGCGGC GGCGGCGGGA GCGCGGGCGG AGGCGCGGGC   540
GGTGCCAAGA CCTCCAAGGG CTCCAGCAAG AAATGCGGCA AGCTCAAGGC CCCCGCGGCC   600
GCGGGCGCCA AGGCGGGCGC GGGCAAGGCG GCCCAGTCCG GGGACTACGG GGGCGCGGGC   660
GACGACTACG TGCTGGGCAG CCTGCGCGTG AGCGGCTCGG GCGGCGGCGG CGCGGGCAAG   720
ACGGTCAAGT GCGTGTTTCT GGATGAGGAC GACGACGACG ACGACGACGA CGACGAGCTG   780
CAGCTGCAGA TCAAACAGGA GCCGGACGAG GAGGACGAGG AACCACCGCA CCAGCAGCTC   840
CTGCAGCCGC CGGGGCAGCA GCCGTCGCAG CTGCTGAGAC GCTACAACGT CGCCAAAGTG   900
CCCGCCAGCC CTACGCTGAG CAGCTCGGCG GAGTCCCCCG AGGGAGCGAG CCTCTACGAC   960
GAGGTGCGGG CCGGCGCGAC CTCGGGCGCC GGGGGCGGCA GCCGCCTCTA CTACAGCTTC  1020
AAGAACATCA CCAAGCAGCA CCCGCCGCCG CTCGCGCAGC CCGCGCTGTC GCCCGCGTCC  1080
TCGCGCTCGG TGTCCACCTC CTCGTCCAGC AGCAGCGGCA GCAGCAGCGG CAGCAGCGGC  1140
GAGGACGCCG ACGACCTGAT GTTCGACCTG AGCTTGAATT TCTCTCAAAG CGCGCACAGC  1200
GCCAGCGAGC AGCAGCTGGG GGGCGGCGCG GCGGCCGGGA ACCTGTCCCT GTCGCTGGTG  1260
GATAAGGATT TGGATTCGTT CAGCGAGGGC AGCCTGGGCT CCCACTTCGA GTTCCCCGAC  1320
TACTGCACGC CGGAGCTGAG CGAGATGATC GCGGGGGACT GGCTGGAGGC GAACTTCTCC  1380
GACCTGGTGT TCACATATTG AAAGGCGCCC GCTGCTCGCT CTTTCTCTCG GAGGGTGCAG  1440
AGCTGGGTTC CTTGGGAGGA AGTTGTAGTG GTGATGATGA TGATGATGAT AATGATGATG  1500
ATGATGGTGG TGTTGATGGT GGCGGTGGTA GGGTGGAGGG GAGAGAAGAA GATGCTGATG  1560
ATATTGATAA GATGTCGTGA CGCAAAGAAA TTGGAAAACA TGATGAAAAT TTTGGTGGAG  1620
TTAAAGTGAA ATGAGTAGTT TTTAAACATT TTTCCTGTCC TTTTTTTGTC CCCCCTCCCT  1680
TCCTTTATCG TGTCTCAAGG TAGTTGCATA CCTAGTCTGG AGTTGTGATT ATTTTCCCAA  1740
AAAATGTGTT TTTGTAATTA CTATTTCTTT TTCCTGAAAT TCGTGATTGC AACAAAGGCA  1800
GAGGGGGCGG CGCGGCGGAG GGGAGGTAGG ACCCGCTCCG GAAGGCGCTG TTTGAAGCTT  1860
GTCGGTCTTT GAAGTCTGGA AGACGTCTGC AGAGGACCCT TTTGGCAGCA CAACTGTTAC  1920
TCTAGGGAGT TGGTGGAGAT ATTTTTTTTT CTTAAGAGAA CTTAAAGAAC TGGTGATTTT  1980
TTTTTAACAA AAAAAGGG
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Seq ID NO: 657 Protein sequence
Protein Accession #: NP_003099.1

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1          11         21         31         41         51
|          |          |          |          |          |
MVQQAESLEA ESNLPREALD TEEGEFMACS PVALDESDPD WCKTASGHIK RPMNAFMVWS    60
KIERRKIMEQ SPDMHNAEIS KRLGKRWKML KDSEKIPFIR EAERLRLKHM ADYPDYKYRP   120
RKKPKMDPSA KPSASQSPEK SAAGGGGGSA GGGAGGAKTS KGSSKKCGKL KAPAAAGAKA   180
GAGKAAQSGD YGGAGDDYVL GSLRVSGSGG GGAGKTVKCV FLDEDDDDDD DDDELQLQIK   240
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QEPDEEDEEP PHQQLLQPPG QQPSQLLRRY NVAKVPASPT LSSSAESPEG ASLYDEVRAG   300
ATSGAGGGSR LYYSFKNITK QHPPPLAQPA LSPASSRSVS TSSSSSSGSS SGSSGEDADD   360
LMFDLSLNFS QSAHSASEQQ LGGGAAAGNL SLSLVDKDLD SFSEGSLGSH FEFPDYCTPE   420
LSEMIAGDWL EANFSDLVFT Y
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Seq ID NO: 658 DNA sequence
Nucleic Acid Accession #: NM_001719
Coding sequence: 123..1418

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1          11         21         31         41         51
|          |          |          |          |          |
GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CCTGCCCCCT     60
CTGCCACCTG GGGCGGTGCG GGCCCGGAGC CCGGAGCCCG GGTAGCGCGT AGAGCCGGCG    120
CGATGCACGT GCGCTCACTG CGAGCTGCGG CGCCGCACAG CTTCGTGGCG CTCTGGGCAC    180
CCCTGTTCCT GCTGCGCTCC GCCCTGGCCG ACTTCAGCCT GGACAACGAG GTGCACTCGA    240
GCTTCATCCA CCGGCGCCTC CGCAGCCAGG AGCGGCGGGA GATGCAGCGC GAGATCCTCT    300
CCATTTTGGG CTTGCCCCAC CGCCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC    360
CCATGTTCAT GCTGGACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGGCG    420
GCCAGGGCTT CTCCTACCCC TACAAGGCCG TCTTCAGTAC CCAGGGCCCC CCTCTGGCCA    480
GCCTGCAAGA TAGCCATTTC CTCACCGACG CCGACATGGT CATGAGCTTC GTCAACCTCG    540
TGGAACATGA CAAGGAATTC TTCCACCCAC GCTACCACCA TCGAGAGTTC CGGTTTGATC    600
TTTCCAAGAT CCCAGAAGGG GAAGCTGTCA CGGCAGCCGA ATTCCGGATC TACAAGGACT    660
ACATCCGGGA ACGCTTCGAC AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAGG    720
AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CCGTACCCTC TGGGCCTCGG    780
AGGAGGGCTG GCTGGTGTTT GACATCACAG CCACCAGCAA CCACTGGGTG GTCAATCCGC    840
GGCACAACCT GGGCCTGCAG CTCTCGGTGG AGACGCTGGA TGGGCAGAGC ATCAACCCCA    900
AGTTGGCGGG CCTGATTGGG CGGCACGGGC CCCAGAACAA GCAGCCCTTC ATGGTGGCTT    960
TCTTCAAGGC CACGGAGGTC CACTTCCGCA GCATCCGGTC CACGGGGAGC AAACAGCGCA   1020
GCCAGAACCG CTCCAAGACG CCCAAGAACC AGGAAGCCCT GCGGATGGCC AACGTGGCAG   1080
AGAACAGCAG CAGCGACCAG AGGCAGGCCT GTAAGAAGCA CGAGCTGTAT GTCAGCTTCC   1140
GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCCTGAAGG CTACGCCGCC TACTACTGTG   1200
AGGGGGAGTG TGCCTTCCCT CTGAACTCCT ACATGAACGC CACCAACCAC GCCATCGTGC   1260
AGACGCTGGT CCACTTCATC AACCCGGAAA CGGTGCCCAA GCCCTGCTGT GCGCCCACGC   1320
AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAACGTCATC CTGAAGAAAT   1380
ACAGAAACAT GGTGGTCCGG GCCTGTGGCT GCCACTAGCT CCTCCGAGAA TTCAGACCCT   1440
TTGGGGCCAA GTTTTTCTGG ATCCTCCATT GCTCGCCTTG GCCAGGAACC AGCAGACCAA   1500
CTGCCTTTTG TGAGACCTTC CCCTCCCTAT CCCCAACTTT AAAGGTGTGA GAGTATTAGG   1560
AAACATGAGC AGCATATGGC TTTTGATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAGA   1620
TCCTACAAGC TGTGCAGGCA AAACCTAGCA GGAAAAAAAA ACAACGCATA AAGAAAAATG   1680
GCCGGGCCAG GTCATTGGCT GGGAAGTCTC AGCCATGCAC GGACTCGTTT CCAGAGGTAA   1740
TTATGAGCGC CTACCAGCCA GGCCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAAGGGGT   1800
GGGCACATTG GTGTCTGTGC GAAAGGAAAA TTGACCCGGA AGTTCCTGTA ATAAATGTCA   1860
CAATAAAACG AATGAATG
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Seq ID NO: 659 Protein sequence
Protein Accession #: NP_001710

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1          11         21         31         41         51
|          |          |          |          |          |
MHVRSLRAAA PHSFVALWAP LFLLRSALAD FSLDNEVHSS FIHRRLRSQE RREMQREILS     60
ILGLPHRPRP HLQGKHNSAP MFMLDLYNAM AVEEGGGPGG QGFSYPYKAV FSTQGPPLAS    120
LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHHREFRFDL SKIPEGEAVT AAEFRIYKDY    180
IRERFDNETF RISVYQVLQE HLGRESDLFL LDSRTLWASE EGWLVFDITA TSNHWVVNPR    240
HNLGLQLSVE TLDGQSINPK LAGLIGRHGP QNKQPFMVAF FKATEVHFRS IRSTGSKQRS    300
QNRSKTPKNQ EALRMANVAE NSSSDQRQAC KKHELYVSFR DLGWQDWIIA PEGYAAYYCE    360
GECAFPLNSY MNATNHAIVQ TLVHFINPET VPKPCCAPTQ LNAISVLYFD DSSNVILKKY    420
RNMVVRACGC H
```

Seq ID NO: 660 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 211..1895

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1          11         21         31         41         51
|          |          |          |          |          |
GGATCTGAGG GGCGCCCAGT CACTTCCTCC ACGTTCTCGT GCTGGGCGGG AGGAGCGGAT     60
GGGGCTTGGG AGGCAGCCTG CTCTCCAGTC CCTATCCACC CACAGGTTTT TTGGGTCGGA    120
GAGGAATTAT CTGATAAAAT TCCTGGGTTA ATATTTTTAA AAACGGAGAG TTTTTAAAAA    180
TGATTTTTTT CCCTCGAAAA TGACCTTTTT ATGCTTCGAA GCAGTTTGTC AACCAGCATA    240
GTGCTTTTTC TTTTCTCTTC TTTTTCTACG ATAAATGAAA GCATTTCTTC AAGAAAAAGG    300
CACAGGTTCC TTGAACAGCT GGATTCTGAT GGCACCATTA CTATAGAGGA GCAGATTGTC    360
CTTGTGCTGA AAGCGAAAGT ACAATGTGAA CTCAACATCA CAGCTCAACT CCAGGAGGGA    420
GAAGGTAATT GTTTCCCTGA ATGGGATGGA CTCATTTGTT GGCCCAGAGG AACAGTGGGG    480
AAAATATCGG CTGTTCCATG CCCTCCTTAT ATTTATGACT TCAACCATAA AGGAGTTGCT    540
TTCCGACACT GTAACCCCAA TGGAACATGG GATTTTATGC ACAGCTTAAA TAAAACATGG    600
GCCAATTATT CAGACTGCCT TCGCTTTCTG CAGCCAGATA TCAGCATAGG AAAGCAAGAA    660
TTCTTTGAAC GCCTCTATGT AATGTATACC GTTGGCTACT CCATCTCTTT TGGTTCCTTG    720
GCTGTGGCTA TTCTCATCAT TGGTTACTTC AGACGATTGC ATTGCACTAG GAACTATATC    780
CACATGCACT TATTTGTGTC TTTCATGCTG AGAGCTACAA GCATCTTTGT CAAAGACAGA    840
GTAGTCCATG CTCACATAGG AGTAAAGGAG CTGGAGTCCC TAATAATGCA GGATGACCCA    900
CAAAATTCCA TTGAGGCAAC TTCTGTGGAC AAATCACAAT ATATCGGGTG CAAGATTGCT    960
GTTGTGATGT TTATTTACTT CCTGGCTACA AATTATTATT GGATCCTGGT GGAAGGTCTC   1020
TACCTGCATA ATCTCATCTT TGTGGCTTTC TTTTCGGACA CCAAATACCT GTGGGGCTTC   1080
ATCTTGATAG GCTGGGGGTT TCCAGCAGCA TTTGTTGCAG CATGGGCTGT GGCACGAGCA   1140
ACTCTGGCTG ATGCGAGGTG CTGGGAACTT AGTGCTGGAG ACATCAAGTG GATTTATCAA   1200
GCACCGATCT TAGCAGCTAT TGGGCTGAAT TTTATTCTGT TTCTGAATAC GGTTAGAGTT   1260
CTAGCTACCA AAATCTGGGA GACCAATGCA GTTGGGCATG ACACAAGGAA GCAATACAGG   1320
AAACTGGCCA AATCGACACT GGTCCTGGTC CTAGTCTTTG GAGTGCATTA CATCGTGTTC   1380
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GTATGCCTGC CTCACTCCTT CACTGGGCTC GGGTGGGAGA TCCGCATGCA CTGTGAGCTC  1440
TTCTTCAACT CCTTTCAGGG TTTCTTTGTG TCTATCATCT ACTGCTACTG CAATGGAGAG  1500
GTTCAGGCAG AGGTGAAGAA GATGTGGAGT CGGTGGAATC TCTCCGTGGA CTGGAAAAGG  1560
ACACCGCCAT GTGGCAGCCG CAGATGCGGC TCAGTGCTCA CCACCGTGAC GCACAGCACC  1620
AGCAGCCAGT CACAGGTGGC GGCCAGCACA CGCATGGTGC TTATCTCTGG CAAAGCTGCC  1680
AAGATCGCCA GCAGACAGCC TGACAGCCAC ATCACTTTAC CTGGCTATGT CTGGAGTAAC  1740
TCAGAGCAGG ACTGCCTGCC ACACTCTTTC CACGAGGAGA CCAAGGAAGA TAGTGGGAGG  1800
CAGGGAGATG ATATTCTAAT GGAGAAGCCT TCCAGGCCTA TGGAATCTAA CCCAGACACT  1860
GAAGGATGCC AAGGAGAAAC TGAGGATGTT CTCTGA
```

Seq ID NO: 661 Protein sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MLRSSLSTSI VLFLFSSFST INESISSRKR HRFLEQLDSD GTITIEEQIV LVLKAKVQCE    60
LNITAQLQEG EGNCFPEWDG LICWPRGTVG KISAVPCPPY IYDFNHKGVA FRHCNPNGTW   120
DFMHSLNKTW ANYSDCLRFL QPDISIGKQE FFERLYVMYT VGYSISFGSL AVAILIIGYF   180
RRLHCTRNYI HMHLFVSFML RATSIFVKDR VVHAHIGVKE LESLIMQDDP QNSIEATSVD   240
KSQYIGCKIA VVMFIYFLAT NYYWILVEGL YLHNLIFVAF FSDTKYLWGF ILIGWGFPAA   300
FVAAWAVARA TLADARCWEL SAGDIKWIYQ APILAAIGLN FILFLNTVRV LATKIWETNA   360
VGHDTRKQYR KLAKSTLVLV LVFGVHYIVF VCLPHSFTGL GWEIRMHCEL FFNSFQGFFV   420
SIIYCYCNGE VQAEVKKMWS RWNLSVDWKR TPPCGSRRCG SVLTTVTHST SSQSQVAAST   480
RMVLISGKAA KIASRQPDSH ITLPGYVWSN SEQDCLPHSF HEETKEDSGR QGDDILMEKP   540
SRPMESNPDT EGCQGETEDV L
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Seq ID NO: 662 DNA sequence
Nucleic Acid Accession #: NM_005048
Coding sequence: 143..1795

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1          11         21         31         41         51
|          |          |          |          |          |
GGCCGGTGGC CCGGGCCCGA CCACCCCAGC TGCGCGTCGT TACTGGCCAC AAGTTTGCTC    60
TGGGCCAGCC AAGTTGGCAA CTTGGAAGCT TCTCCCGGGC TCTGGAGGAG GGTCCCTGCT   120
TCTTCCTACA GCCGTTCCGG GCATGGCCGG GCTGGGGGCG TCGCTCCACG TCTGGGGTTG   180
GCTAATGCTC GGCAGCTGCC TCCTGGCCAG AGCCCAGCTG GATTCTGATG GCACCATTAC   240
TATAGAGGAG CAGATTGTCC TTGTGCTGAA AGCGAAAGTA CAATGTGAAC TCAACATCAC   300
AGCTCAACTC CAGGAGGGAG AAGGTAATTG TTTCCCTGAA TGGGATGGAC TCATTTGTTG   360
GCCCAGAGGA ACAGTGGGGA AAATATCGGC TGTTCCATGC CCTCCTTATA TTTATGACTT   420
CAACCATAAA GGAGTTGCTT TCCGACACTG TAACCCCAAT GGAACATGGG ATTTTATGCA   480
CAGCTTAAAT AAAACATGGG CCAATTATTC AGACTGCCTT CGCTTTCTGC AGCCAGATAT   540
CAGCATAGGA AAGCAAGAAT TCTTTGAACG CCTCTATGTA ATGTATACCG TTGGCTACTC   600
CATCTCTTTT GGTTCCTTGG CTGTGGCTAT TCTCATCATT GGTTACTTCA GACGATTGCA   660
TTGCACTAGG AACTATATCC ACATGCACTT ATTTGTGTCT TTCATGCTGA GAGCTACAAG   720
CATCTTTGTC AAAGACAGAG TAGTCCATGC TCACATAGGA GTAAAGGAGC TGGAGTCCCT   780
AATAATGCAG GATGACCCAC AAAATTCCAT TGAGGCAACT TCTGTGGACA AATCACAATA   840
TATCGGGTGC AAGATTGCTG TTGTGATGTT TATTTACTTC CTGGCTACAA ATTATTATTG   900
GATCCTGGTG GAAGGTCTCT ACCTGCATAA TCTCATCTTT GTGGCTTTCT TTTCGGACAC   960
CAAATACCTG TGGGGCTTCA TCTTGATAGG CTGGGGGTTT CCAGCAGCAT TTGTTGCAGC  1020
ATGGGCTGTG GCACGAGCAA CTCTGGCTGA TGCGAGGTGC TGGGAACTTA GTGCTGGAGA  1080
CATCAAGTGG ATTTATCAAG CACCGATCTT AGCAGCTATT GGGCTGAATT TTATTCTGTT  1140
TCTGAATACG GTTAGAGTTC TAGCTACCAA AATCTGGGAG ACCAATGCAG TTGGGCATGA  1200
CACAAGGAAG CAATACAGGA AACTGGCCAA ATCGACACTG GTCCTGGTCC TAGTCTTTGG  1260
AGTGCATTAC ATCGTGTTCG TATGCCTGCC TCACTCCTTC ACTGGGCTCG GGTGGGAGAT  1320
CCGCATGCAC TGTGAGCTCT TCTTCAACTC CTTTCAGGGT TTCTTTGTGT CTATCATCTA  1380
CTGCTACTGC AATGGAGAGG TTCAGGCAGA GGTGAAGAAG ATGTGGAGTC GGTGGAATCT  1440
CTCCGTGGAC TGGAAAAGGA CACCGCCATG TGGCAGCCGC AGATGCGGCT CAGTGCTCAC  1500
CACCGTGACG CACAGCACCA GCAGCCAGTC ACAGGTGGCG GCCAGCACAC GCATGGTGCT  1560
TATCTCTGGC AAAGCTGCCA AGATCGCCAG CAGACAGCCT GACAGCCACA TCACTTTACC  1620
TGGCTATGTC TGGAGTAACT CAGAGCAGGA CTGCCTGCCA CACTCTTTCC ACGAGGAGAC  1680
CAAGGAAGAT AGTGGGAGGC AGGGAGATGA TATTCTAATG GAGAAGCCTT CCAGGCCTAT  1740
GGAATCTAAC CCAGACACTG AAGGATGCCA AGGAGAAACT GAGGATGTTC TCTGAATGGA  1800
CATTTGTGGC TGACTTTCAT GGGCTGGTCC AATGGCTGGT TGTGTGAGAG GGCTTGGCTG  1860
ATACTCCTAT GCTTGAGTTC AAAGGCTGAA AATTCAGTTA AGGTGTTACT TAATAATAGT  1920
TTTTAGGCTC CATGAATTGG CTCCTGTAAA TACTAACGAC ATGAAAATGC AAGTGTCAAT  1980
GGAGTAGTTT ATTACCTTCT ATTGGCATCA AGTTTTCCTC TAAATTAATG TATGGTATTT  2040
GCTCTGTGAT TGTTCATTTT TTTCTGCTAC TTTTGGGTAG AAAAAAGATT CAATTGCTTG  2100
GCTGTAGCTT TCTCTCATAT ATATCACCCT AAATATAATG AAGATCTTTT AGTGTGTATC  2160
ATTTTCCTTT TAGAAACTAG TATTCTCTTA TTTCTTACTT TAATGTACTT CTATCACTGC  2220
ATTTATTTTG CCTGTGCATA GGAGCAATTA GGATCTAAAA AAATATATGG GAAGATAAAA  2280
GATCTAAGAA CAAGTACTTG CTGGAAAATT AGTTGGCTGG ACATTGATAA AATAATGCAT  2340
TTATAACAAT TACATGTGTT TTTGGGAACA AGGAAAATTT CTCAAAAAAG AATATTTCAC  2400
ACATCCCTTC TTTTGAATGG CCTCTTTGTG ACCAGCCAGA CCTCAGGTCT TCACTCTTTC  2460
TTCTTTGTAA ACCATGTCAT GTGGAAAGAT TTCCTCAGTT AGTGAGCTTG TGTCTGCAAA  2520
TTGATTTTGT TTGTAATGTA TTTTGATAGC AAATCATGCT GCATCTATAT CTTTTTCTTG  2580
TTTGAGCTGT TACTACATTG TACATGGCAT GTGGGATCAA TTAAAAATTT GTTTTAAAAA  2640
T
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Seq ID NO: 663 Protein sequence
Protein Accession #: NP_005039

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1          11         21         31         41         51
|          |          |          |          |          |
MAGLGASLHV WGWLMLGSCL LARAQLDSDG TITIEEQIVL VLKAKVQCEL NITAQLQEGE    60
GNCFPEWDGL ICWPRGTVGK ISAVPCPPYI YDFNHKGVAF RHCNPNGTWD FMHSLNKTWA   120
NYSDCLRFLQ PDISIGKQEF FERLYVMYTV GYSISFGSLA VAILIIGYFR RLHCTRNYIH   180
MHLFVSFMLR ATSIFVKDRV VHAHIGVKEL ESLIMQDDPQ NSIEATSVDK SQYIGCKIAV   240
```

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VMFIYFLATN YYWILVEGLY LHNLIFVAFF SDTKYLWGFI LIGWGFPAAF VAAWAVARAT   300
LADARCWELS AGDIKWIYQA PILAAIGLNF ILFLNTVRVL ATKIWETNAV GHDTRKQYRK   360
LAKSTLVLVL VFGVHYIVFV CLPHSFTGLG WEIRMHCELF FNSFQGFFVS IIYCYCNGEV   420
QAEVKKMWSR WNLSVDWKRT PPCGSRRCGS VLTTVTHSTS SQSQVAASTR MVLISGKAAK   480
IASRQPDSHI TLPGYVWSNS EQDCLPHSFH EETKEDSGRQ GDDILMEKPS RPMESNPDTE   540
GCQGETEDVL
```

Seq ID NO: 664 DNA sequence
Nucleic Acid Accession #: NM_012152
Coding sequence: 43..1104

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1          11         21         31         41         51
|          |          |          |          |          |
CTTCTTTAAA TTTCTTTCTA GGATGTTCAC TTCTTCTCCA CAATGAATGA GTGTCACTAT     60
GACAAGCACA TGGACTTTTT TTATAATAGG AGCAACACTG ATACTGTCGA TGACTGGACA    120
GGAACAAAGC TTGTGATTGT TTTGTGTGTT GGGACGTTTT TCTGCCTGTT TATTTTTTTT    180
TCTAATTCTC TGGTCATCGC GGCAGTGATC AAAAACAGAA AATTTCATTT CCCCTTCTAC    240
TACCTGTTGG CTAATTTAGC TGCTGCCGAT TTCTTCGCTG GAATTGCCTA TGTATTCCTG    300
ATGTTTAACA CAGGCCCAGT TTCAAAAACT TTGACTGTCA ACCGCTGGTT TCTCCGTCAG    360
GGGCTTCTGG ACAGTAGCTT GACTGCTTCC CTCACCAACT TGCTGGTTAT CGCCGTGGAG    420
AGGCACATGT CAATCATGAG GATGCGGGTC CATAGCAACC TGACCAAAAA GAGGGTGACA    480
CTGCTCATTT TGCTTGTCTG GGCCATCGCC ATTTTTATGG GGGCGGTCCC CACACTGGGC    540
TGGAATTGCC TCTGCAACAT CTCTGCCTGC TCTTCCCTGG CCCCCATTTA CAGCAGGAGT    600
TACCTTGTTT TCTGGACAGT GTCCAACCTC ATGGCCTTCC TCATCATGGT TGTGGTGTAC    660
CTGCGGATCT ACGTGTACGT CAAGAGGAAA ACCAACGTCT TGTCTCCGCA TACAAGTGGG    720
TCCATCAGCC GCCGGAGGAC ACCCATGAAG CTAATGAAGA CGGTGATGAC TGTCTTAGGG    780
GCGTTTGTGG TATGCTGGAC CCCGGGCCTG GTGGTTCTGC TCCTCGACGG CCTGAACTGC    840
AGGCAGTGTG GCGTGCAGCA TGTGAAAAGG TGGTTCCTGC TGCTGGCGCT GCTCAACTCC    900
GTCGTGAACC CCATCATCTA CTCCTACAAG GACGAGGACA TGTATGGCAC CATGAAGAAG    960
ATGATCTGCT GCTTCTCTCA GGAGAACCCA GAGAGGCGTC CCTCTCGCAT CCCCTCCACA   1020
GTCCTCAGCA GGAGTGACAC AGGCAGCCAG TACATAGAGG ATAGTATTAG CCAAGGTGCA   1080
GTCTGCAATA AAAGCACTTC CTAAACTCTG GATGCCTCTC GGCCCACCCA GGTGATGACT   1140
GTCTTAGG
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Seq ID NO: 665 Protein sequence
Protein Accession #: NP_036284

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1          11         21         31         41         51
|          |          |          |          |          |
MNECHYDKHM DFFYNRSNTD TVDDWTGTKL VIVLCVGTFF CLFIFFSNSL VIAAVIKNRK     60
FHFPFYYLLA NLAAADFFAG IAYVFLMFNT GPVSKTLTVN RWFLRQGLLD SSLTASLTNL    120
LVIAVERHMS IMRMRVHSNL TKKRVTLLIL LVWAIAIFMG AVPTLGWNCL CNISACSSLA    180
PIYSRSYLVF WTVSNLMAFL IMVVVYLRIY VYVKRKTNVL SPHTSGSISR RRTPMKLMKT    240
VMTVLGAFVV CWTPGLVVLL LDGLNCRQCG VQHVKRWFLL LALLNSVVNP IIYSYKDEDM    300
YGTMKKMICC FSQENPERRP SRIPSTVLSR SDTGSQYIED SISQGAVCNK STS
```

Seq ID NO: 666 DNA sequence
Nucleic Acid Accession #: NM_002821
Coding sequence: 150..3362

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1          11         21         31         41         51
|          |          |          |          |          |
AACTCCCGCC TCGGGACGCC TCGGGGTCGG GCTCCGGCTG CGGCTGCTGC TGCGGCGCCC     60
GCGCTCCGGT GCGTCCGCCT CCTGTGCCCG CCGCGGAGCA GTCTGCGGCC CGCCGTGCGC    120
CCTCAGCTCC TTTTCCTGAG CCCGCCGCGA TGGGAGCTGC GCGGGGATCC CCGGCCAGAC    180
CCCGCCGGTT GCCTCTGCTC AGCGTCCTGC TGCTGCCGCT GCTGGGCGGT ACCCAGACAG    240
CCATTGTCTT CATCAAGCAG CCGTCCTCCC AGGATGCACT GCAGGGGCGC CGGGCGCTGC    300
TTCGCTGTGA GGTTGAGGCT CCGGGCCCGG TACATGTGTA CTGGCTGCTC GATGGGGCCC    360
CTGTCCAGGA CACGGAGCGG CGTTTCGCCC AGGGCAGCAG CCTGAGCTTT GCAGCTGTGG    420
ACCGGCTGCA GGACTCTGGC ACCTTCCAGT GTGTGGCTCG GGATGATGTC ACTGGAGAAG    480
AAGCCCGCAG TGCCAACGCC TCCTTCAACA TCAAATGGAT TGAGGCAGGT CCTGTGGTCC    540
TGAAGCATCC AGCCTCGGAA GCTGAGATCC AGCCACAGAC CCAGGTCACA CTTCGTTGCC    600
ACATTGATGG GCACCCTCGG CCCACCTACC AATGGTTCCG AGATGGGACC CCCCTTTCTG    660
ATGGTCAGAG CAACCACACA GTCAGCAGCA AGGAGCGGAA CCTGACGCTC CGGCCAGCTG    720
GTCCTGAGCA TAGTGGGCTG TATTCCTGCT GCGCCCACAG TGCTTTTGGC CAGGCTTGCA    780
GCAGCCAGAA CTTCACCTTG AGCATTGCTG ATGAAAGCTT TGCCAGGGTG GTGCTGGCAC    840
CCCAGGACGT GGTAGTAGCG AGGTATGAGG AGGCCATGTT CCATTGCCAG TTCTCAGCCC    900
AGCCACCCCC GAGCCTGCAG TGGCTCTTTG AGGATGAGAC TCCCATCACT AACCGCAGTC    960
GCCCCCCACA CCTCCGCAGA GCCACAGTGT TTGCCAACGG GTCTCTGCTG CTGACCCAGG   1020
TCCGGCCACG CAATGCAGGG ATCTACCGCT GCATTGGCCA GGGGCAGAGG GGCCCACCCA   1080
TCATCCTGGA AGCCACACTT CACCTAGCAG AGATTGAAGA CATGCCGCTA TTTGAGCCAC   1140
GGGTGTTTAC AGCTGGCAGC GAGGAGCGTG TGACCTGCCT TCCCCCCAAG GGTCTGCCAG   1200
AGCCCAGCGT GTGGTGGGAG CACGCGGGAG TCCGGCTGCC CACCCATGGC AGGGTCTACC   1260
AGAAGGGCCA CGAGCTGGTG TTGGCCAATA TTGCTGAAAG TGATGCTGGT GTCTACACCT   1320
GCCACGCGGC CAACCTGGCT GGTCAGCGGA GACAGGATGT CAACATCACT GTGGCCACTG   1380
TGCCCTCCTG GCTGAAGAAG CCCCAAGACA GCCAGCTGGA GGAGGGCAAA CCCGGCTACT   1440
TGGATTGCCT GACCCAGGCC ACACCAAAAC CTACAGTTGT CTGGTACAGA AACCAGATGC   1500
TCATCTCAGA GGACTCACGG TTCGAGGTCT TCAAGAATGG GACCTTGCGC ATCAACAGCG   1560
TGGAGGTGTA TGATGGGACA TGGTACCGTT GTATGAGCAG CACCCCAGCC GGCAGCATCG   1620
AGGCGCAAGC CCGTGTCCAA GTGCTGGAAA AGCTCAAGTT CACACCACCA CCCCAGCCAC   1680
AGCAGTGCAT GGAGTTTGAC AAGGAGGCCA CGGTGCCCTG TTCAGCCACA GGCCGAGAGA   1740
AGCCCACTAT TAAGTGGGAA CGGGCAGATG GGAGCAGCCT CCCAGAGTGG GTGACAGACA   1800
ACGCTGGGAC CCTGCATTTT GCCCGGGTGA CTCGAGATGA CGCTGGCAAC TACACTTGCA   1860
TTGCCTCCAA CGGGCCGCAG GGCCAGATTC GTGCCCATGT CCAGCTCACT GTGGCAGTTT   1920
TTATCACCTT CAAAGTGGAA CCAGAGCGTA CGACTGTGTA CCAGGGCCAC ACAGCCCTAC   1980
TGCAGTGCGA GGCCCAGGGG GACCCCAAGC CGCTGATTCA GTGGAAAGGC AAGGACCGCA   2040
TCCTGGACCC CACCAAGCTG GGACCCAGGA TGCACATCTT CCAGAATGGC TCCCTGGTGA   2100
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TCCATGACGT GGCCCCTGAG GACTCAGGCC GCTACACCTG CATTGCAGGC AACAGCTGCA  2160
ACATCAAGCA CACGGAGGCC CCCCTCTATG TCGTGGACAA GCCTGTGCCG GAGGAGTCGG  2220
AGGGCCCTGG CAGCCCTCCC CCCTACAAGA TGATCCAGAC CATTGGGTTG TCGGTGGGTG  2280
CCGCTGTGGC CTACATCATT GCCGTGCTGG GCCTCATGTT CTACTGCAAG AAGCGCTGCA  2340
AAGCCAAGCG GCTGCAGAAG CAGCCCGAGG GCGAGGAGCC AGAGATGGAA TGCCTCAACG  2400
GAGGGCCTTT GCAGAACGGG CAGCCCTCAG CAGAGATCCA AGAAGAAGTG GCCTTGACCA  2460
GCTTGGGCTC CGGCCCCGCG GCCACCAACA AACGCCACAG CACAAGTGAT AAGATGCACT  2520
TCCCACGGTC TAGCCTGCAG CCCATCACCA CGCTGGGGAA GAGTGAGTTT GGGGAGGTGT  2580
TCCTGGCAAA GGCTCAGGGC TTGGAGGAGG GAGTGGCAGA GACCCTGGTA CTTGTGAAGA  2640
GCCTGCAGAC GAAGGATGAG CAGCAGCAGC TGGACTTCCG GAGGGAGTTG GAGATGTTTG  2700
GGAAGCTGAA CCACGCCAAC GTGGTGCGGC TCCTGGGGCT GTGCCGGGAG GCTGAGCCCC  2760
ACTACATGGT GCTGGAATAT GTGGATCTGG GAGACCTCAA GCAGTTCCTG AGGATTTCCA  2820
AGAGCAAGGA TGAAAAATTG AAGTCACAGC CCCTCAGCAC CAAGCAGAAG GTGGCCCTAT  2880
GCACCCAGGT AGCCCTGGGC ATGGAGCACC TGTCCAACAA CCGCTTTGTG CATAAGGACT  2940
TGGCTGCGCG TAACTGCCTG GTCAGTGCCC AGAGACAAGT GAAGGTGTCT GCCCTGGGCC  3000
TCAGCAAGGA TGTGTACAAC AGTGAGTACT ACCACTTCCG CCAGGCCTGG GTGCCGCTGC  3060
GCTGGATGTC CCCCGAGGCC ATCCTGGAGG GTGACTTCTC TACCAAGTCT GATGTCTGGG  3120
CCTTCGGTGT GCTGATGTGG GAAGTGTTTA CACATGGAGA GATGCCCCAT GGTGGGCAGG  3180
CAGATGATGA AGTACTGGCA GATTTGCAGG CTGGGAAGGC TAGACTTCCT CAGCCCGAGG  3240
GCTGCCCTTC CAAACTCTAT CGGCTGATGC AGCGCTGCTG GGCCCTCAGC CCCAAGGACC  3300
GGCCCTCCTT CAGTGAGATT GCCAGCGCCC TGGGAGACAG CACCGTGGAC AGCAAGCCGT  3360
GAGGAGGGAG CCCGCTCAGG ATGGCCTGGG CAGGGGAGGA CATCTCTAGA GGGAAGCTCA  3420
CAGCATGATG GGCAAGATCC CTGTCCTCCT GGGCCCTGAG GTGCCCTAGT GCAACAGGCA  3480
TTGCTGAGGT CTGAGCAGGG CCTGGCCTTT CCTCCTCTTC CTCACCCTCA TCCTTTGGGA  3540
GGCTGACTTG GACCCAAACT GGGCGACTAG GGCTTTGAGC TGGGCAGTTT CCCCTGCCAC  3600
CTCTTCCTCT ATCAGGGACA GTGTGGGTGC CACAGGTAAC CCCAATTTCT GGCCTTCAAC  3660
TTCTCCCCTT GACCGGGTCC AACTCTGCCA CTCATCTGCC AACTTTGCCT GGGGAGGGCT  3720
AGGCTTGGGA TGAGCTGGGT TTGTGGGGAG TTCCTTAATA TTCTCAAGTT CTGGGCACAC  3780
AGGGTTAATG AGTCTCTTGC CCACTGGTCC ACTTGGGGGT CTAGACCAGG ATTATAGAGG  3840
ACACAGCAAG TGAGTCCTCC CCACTCTGGG CTTGTGCACA CTGACCCAGA CCCACGTCTT  3900
CCCCACCCTT CTCTCCTTTC CTCATCCTAA GTGCCTGGCA GATGAAGGAG TTTTCAGGAG  3960
CTTTTGACAC TATATAAACC GCCCTTTTTG TATGCACCAC GGGCGGCTTT TATATGTAAT  4020
TGCAGCGTGG GGTGGGTGGG CATGGGAGGT AGGGGTGGGC CCTGGAGATG AGGAGGGTGG  4080
GCCATCCTTA CCCCACACTT TTATTGTTGT CGTTTTTTGT TTGTTTTGTT TTTTTGTTTT  4140
TGTTTTTGTT TTTACACTCG CTGCTCTCAA TAAATAAGCC TTTTTTA
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Seq ID NO: 667 Protein sequence
Protein Accession #: NP_002812

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1          11         21         31         41         51
|          |          |          |          |          |
MGAARGSPAR PRRLPLLSVL LLPLLGGTQT AIVFIKQPSS QDALQGRRAL LRCEVEAPGP    60
VHVYWLLDGA PVQDTERRFA QGSSLSFAAV DRLQDSGTFQ CVARDDVTGE EARSANASFN   120
IKWIEAGPVV LKHPASEAEI QPQTQVTLRC HIDGHPRPTY QWFRDGTPLS DGQSNHTVSS   180
KERNLTLRPA GPEHSGLYSC CAHSAFGQAC SSQNFTLSIA DESFARVVLA PQDVVVARYE   240
EAMFHCQFSA QPPPSLQWLF EDETPITNRS RPPHLRRATV FANGSLLLTQ VRPRNAGIYR   300
CIGQGQRGPP IILEATLHLA EIEDMPLFEP RVFTAGSEER VTCLPPKGLP EPSVWWEHAG   360
VRLPTHGRVY QKGHELVLAN IAESDAGVYT CHAANLAGQR RQDVNITVAT VPSWLKKPQD   420
SQLEEGKPGY LDCLTQATPK PTVVWYRNQM LISEDSRFEV FKNGTLRINS VEVYDGTWYR   480
CMSSTPAGSI EAQARVQVLE KLKFTPPPQP QQCMEFDKEA TVPCSATGRE KPTIKWERAD   540
GSSLPEWVTD NAGTLHFARV TRDDAGNYTC IASNGPQGQI RAHVQLTVAV FITFKVEPER   600
TTVYQGHTAL LQCEAQGDPK PLIQWKGKDR ILDPTKLGPR MHIFQNGSLV IHDVAPEDSG   660
RYTCIAGNSC NIKHTEAPLY VVDKPVPEES EGPGSPPPYK MIQTIGLSVG AAVAYIIAVL   720
GLMFYCKKRC KAKRLQKQPE GEEPEMECLN GGPLQNGQPS AEIQEEVALT SLGSGPAATN   780
KRHSTSDKMH FPRSSLQPIT TLGKSEFGEV FLAKAQGLEE GVAETLVLVK SLQTKDEQQQ   840
LDFRRELEMF GKLNHANVVR LLGLCREAEP HYMVLEYVDL GDLKQFLRIS KSKDEKLKSQ   900
PLSTKQKVAL CTQVALGMEH LSNNRFVHKD LAARNCLVSA QRQVKVSALG LSKDVYNSEY   960
YHFRQAWVPL RWMSPEAILE GDFSTKSDVW AFGVLMWEVF THGEMPHGGQ ADDEVLADLQ  1020
AGKARLPQPE GCPSKLYRLM QRCWALSPKD RPSFSEIASA LGDSTVDSKP
```

Seq ID NO: 668 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1389

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1          11         21         31         41         51
|          |          |          |          |          |
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCAGA GAGATTTAGA TGACAGAGAA    60
ACCCTTGTTT CTGAACATGA GTATAAAGAG AAAACCTGTC AGTCTGCTGC TCTTTTTAAT   120
GTTGTCAACT CGATTATAGG ATCTGGTATA ATAGGATTGC CTTATTCAAT GAAGCAAGCT   180
GGGTTTCCTT TGGGAATATT GCTTTTATTC TGGGTTTCAT ATGTTACGGA CTTTTCCCTT   240
GTTTTATTGA TAAAAGGAGG GGCCCTCTCT GGAACAGATA CCTACCAGTC TTTGGTCAAT   300
AAAACTTTCG GCTTTCCAGG GTATCTGCTC CTCTCTGTTC TTCAGTTTTT GTATCCTTTT   360
ATAGCAATGA TAAGTTACAA TATAATAGCT GGAGATACTT TGAGCAAAGT TTTTCAAAGA   420
ATCCCAGGAG TTGATCCTGA AAACGTGTTT ATTGGTCGCC ACTTCATTAT TGGACTTTCC   480
ACAGTTACCT TTACTCTGCC TTTATCCTTG TACCGAAATA TAGCAAAGCT TGGAAAGGTC   540
TCCCTCATCT CTACAGGTTT AACAACTCTG ATTCTTGGAA TTGTAATGGC AAGGGCAATT   600
TCACTGGGTC CACACATACC AAAAACAGAA GACGCTTGGG TATTTGCAAA GCCCAATGCC   660
ATTCAAGCGG TCGGGGTTAT GTCTTTTGCA TTTATTTGCC ACCATAACTC CTTCTTAGTT   720
TACAGTTCTC TAGAAGAACC CACAGTAGCT AAGTGGTCCC GCCTTATCCA TATGTCCATC   780
GTGATTTCTG TATTTATCTG TATATTCTTT GCTACATGTG GATACTTGAC ATTTACTGGC   840
TTCACCCAAG GGGACTTATT TGAAAATTAC TGCAGAAATG ATGACCTGGT AACATTTGGA   900
AGATTTTGTT ATGGTGTCAC TGTCATTTTG ACATACCCTA TGGAATGCTT TGTGACAAGA   960
GAGGTAATTG CCAATGTGTT TTTTGGTGGG AATCTTTCAT CGGTTTTCCA CATTGTTGTA  1020
ACAGTGATGG TCATCACTGT AGCCACGCTT GTGTCATTGC TGATTGATTG CCTCGGGATA  1080
GTTCTAGAAC TCAATGGTGT GCTCTGTGCA ACTCCCCTCA TTTTTATCAT TCCATCAGCC  1140
TGTTATCTGA AACTGTCTGA AGAACCAAGG ACACACTCCG ATAAGATTAT GTCTTGTGTC  1200
ATGCTTCCCA TTGGTGCTGT GGTGATGGTT TTTGGATTCG TCATGGCTAT TACAAATACT  1260
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CAAGACTGCA CCCATGGGCA GGAAATGTTC TACTGCTTTC CTGACAATTT CTCTCTCACA  1320
AATACCTCAG AGTCTCATGT TCAGCAGACA ACACAACTTT CTACTTTAAA TATTAGTATC  1380
TTTCAATGA
```

Seq ID NO: 669 Protein sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MGYQRQEPVI PPQRDLDDRE TLVSEHEYKE KTCQSAALFN VVNSIIGSGI IGLPYSMKQA    60
GFPLGILLLF WVSYVTDFSL VLLIKGGALS GTDTYQSLVN KTFGFPGYLL LSVLQFLYPF   120
IAMISYNIIA GDTLSKVFQR IPGVDPENVF IGRHFIIGLS TVTFTLPLSL YRNIAKLGKV   180
SLISTGLTTL ILGIVMARAI SLGPHIPKTE DAWVFAKPNA IQAVGVMSFA FICHHNSFLV   240
YSSLEEPTVA KWSRLIHMSI VISVFICIFF ATCGYLTFTG FTQGDLFENY CRNDDLVTFG   300
RFCYGVTVIL TYPMECFVTR EVIANVFFGG NLSSVFHIVV TVMVITVATL VSLLIDCLGI   360
VLELNGVLCA TPLIFIIPSA CYLKLSEEPR THSDKIMSCV MLPIGAVVMV FGFVMAITNT   420
QDCTHGQEMF YCFPDNFSLT NTSESHVQQT TQLSTLNISI FQ
```

Seq ID NO: 670 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1284

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCAGA GAGGATTGCC TTATTCAATG    60
AAGCAAGCTG GGTTTCCTTT GGGAATATTG CTTTTATTCT GGGTTTCATA TGTTACAGAC   120
TTTTCCCTTG TTTTATTGAT AAAAGGAGGG GCCCTCTCTG GAACAGATAC CTACCAGTCT   180
TTGGTCAATA AAACTTTCGG CTTTCCAGGG TATCTGCTCC TCTCTGTTCT TCAGTTTTTG   240
TATCCTTTTA TAGCAATGAT AAGTTACAAT ATAATAGCTG GAGATACTTT GAGCAAAGTT   300
TTTCAAAGAA TCCCAGGAGT TGATCCTGAA AACGTGTTTA TTGGTCGCCA CTTCATTATT   360
GGACTTTCCA CAGTTACCTT TACTCTGCCT TTATCCTTGT ACCGAAATAT AGCAAAGCTT   420
GGAAAGGTCT CCCTCATCTC TACAGGTTTA ACAACTCTGA TTCTTGGAAT TGTAATGGCA   480
AGGGCAATTT CACTGGGTCC ACACATACCA AAAACAGAAG ACGCTTGGGT ATTTGCAAAG   540
CCCAATGCCA TTCAAGCGGT CGGGGTTATG TCTTTTGCAT TTATTTGCCA CCATAACTCC   600
TTCTTAGTTT ACAGTTCTCT AGAAGAACCC ACAGTAGCTA AGTGGTCCCG CCTTATCCAT   660
ATGTCCATCG TGATTTCTGT ATTTATCTGT ATATTCTTTG CTACATGTGG ATACTTGACA   720
TTTACTGGCT TCACCCAAGG GGACTTATTT GAAAATTACT GCAGAAATGA TGACCTGGTA   780
ACATTTGGAA GATTTTGTTA TGGTGTCACT GTCATTTTGA CATACCCTAT GGAATGCTTT   840
GTGACAAGAG AGGTAATTGC CAATGTGTTT TTTGGTGGGA ATCTTTCATC GGTTTTCCAC   900
ATTGTTGTAA CAGTGATGGT CATCACTGTA GCCACGCTTG TGTCATTGCT GATTGATTGC   960
CTCGGGATAG TTCTAGAACT CAATGGTGTG CTCTGTGCAA CTCCCCTCAT TTTTATCATT  1020
CCATCAGCCT GTTATCTGAA ACTGTCTGAA GAACCAAGGA CACACTCCGA TAAGATTATG  1080
TCTTGTGTCA TGCTTCCCAT TGGTGCTGTG GTGATGGTTT TTGGATTCGT CATGGCTATT  1140
ACAAATACTC AAGACTGCAC CCATGGGCAG GAAATGTTCT ACTGCTTTCC TGACAATTTC  1200
TCTCTCACAA ATACCTCAGA GTCTCATGTT CAGCAGACAA CACAACTTTC TACTTTAAAT  1260
ATTAGTATCT TTCAACTCGA GTAA
```

Seq ID NO: 671 Protein sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MGYQRQEPVI PPQRGLPYSM KQAGFPLGIL LLFWVSYVTD FSLVLLIKGG ALSGTDTYQS    60
LVNKTFGFPG YLLLSVLQFL YPFIAMISYN IIAGDTLSKV FQRIPGVDPE NVFIGRHFII   120
GLSTVTFTLP LSLYRNIAKL GKVSLISTGL TTLILGIVMA RAISLGPHIP KTEDAWVFAK   180
PNAIQAVGVM SFAFICHHNS FLVYSSLEEP TVAKWSRLIH MSIVISVFIC IFFATCGYLT   240
FTGFTQGDLF ENYCRNDDLV TFGRFCYGVT VILTYPMECF VTREVIANVF FGGNLSSVFH   300
IVVTVMVITV ATLVSLLIDC LGIVLELNGV LCATPLIFII PSACYLKLSE EPRTHSDKIM   360
SCVMLPIGAV VMVFGFVMAI TNTQDCTHGQ EMFYCFPDNF SLTNTSESHV QQTTQLSTLN   420
ISIFQLE
```

Seq ID NO: 672 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1203

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCAGT TTTCCCTTGT TTTATTGATA    60
AAAGGAGGGG CCCTCTCTGG AACAGATACC TACCAGTCTT TGGTCAATAA AACTTTCGGC   120
TTTCCAGGGT ATCTGCTCCT CTCTGTTCTT CAGTTTTTGT ATCCTTTTAT AGCAATGATA   180
AGTTACAATA TAATAGCTGG AGATACTTTG AGCAAAGTTT TTCAAAGAAT CCCAGGAGTT   240
GATCCTGAAA ACGTGTTTAT TGGTCGCCAC TTCATTATTG GACTTTCCAC AGTTACCTTT   300
ACTCTGCCTT TATCCTTGTA CCGAAATATA GCAAAGCTTG GAAAGGTCTC CCTCATCTCT   360
ACAGGTTTAA CAACTCTGAT TCTTGGAATT GTAATGGCAA GGGCAATTTC ACTGGGTCCA   420
CACATACCAA AAACAGAAGA CGCTTGGGTA TTTGCAAAGC CCAATGCCAT TCAAGCGGTC   480
GGGGTTATGT CTTTTGCATT TATTTGCCAC CATAACTCCT TCTTAGTTTA CAGTTCTCTA   540
GAAGAACCCA CAGTAGCTAA GTGGTCCCGC CTTATCCATA TGTCCATCGT GATTTCTGTA   600
TTTATCTGTA TATTCTTTGC TACATGTGGA TACTTGACAT TTACTGGCTT CACCCAAGGG   660
GACTTATTTG AAAATTACTG CAGAAATGAT GACCTGGTAA CATTTGGAAG ATTTTGTTAT   720
GGTGTCACTG TCATTTTGAC ATACCCTATG GAATGCTTTG TGACAAGAGA GGTAATTGCC   780
AATGTGTTTT TTGGTGGGAA TCTTTCATCG GTTTTCCACA TTGTTGTAAC AGTGATGGTC   840
ATCACTGTAG CCACGCTTGT GTCATTGCTG ATTGATTGCC TCGGGATAGT TCTAGAACTC   900
AATGGTGTGC TCTGTGCAAC TCCCCTCATT TTTATCATTC CATCAGCCTG TTATCTGAAA   960
CTGTCTGAAG AACCAAGGAC ACACTCCGAT AAGATTATGT CTTGTGTCAT GCTTCCCATT  1020
GGTGCTGTGG TGATGGTTTT TGGATTCGTC ATGGCTATTA CAAATACTCA AGACTGCACC  1080
CATGGGCAGG AAATGTTCTA CTGCTTTCCT GACAATTTCT CTCTCACAAA TACCTCAGAG  1140
TCTCATGTTC AGCAGACAAC ACAACTTTCT ACTTTAAATA TTAGTATCTT TCAACTCGAG  1200
```

TAA

Seq ID NO: 673 Protein sequence
Protein Accession #: Eos sequence

```
1          11         21         31         41         51
|          |          |          |          |          |
MGYQRQEPVI PPQFSLVLLI KGGALSGTDT YQSLVNKTFG FPGYLLLSVL QFLYPFIAMI    60
SYNIIAGDTL SKVFQRIPGV DPENVFIGRH FIIGLSTVTF TLPLSLYRNI AKLGKVSLIS   120
TGLTTLILGI VMARAISLGP HIPKTEDAWV FAKPNAIQAV GVMSFAFICH HNSFLVYSSL   180
EEPTVAKWSR LIHMSIVISV FICIFFATCG YLTFTGFTQG DLFENYCRND DLVTFGRFCY   240
GVTVILTYPM ECFVTREVIA NVFFGGNLSS VFHIVVTVMV ITVATLVSLL IDCLGIVLEL   300
NGVLCATPLI FIIPSACYLK LSEEPRTHSD KIMSCVMLPI GAVVMVFGFV MAITNTQDCT   360
HGQEMFYCFP DNFSLTNTSE SHVQQTTQLS TLNISIFQLE
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Seq ID NO: 674 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1140

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1          11         21         31         41         51
|          |          |          |          |          |
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCAGG TCAATAAAAC TTTCGGCTTT    60
CCAGGGTATC TGCTCCTCTC TGTTCTTCAG TTTTTGTATC CTTTTATAGC AATGATAAGT   120
TACAATATAA TAGCTGGAGA TACTTTGAGC AAAGTTTTTC AAAGAATCCC AGGAGTTGAT   180
CCTGAAAACG TGTTTATTGG TCGCCACTTC ATTATTGGAC TTTCCACAGT TACCTTTACT   240
CTGCCTTTAT CCTTGTACCG AAATATAGCA AAGCTTGGAA AGGTCTCCCT CATCTCTACA   300
GGTTTAACAA CTCTGATTCT TGGAATTGTA ATGGCAAGGG CAATTTCACT GGGTCCACAC   360
ATACCAAAAA CAGAAGACGC TTGGGTATTT GCAAAGCCCA ATGCCATTCA AGCGGTCGGG   420
GTTATGTCTT TTGCATTTAT TTGCCACCAT AACTCCTTCT TAGTTTACAG TTCTCTAGAA   480
GAACCCACAG TAGCTAAGTG GTCCCGCCTT ATCCATATGT CCATCGTGAT TTCTGTATTT   540
ATCTGTATAT TCTTTGCTAC ATGTGGATAC TTGACATTTA CTGGCTTCAC CCAAGGGGAC   600
TTATTTGAAA ATTACTGCAG AAATGATGAC CTGGTAACAT TTGGAAGATT TTGTTATGGT   660
GTCACTGTCA TTTTGACATA CCCTATGGAA TGCTTTGTGA CAAGAGAGGT AATTGCCAAT   720
GTGTTTTTTG GTGGGAATCT TTCATCGGTT TTCCACATTG TTGTAACAGT GATGGTCATC   780
ACTGTAGCCA CGCTTGTGTC ATTGCTGATT GATTGCCTCG GGATAGTTCT AGAACTCAAT   840
GGTGTGCTCT GTGCAACTCC CCTCATTTTT ATCATTCCAT CAGCCTGTTA TCTGAAACTG   900
TCTGAAGAAC CAAGGACACA CTCCGATAAG ATTATGTCTT GTGTCATGCT TCCCATTGGT   960
GCTGTGGTGA TGGTTTTTGG ATTCGTCATG GCTATTACAA ATACTCAAGA CTGCACCCAT  1020
GGGCAGGAAA TGTTCTACTG CTTTCCTGAC AATTTCTCTC TCACAAATAC CTCAGAGTCT  1080
CATGTTCAGC AGACAACACA ACTTTCTACT TTAAATATTA GTATCTTTCA ACTCGAGTAA
```

Seq ID NO: 675 Protein sequence
Protein Accession #: Eos sequence

```
1          11         21         31         41         51
|          |          |          |          |          |
MGYQRQEPVI PPQVNKTFGF PGYLLLSVLQ FLYPFIAMIS YNIIAGDTLS KVFQRIPGVD    60
PENVFIGRHF IIGLSTVTFT LPLSLYRNIA KLGKVSLIST GLTTLILGIV MARAISLGPH   120
IPKTEDAWVF AKPNAIQAVG VMSFAFICHH NSFLVYSSLE EPTVAKWSRL IHMSIVISVF   180
ICIFFATCGY LTFTGFTQGD LFENYCRNDD LVTFGRFCYG VTVILTYPME CFVTREVIAN   240
VFFGGNLSSV FHIVVTVMVI TVATLVSLLI DCLGIVLELN GVLCATPLIF IIPSACYLKL   300
SEEPRTHSDK IMSCVMLPIG AVVMVFGFVM AITNTQDCTH GQEMFYCFPD NFSLTNTSES   360
HVQQTTQLST LNISIFQLE
```

Seq ID NO: 676 DNA sequence
Nucleic Acid Accession #: NM_006853.1
Coding sequence: 26..874

```
1          11         21         31         41         51
|          |          |          |          |          |
AGGAATCTGC GCTCGGGTTC CGCAGATGCA GAGGTTGAGG TGGCTGCGGG ACTGGAAGTC    60
ATCGGGCAGA GGTCTCACAG CAGCCAAGGA ACCTGGGGCC CGCTCCTCCC CCCTCCAGGC   120
CATGAGGATT CTGCAGTTAA TCCTGCTTGC TCTGGCAACA GGGCTTGTAG GGGGAGAGAC   180
CAGGATCATC AAGGGGTTCG AGTGCAAGCC TCACTCCCAG CCCTGGCAGG CAGCCCTGTT   240
CGAGAAGACG CGGCTACTCT GTGGGGCGAC GCTCATCGCC CCCAGATGGC TCCTGACAGC   300
AGCCCACTGC CTCAAGCCCC GCTACATAGT TCACCTGGGG CAGCACAACC TCCAGAAGGA   360
GGAGGGCTGT GAGCAGACCC GGACAGCCAC TGAGTCCTTC CCCCACCCCG GCTTCAACAA   420
CAGCCTCCCC AACAAAGACC ACCGCAATGA CATCATGCTG GTGAAGATGG CATCGCCAGT   480
CTCCATCACC TGGGCTGTGC GACCCCTCAC CCTCTCCTCA CGCTGTGTCA CTGCTGGCAC   540
CAGCTGCCTC ATTTCCGGCT GGGGCAGCAC GTCCAGCCCC CAGTTACGCC TGCCTCACAC   600
CTTGCGATGC GCCAACATCA CCATCATTGA GCACCAGAAG TGTGAGAACG CCTACCCCGG   660
CAACATCACA GACACCATGG TGTGTGCCAG CGTGCAGGAA GGGGGCAAGG ACTCCTGCCA   720
GGGTGACTCC GGGGGCCCTC TGGTCTGTAA CCAGTCTCTT CAAGGCATTA TCTCCTGGGG   780
CCAGGATCCG TGTGCGATCA CCCGAAAGCC TGGTGTCTAC ACGAAAGTCT GCAAATATGT   840
GGACTGGATC CAGGAGACGA TGAAGAACAA TTAGACTGGA CCCACCCACC ACAGCCCATC   900
ACCCTCCATT TCCACTTGGT GTTTGGTTCC TGTTCACTCT GTTAATAAGA AACCCTAAGC   960
CAAGACCCTC TACGAACATT CTTTGGGCCT CCTGGACTAC AGGAGATGCT GTCACTTAAT  1020
AATCAACCTG GGGTTCGAAA TCAGTGAGAC CTGGATTCAA ATTCTGCCTT GAAATATTGT  1080
GACTCTGGGA ATGACAACAC CTGGTTTGTT CTCTGTTGTA TCCCCAGCCC CAAAGACAGC  1140
TCCTGGCCAT ATATCAAGGT TTCAATAAAT ATTTGCTAAA TGAGTG
```

Seq ID NO: 677 Protein sequence
Protein Accession #: NP_006844.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MRILQLILLA LATGLVGGET RIIKGFECKP HSQPWQAALF EKTRLLCGAT LIAPRWLLTA    60
```

```
AHCLKPRYIV HLGQHNLQKE EGCEQTRTAT ESFPHPGFNN SLPNKDHRND IMLVKMASPV   120
SITWAVRPLT LSSRCVTAGT SCLISGWGST SSPQLRLPHT LRCANITIIE HQKCENAYPG   180
NITDTMVCAS VQEGGKDSCQ GDSGGPLVCN QSLQGIISWG QDPCAITRKP GVYTKVCKYV   240
DWIQETMKNN
```

Seq ID NO: 678 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..933

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGTGCAGCA ATGGACGGTG CATCCCGGGC GCCTGGCAGT GTGACGGGCT GCCTGACTGC    60
TTCGACAAGA GTGATGAGAA GGAGTGCCCC AAGGCTAAGT CGAAATGTGG CCCGACCTTC   120
TTCCCCTGTG CCAGCGGCAT CCATTGCATC ATTGGTCGCT TCCGGTGCAA TGGGTTTGAG   180
GACTGTCCCG ATGGCAGCGA TGAAGAGAAC TGCACAGCAA ACCCTCTGCT TTGCTCCACC   240
GCCCGCTACC ACTGCAAGAA CGGCCTCTGT ATTGACAAGA GCTTCATCTG CGATGGACAG   300
AATAACTGTC AAGACAACAG TGATGAGGAA AGCTGTGAAA GTTCTCAAGA ACCCGGCAGT   360
GGGCAGGTGT TTGTGACTTC AGAGAACCAA CTTGTGTATT ACCCCAGCAT CACCTATGCC   420
ATCATCGGCA GCTCCGTCAT TTTTGTGCTG GTGGTGGCCC TGCTGGCACT GGTCTTGCAC   480
CACCAGCGGA AGCGGAACAA CCTCATGACG CTGCCCGTGC ACCGGCTGCA GCACCCTGTG   540
CTGCTGTCCC GCCTGGTGGT CCTGGACCAC CCCCACCACT GCAACGTCAC CTACAACGTC   600
AATAATGGCA TCCAGTATGT GGCCAGCCAG GCGGAGCAGA ATGCGTCGGA AGTAGGCTCC   660
CCACCCTCCT ACTCCGAGGC CTTGCTGGAC CAGAGGCCTG CGTGGTATGA CCTTCCTCCA   720
CCGCCCTACT CTTCTGACAC GGAATCTCTG AACCAAGCCG ACCTGCCCCC CTACCGCTCC   780
CGGTCCGGGA GTGCCAACAG TGCCAGCTCC CAGGCAGCCA GCAGCCTCCT GAGCGTGGAA   840
GACACCAGCC ACAGCCCGGG GCAGCCTGGC CCCCAGGAGG GCACTGCTGA GCCCAGGGAC   900
TCTGAGCCCA GCCAGGGCAC TGAAGAAGTA TAA
```

Seq ID NO: 679 Protein sequence
Protein Accession #: Eos sequence

```
1          11         21         31         41         51
|          |          |          |          |          |
MCSNGRCIPG AWQCDGLPDC FDKSDEKECP KAKSKCGPTF FPCASGIHCI IGRFRCNGFE    60
DCPDGSDEEN CTANPLLCST ARYHCKNGLC IDKSFICDGQ NNCQDNSDEE SCESSQEPGS   120
GQVFVTSENQ LVYYPSITYA IIGSSVIFVL VVALLALVLH HQRKRNNLMT LPVHRLQHPV   180
LLSRLVVLDH PHHCNVTYNV NNGIQYVASQ AEQNASEVGS PPSYSEALLD QRPAWYDLPP   240
PPYSSDTESL NQADLPPYRS RSGSANSASS QAASSLLSVE DTSHSPGQPG PQEGTAEPRD   300
SEPSQGTEEV
```

Seq ID NO: 680 DNA sequence
Nucleic Acid Accession #: S78203.1
Coding sequence: 1..2190

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGAATCCTT TCCAGAAAAA TGAGTCCAAG GAAACTCTTT TTTCACCTGT CTCCATTGAA    60
GAGGTACCAC CTCGACCACC TAGCCCTCCA AAGAAGCCAT CTCCGACAAT CTGTGGCTCC   120
AACTATCCAC TGAGCATTGC CTTCATTGTG GTGAATGAAT TCTGCGAGCG CTTTTCCTAT   180
TATGGAATGA AAGCTGTGCT GATCCTGTAT TTCCTGTATT TCCTGCACTG GAATGAAGAT   240
ACCTCCACAT CTATATACCA TGCCTTCAGC AGCCTCTGTT ATTTTACTCC CATCCTGGGA   300
GCAGCCATTG CTGACTCGTG GTTGGGAAAA TTCAAGACAA TCATCTATCT CTCCTTGGTG   360
TATGTGCTTG GCCATGTGAT CAAGTCCTTG GGTGCCTTAC CAATACTGGG AGGACAAGTG   420
GTACACACAG TCCTATCATT GATCGGCCTG AGTCTAATAG CTTTGGGGAC AGGAGGCATC   480
AAACCCTGTG TGGCAGCTTT TGGTGGAGAC CAGTTTGAAG AAAAACATGC AGAGGAACGG   540
ACTAGATACT TCTCAGTCTT CTACCTGTCC ATCAATGCAG GGAGCTTGAT TTCTACATTT   600
ATCACACCCA TGCTGAGAGG AGATGTGCAA TGTTTTGGAG AAGACTGCTA TGCATTGGCT   660
TTTGGAGTTC CAGGACTGCT CATGGTAATT GCACTTGTTG TGTTTGCAAT GGGAAGCAAA   720
ATATACAATA AACCACCCCC TGAAGGAAAC ATAGTGGCTC AAGTTTTCAA ATGTATCTGG   780
TTTGCTATTT CCAATCGTTT CAAGAACCGT TCTGGAGACA TTCCAAAGCG ACAGCACTGG   840
CTAGACTGGG CAGCTGAGAA ATATCCAAAG CAGCTCATTA TGGATGTAAA GGCACTGACC   900
AGGGTACTAT TCCTTTATAT CCCATTGCCC ATGTTCTGGG CTCTTTTGGA TCAGCAGGGT   960
TCACGATGGA CTTTGCAAGC CATCAGGATG AATAGGAATT TGGGGTTTTT TGTGCTTCAG  1020
CCGGACCAGA TGCAGGTTCT AAATCCCTTT CTGGTTCTTA TCTTCATCCC GTTGTTTGAC  1080
TTTGTCATTT ATCGTCTGGT CTCCAAGTGT GGAATTAACT TCTCATCACT TAGGAAAATG  1140
GCTGTTGGTA TGATCCTAGC GTGCCTGGCA TTTGCAGTTG CGGCAGCTGT AGAGATAAAA  1200
ATAAATGAAA TGGCCCCAGC CCAGTCAGGT CCCCAGGAGG TTTTCCTACA AGTCTTGAAT  1260
CTGGCAGATG ATGAGGTGAA GGTGACAGTG GTGGGAAATG AAAACAATTC TCTGTTGATA  1320
GAGTCCATCA AATCCTTTCA GAAAACACCA CACTATTCCA AACTGCACCT GAAAACAAAA  1380
AGCCAGGATT TTCACTTCCA CCTGAAATAT CACAATTTGT CTCTCTACAC TGAGCATTCT  1440
GTGCAGGAGA AGAACTGGTA CAGTCTTGTC ATTCGTGAAG ATGGGAACAG TATCTCCAGC  1500
ATGATGGTAA AGGATACAGA AAGCAAAACA ACCAATGGGA TGACAACCGT GAGGTTTGTT  1560
AACACTTTGC ATAAAGATGT CAACATCTCC CTGAGTACAG ATACCTCTCT CAATGTTGGT  1620
GAAGACTATG GTGTGTCTGC TTATAGAACT GTGCAAAGAG GAGAATACCC TGCAGTGCAC  1680
TGTAGAACAG AAGATAAGAA CTTTTCTCTG AATTTGGGTC TTCTAGACTT TGGTGCAGCA  1740
TATCTGTTTG TTATTACTAA TAACACCAAT CAGGGTCTTC AGGCCTGGAA GATTGAAGAC  1800
ATTCCAGCCA ACAAAATGTC CATTGCGTGG CAGCTACCAC AATATGCCCT GGTTACAGCT  1860
GGGGAGGTCA TGTTCTCTGT CACAGGTCTT GAGTTTTCTT ATTCTCAGGC TCCCTCTAGC  1920
ATGAAATCTG TGCTCCAGGC AGCTTGGCTA TTGACAATTG CAGTTGGGAA TATCATCGTG  1980
CTTGTTGTGG CACAGTTCAG TGGCCTGGTA CAGTGGGCCG AATTCATTTT GTTTTCCTGC  2040
CTCCTGCTGG TGATCTGCCT GATCTTCTCC ATCATGGGCT ACTACTATGT TCCTGTAAAG  2100
ACAGAGGATA TGCGGGGTCC AGCAGATAAG CACATTCCTC ACATCCAGGG GAACATGATC  2160
AAACTAGAGA CCAAGAAGAC AAAACTCTGA
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Seq ID NO: 681 Protein sequence
Protein Accession #: AAB34388.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MNPFQKNESK ETLFSPVSIE EVPPRPPSPP KKPSPTICGS NYPLSIAFIV VNEFCERFSY    60
YGMKAVLILY FLYFLHWNED TSTSIYHAFS SLCYFTPILG AAIADSWLGK FKTIIYLSLV   120
YVLGHVIKSL GALPILGGQV VHTVLSLIGL SLIALGTGGI KPCVAAFGGD QFEEKHAEER   180
TRYFSVFYLS INAGSLISTF ITPMLRGDVQ CFGEDCYALA FGVPGLLMVI ALVVFAMGSK   240
IYNKPPPEGN IVAQVFKCIW FAISNRFKNR SGDIPKRQHW LDWAAEKYPK QLIMDVKALT   300
RVLFLYIPLP MFWALLDQQG SRWTLQAIRM NRNLGFFVLQ PDQMQVLNPF LVLIFIPLFD   360
FVIYRLVSKC GINFSSLRKM AVGMILACLA FAVAAAVEIK INEMAPAQSG PQEVFLQVLN   420
LADDEVKVTV VGNENNSLLI ESIKSFQKTP HYSKLHLKTK SQDFHFHLKY HNLSLYTEHS   480
VQEKNWYSLV IREDGNSISS MMVKDTESKT TNGMTTVRFV NTLHKDVNIS LSTDTSLNVG   540
EDYGVSAYRT VQRGEYPAVH CRTEDKNFSL NLGLLDFGAA YLFVITNNTN QGLQAWKIED   600
IPANKMSIAW QLPQYALVTA GEVMFSVTGL EFSYSQAPSS MKSVLQAAWL LTIAVGNIIV   660
LVVAQFSGLV QWAEFILFSC LLLVICLIFS IMGYYYVPVK TEDMRGPADK HIPHIQGNMI   720
KLETKKTKL
```

Seq ID NO: 682 DNA sequence
Nucleic Acid Accession #: NM_016077.1
Coding sequence: 128..667

```
1          11         21         31         41         51
|          |          |          |          |          |
TCGCTTTGTG ATTCTTGATC CGGAACTTTG TCACCCAGGA ACCCCGGAAG AGGTAGCTCA    60
CGCGATAGAA ACGTGTTCGC TTGCCCAGAA GAAGGGAAGG CGCGAGTGAG GAAAGGAGGT   120
ACTGTAGATG CCCTCCAAAT CCTTGGTTAT GGAATATTTG GCTCATCCCA GTACACTCGG   180
CTTGGCTGTT GGAGTTGCTT GTGGCATGTG CCTGGGCTGG AGCCTTCGAG TATGCTTTGG   240
GATGCTCCCC AAAAGCAAGA CGAGCAAGAC ACACACAGAT ACTGAAAGTG AAGCAAGCAT   300
CTTGGGAGAC AGCGGGGAGT ACAAGATGAT TCTTGTGGTT CGAAATGACT TAAAGATGGG   360
AAAAGGGAAA GTGGCTGCCC AGTGCTCTCA TGCTGCTGTT TCAGCCTACA AGCAGATTCA   420
AAGAAGAAAT CCTGAAATGC TCAAACAATG GGAATACTGT GGCCAGCCCA AGGTGGTGGT   480
CAAAGCTCCT GATGAAGAAA CCCTGATTGC ATTATTGGCC CATGCAAAAA TGCTGGGACT   540
GACTGTAAGT TTAATTCAAG ATGCTGGACG TACTCAGATT GCACCAGGCT CTCAAACTGT   600
CCTAGGGATT GGGCCAGGAC CAGCAGACCT AATTGACAAA GTCACTGGTC ACCTAAAACT   660
TTACTAGGTG GACTTTGATA TGACAACAAC CCCTCCATCA CAAGTGTTTG AAGCCTGTCA   720
GATTCTAACA ACAAAAGCTG AATTTCTTCA CCCAACTTAA ATGTTCTTGA GATGAAAATA   780
AAACCTATTC CCATGTTCTA AAAAAA
```

Seq ID NO: 683 Protein sequence
Protein Accession #: NP_057161.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MPSKSLVMEY LAHPSTLGLA VGVACGMCLG WSLRVCFGML PKSKTSKTHT DTESEASILG    60
DSGEYKMILV VRNDLKMGKG KVAAQCSHAA VSAYKQIQRR NPEMLKQWEY CGQPKVVVKA   120
PDEETLIALL AHAKMLGLTV SLIQDAGRTQ IAPGSQTVLG IGPGPADLID KVTGHLKLY
```

Seq ID NO: 684 DNA sequence
Nucleic Acid Accession #: NM_004864.1
Coding sequence: 26..952

```
1          11         21         31         41         51
|          |          |          |          |          |
CGGAACGAGG GCAACCTGCA CAGCCATGCC CGGGCAAGAA CTCAGGACGG TGAATGGCTC    60
TCAGATGCTC CTGGTGTTGC TGGTGCTCTC GTGGCTGCCG CATGGGGGCG CCCTGTCTCT   120
GGCCGAGGCG AGCCGCGCAA GTTTCCCGGG ACCCTCAGAG TTGCACTCCG AAGACTCCAG   180
ATTCCGAGAG TTGCGGAAAC GCTACGAGGA CCTGCTAACC AGGCTGCGGG CCAACCAGAG   240
CTGGGAAGAT TCGAACACCG ACCTCGTCCC GGCCCCTGCA GTCCGGATAC TCACGCCAGA   300
AGTGCGGCTG GGATCCGGCG GCCACCTGCA CCTGCGTATC TCTCGGGCCG CCCTTCCCGA   360
GGGGCTCCCC GAGGCCTCCC GCCTTCACCG GGCTCTGTTC CGGCTGTCCC CGACGGCGTC   420
AAGGTCGTGG GACGTGACAC GACCGCTGCG GCGTCAGCTC AGCCTTGCAA GACCCCAAGC   480
GCCCGCGCTG CACCTGCGAC TGTCGCCGCC GCCGTCGCAG TCGGACCAAC TGCTGGCAGA   540
ATCTTCGTCC GCACGGCCCC AGCTGGAGTT GCACTTGCGG CCGCAAGCCG CCAGGGGGCG   600
CCGCAGAGCG CGTGCGCGCA ACGGGGACGA CTGTCCGCTC GGGCCCGGGC GTTGCTGCCG   660
TCTGCACACG GTCCGCGCGT CGCTGGAAGA CCTGGGCTGG GCCGATTGGG TGCTGTCGCC   720
ACGGGAGGTG CAAGTGACCA TGTGCATCGG CGCGTGCCCG AGCCAGTTCC GGGCGGCAAA   780
CATGCACGCG CAGATCAAGA CGAGCCTGCA CCGCCTGAAG CCCGACACGG AGCCAGCGCC   840
CTGCTGCGTG CCCGCCAGCT ACAATCCCAT GGTGCTCATT CAAAAGACCG ACACCGGGGT   900
GTCGCTCCAG ACCTATGATG ACTTGTTAGC CAAAGACTGC CACTGCATAT GAGCAGTCCT   960
GGTCCTTCCA CTGTGCACCT GCGCGGGGGA GGCGACCTCA GTTGTCCTGC CCTGTGGAAT  1020
GGGCTCAAGG TTCCTGAGAC ACCCGATTCC TGCCCAAACA GCTGTATTTA TATAAGTCTG  1080
TTATTTATTA TTAATTTATT GGGGTGACCT TCTTGGGGAC TCGGGGGCTG GTCTGATGGA  1140
ACTGTGTATT TATTTAAAAC TCTGGTGATA AAAATAAAGC TGTCTGAACT GTTAAAAAAA  1200
AAAA
```

Seq ID NO: 685 Protein sequence
Protein Accession #: NP_004855.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MPGQELRTVN GSQMLLVLLV LSWLPHGGAL SLAEASRASF PGPSELHSED SRFRELRKRY    60
EDLLTRLRAN QSWEDSNTDL VPAPAVRILT PEVRLGSGGH LHLRISRAAL PEGLPEASRL   120
HRALFRLSPT ASRSWDVTRP LRRQLSLARP QAPALHLRLS PPPSQSDQLL AESSSARPQL   180
ELHLRPQAAR GRRRARARNG DDCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC   240
IGACPSQFRA ANMHAQIKTS LHRLKPDTEP APCCVPASYN PMVLIQKTDT GVSLQTYDDL   300
LAKDCHCI
```

Seq ID NO: 686 DNA sequence

Nucleic Acid Accession #: NM_002423.2
Coding sequence: 48..851

```
1          11         21         31         41         51
|          |          |          |          |          |
ACCAAATCAA CCATAGGTCC AAGAACAATT GTCTCTGGAC GGCAGCTATG CGACTCACCG   60
TGCTGTGTGC TGTGTGCCTG CTGCCTGGCA GCCTGGCCCT GCCGCTGCCT CAGGAGGCGG  120
GAGGCATGAG TGAGCTACAG TGGGAACAGG CTCAGGACTA TCTCAAGAGA TTTTATCTCT  180
ATGACTCAGA AACAAAAAAT GCCAACAGTT TAGAAGCCAA ACTCAAGGAG ATGCAAAAAT  240
TCTTTGGCCT ACCTATAACT GGAATGTTAA ACTCCCGCGT CATAGAAATA ATGCAGAAGC  300
CCAGATGTGG AGTGCCAGAT GTTGCAGAAT ACTCACTATT TCCAAATAGC CCAAAATGGA  360
CTTCCAAAGT GGTCACCTAC AGGATCGTAT CATATACTCG AGACTTACCG CATATTACAG  420
TGGATCGATT AGTGTCAAAG GCTTTAAACA TGTGGGGCAA AGAGATCCCC CTGCATTTCA  480
GGAAAGTTGT ATGGGGAACT GCTGACATCA TGATTGGCTT TGCGCGAGGA GCTCATGGGG  540
ACTCCTACCC ATTTGATGGG CCAGGAAACA CGCTGGCTCA TGCCTTTGCG CCTGGGACAG  600
GTCTCGGAGG AGATGCTCAC TTCGATGAGG ATGAACGCTG GACGGATGGT AGCAGTCTAG  660
GGATTAACTT CCTGTATGCT GCAACTCATG AACTTGGCCA TTCTTTGGGT ATGGGACATT  720
CCTCTGATCC TAATGCAGTG ATGTATCCAA CCTATGGAAA TGGAGATCCC CAAAATTTTA  780
AACTTTCCCA GGATGATATT AAAGGCATTC AGAAACTATA TGGAAAGAGA AGTAATTCAA  840
GAAAGAAATA GAAACTTCAG GCAGAACATC CATTCATTCA TTCATTGGAT TGTATATCAT  900
TGTTGCACAA TCAGAATTGA TAAGCACTGT TCCTCCACTC CATTTAGCAA TTATGTCACC  960
CTTTTTTATT GCAGTTGGTT TTTGAATGTC TTTCACTCCT TTTATTGGTT AAACTCCTTT 1020
ATGGTGTGAC TGTGTCTTAT TCCATCTATG AGCTTTGTCA GTGCGCGTAG ATGTCAATAA 1080
ATGTTACATA CACAAATAAA TAAAATGTTT ATTCCATGGT AAATTTA
```

Seq ID NO: 687 Protein sequence
Protein Accession #: NP_002414.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MRLTVLCAVC LLPGSLALPL PQEAGGMSEL QWEQAQDYLK RFYLYDSETK NANSLEAKLK   60
EMQKFFGLPI TGMLNSRVIE IMQKPRCGVP DVAEYSLFPN SPKWTSKVVT YRIVSYTRDL  120
PHITVDRLVS KALNMWGKEI PLHFRKVVWG TADIMIGFAR GAHGDSYPFD GPGNTLAHAF  180
APGTGLGGDA HFDEDERWTD GSSLGINFLY AATHELGHSL GMGHSSDPNA VMYPTYGNGD  240
PQNFKLSQDD IKGIQKLYGK RSNSRKK
```

Seq ID NO: 688 DNA sequence
Nucleic Acid Accession #: NM_005221.3
Coding sequence: 1..870

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGACAGGAG TGTTTGACAG AAGGGTCCCC AGCATCCGAT CCGGCGACTT CCAAGCTCCG   60
TTCCAGACGT CCGCAGCTAT GCACCATCCG TCTCAGGAAT CGCCAACTTT GCCCGAGTCT  120
TCAGCTACCG ATTCTGACTA CTACAGCCCT ACGGGGGGAG CCCCGCACGG CTACTGCTCT  180
CCTACCTCGG CTTCCTATGG CAAAGCTCTC AACCCCTACC AGTATCAGTA TCACGGCGTG  240
AACGGCTCCG CCGGGAGCTA CCCAGCCAAA GCTTATGCCG ACTATAGCTA CGCTAGCTCC  300
TACCACCAGT ACGGCGGCGC CTACAACCGC GTCCCAAGCG CCACCAACCA GCCAGAGAAA  360
GAAGTGACCG AGCCCGAGGT GAGAATGGTG AATGGCAAAC CAAAGAAAGT TCGTAAACCC  420
AGGACTATTT ATTCCAGCTT TCAGCTGGCC GCATTACAGA GAAGGTTTCA GAAGACTCAG  480
TACCTCGCCT TGCCGGAACG CGCCGAGCTG GCCGCCTCGC TGGGATTGAC ACAAACACAG  540
GTGAAAATCT GGTTTCAGAA CAAAAGATCC AAGATCAAGA AGATCATGAA AAACGGGGAG  600
ATGCCCCCGG AGCACAGTCC CAGCTCCAGC GACCCAATGG CGTGTAACTC GCCGCAGTCT  660
CCAGCGGTGT GGGAGCCCCA GGGCTCGTCC CGCTCGCTCA GCCACCACCC TCATGCCCAC  720
CCTCCGACCT CCAACCAGTC CCCAGCGTCC AGCTACCTGG AGAACTCTGC ATCCTGGTAC  780
ACAAGTGCAG CCAGCTCAAT CAATTCCCAC CTGCCGCCGC CGGGCTCCTT ACAGCACCCG  840
CTGGCGCTGG CCTCCGGGAC ACTCTATTAG
```

Seq ID NO: 689 Protein sequence
Protein Accession #: NP_005212.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MTGVFDRRVP SIRSGDFQAP FQTSAAMHHP SQESPTLPES SATDSDYYSP TGGAPHGYCS   60
PTSASYGKAL NPYQYQYHGV NGSAGSYPAK AYADYSYASS YHQYGGAYNR VPSATNQPEK  120
EVTEPEVRMV NGKPKKVRKP RTIYSSFQLA ALQRRFQKTQ YLALPERAEL AASLGLTQTQ  180
VKIWFQNKRS KIKKIMKNGE MPPEHSPSSS DPMACNSPQS PAVWEPQGSS RSLSHHPHAH  240
PPTSNQSPAS SYLENSASWY TSAASSINSH LPPPGSLQHP LALASGTLY
```

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

1. A method of detecting a lung cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16.

2. The method of claim 1, wherein the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-16.

3. The method of claim 1, wherein the biological sample is a tissue sample.

4. The method of claim 1, wherein the biological sample comprises isolated nucleic acids.

5. The method of claim 4, wherein the nucleic acids are mRNA.

6. The method of claim 4, further comprising the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

7. The method of claim 1, wherein the polynucleotide comprises a sequence as shown in Tables 1A-16.

8. The method of claim 1, wherein the polynucleotide is labeled.

9. The method of claim 8, wherein the label is a fluorescent label.

10. The method of claim 1, wherein the polynucleotide is immobilized on a solid surface.

11. The method of claim 1, wherein the patient is undergoing a therapeutic regimen to treat lung cancer.

12. The method of claim 1, wherein the patient is suspected of having lung cancer.

13. A method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of:

(i) providing a biological sample from a patient undergoing the therapeutic treatment; and

(ii) determining the level of a lung cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy.

14. The method of claim 13, further comprising the step of: (iii) comparing the level of the lung cancer-associated transcript to a level of the lung cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

15. The method of claim 13, wherein the patient is a human.

16. A method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of:

(i) providing a biological sample from a patient undergoing the therapeutic treatment; and

(ii) determining the level of a lung cancer-associated antibody in the biological sample by contacting the biological sample with a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, wherein the polypeptide specifically binds to the lung cancer-associated antibody, thereby monitoring the efficacy of the therapy.

17. The method of claim 16, further comprising the step of: (iii) comparing the level of the lung cancer-associated antibody to a level of the lung cancer-associated antibody in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

18. The method of claim 16, wherein the patient is a human.

19. A method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of:

(i) providing a biological sample from a patient undergoing the therapeutic treatment; and

(ii) determining the level of a lung cancer-associated polypeptide in the biological sample by contacting the biological sample with an antibody, wherein the antibody specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy.

20. The method of claim 19, further comprising the step of: (iii) comparing the level of the lung cancer-associated polypeptide to a level of the lung cancer-associated polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

21. The method of claim 19, wherein the patient is a human.

22. An isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1A-16.

23. The nucleic acid molecule of claim 22, which is labeled.

24. The nucleic acid of claim 23, wherein the label is a fluorescent label

25. An expression vector comprising the nucleic acid of claim 22.

26. A host cell comprising the expression vector of claim 25.

27. An isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16.

28. An antibody that specifically binds a polypeptide of claim 27.

29. The antibody of claim 28, further conjugated to an effector component.

30. The antibody of claim 29, wherein the effector component is a fluorescent label.

31. The antibody of claim 29, wherein the effector component is a radioisotope or a cytotoxic chemical.

32. The antibody of claim 29, which is an antibody fragment.

33. The antibody of claim 29, which is a humanized antibody

34. A method of detecting a lung cancer cell in a biological sample from a patient, the method comprising contacting the biological sample with an antibody of claim 28.

35. The method of claim 34, wherein the antibody is further conjugated to an effector component.

36. The method of claim 35, wherein the effector component is a fluorescent label.

37. A method of detecting antibodies specific to lung cancer in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprises a sequence from Tables 1A-16.

38. A method for identifying a compound that modulates a lung cancer-associated polypeptide, the method comprising the steps of:

(i) contacting the compound with a lung cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16; and

(ii) determining the functional effect of the compound upon the polypeptide.

39. The method of claim 38, wherein the functional effect is a physical effect.

40. The method of claim 38, wherein the functional effect is a chemical effect.

41. The method of claim 38, wherein the polypeptide is expressed in a eukaryotic host cell or cell membrane.

42. The method of claim 38, wherein the functional effect is determined by measuring ligand binding to the polypeptide.

43. The method of claim 38, wherein the polypeptide is recombinant.

44. A method of inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified using the method of claim 38.

45. The method of claim 44, wherein the compound is an antibody.

46. The method of claim 45, wherein the patient is a human.

47. A drug screening assay comprising the steps of

(i) administering a test compound to a mammal having lung cancer or a cell isolated therefrom;

(ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of lung cancer.

48. The assay of claim 47, wherein the control is a mammal with lung cancer or a cell therefrom that has not been treated with the test compound.

49. The assay of claim 47, wherein the control is a normal cell or mammal.

50. A method for treating a mammal having lung cancer comprising administering a compound identified by the assay of claim 47.

51. A pharmaceutiPcal composition for treating a mammal having lung cancer, the composition comprising a compound identified by the assay of claim 47 and a physiologically acceptable excipient.

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

REVISED VERSION

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
31 October 2002 (31.10.2002)

PCT

(10) International Publication Number
WO 2002/086443 A2

(51) International Patent Classification[7]: C07H 21/02, 21/04, C12Q 1/68

(21) International Application Number: PCT/US2002/012476

(22) International Filing Date: 18 April 2002 (18.04.2002)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

60/284,770	18 April 2001 (18.04.2001)	US
60/290,492	10 May 2001 (10.05.2001)	US
60/339,245	9 November 2001 (09.11.2001)	US
60/350,666	13 November 2001 (13.11.2001)	US
60/334,370	29 November 2001 (29.11.2001)	US
60/372,246	12 April 2002 (12.04.2002)	US

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(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Declaration under Rule 4.17:
— *of inventorship (Rule 4.17(iv)) for US only*

Published:
— *with declaration under Article 17(2)(a); without abstract; title not checked by the International Searching Authority*

(48) Date of publication of this revised version: 17 June 2004

(15) Information about Correction:
see PCT Gazette No. 25/2004 of 17 June 2004, Section II

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 2002/086443 A2

(54) Title: METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF LUNG CANCER

(57) Abstract:

PATENT COOPERATION TREATY

PCT

DECLARATION OF NON-ESTABLISHMENT OF INTERNATIONAL SEARCH REPORT

(PCT Article 17(2)(a), Rule 13*ter*.1(c) and 39)

Applicant's or agent's file reference 18501-15-3PC	**IMPORTANT DECLARATION**	Date of mailing (day/month/year) 15 AUG 2003
International application No. PCT/US02/12476	International filing date *(day/month/year)* 18 April 2002 (18.04.2002)	(Earliest) Priority date *(day/month/year)* 10 May 2001 (10.05.2001)
International Patent Classification (IPC) or both national classification and IPC IPC(7): C07H 21/02, 21/04; C12Q 1/68 and US Cl.: 435/6, 536/23.1, 23.5		
Applicant EOS BIOTECHNOLOGY, INC		

This International Searching Authority hereby declares, according to Article 17(2)(a), that **no international search report will be established** on the international application for the reasons indicated below.

1. ☐ The subject matter of the international application relates to:
   - a. ☐ scientific theories.
   - b. ☐ mathematical theories
   - c. ☐ plant varieties.
   - d. ☐ animal varieties.
   - e. ☐ essential biological processes for the production of plants and animals, other than microbiological processes and the products of such processes.
   - f. ☐ schemes, rules or methods of doing business.
   - g. ☐ schemes, rules or methods of performing purely mental acts.
   - h. ☐ schemes, rules or methods of playing games.
   - i. ☐ methods for treatment of the human body by surgery or therapy.
   - j. ☐ methods for treatment of the animal body by surgery or therapy.
   - k. ☐ diagnostic methods practised on the human or animal body.
   - l. ☐ mere presentations of information.
   - m. ☐ computer programs for which this International Searching Authority is not equipped to search prior art.

2. ☐ The failure of the following parts of the international application to comply with prescribed requirements prevents a meaningful search from being carried out:
   ☐ the description ☐ the claims ☐ the drawings

3. ☒ The failure of the nucleotide and/or amino acid sequence listing to comply with the standard provided for in Annex C of the Administrative Instructions prevents a meaningful search from being carried out:
   - ☐ the written form has not been furnished or does not comply with the standard.
   - ☒ the computer readable form has not been furnished or does not comply with the standard.

4. Further comments:

Name and mailing address of the ISA/US	Authorized officer
Mail Stop PCT, Attn: ISA/US Commissioner for Patents P.O. Box 1450 Alexandria, Virginia 22313-1450	Carla Myers CARLA J. MYERS PRIMARY EXAMINER
Facsimile No. (703)305-3230	Telephone No. 703-308-0196

Form PCT/ISA/203 (July 1998)

PATENT COOPERATION TREATY

From the INTERNATIONAL SEARCHING AUTHORITY

To:
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PCT

NOTIFICATION OF TRANSMITTAL OF THE INTERNATIONAL SEARCH REPORT OR THE DECLARATION

(PCT Rule 44.1)

Date of Mailing (*day/month/year*)	15 AUG 2003
Applicant's or agent's file reference 18501-15-3PC	**FOR FURTHER ACTION** See paragraphs 1 and 4 below
International application No. PCT/US02/12476	International filing date (*day/month/year*) 18 April 2002 (18.04.2002)
Applicant EOS BIOTECHNOLOGY, INC	

1. ☐ The applicant is hereby notified that the international search report has been established and is transmitted herewith.

   Filing of amendments and statement under Article 19:
   The applicant is entitled, if he so wishes, to amend the claims of the international application (see Rule 46):

   When? The time limit for filing such amendments is normally two months from the date of transmittal of the international search report.

   Where? Directly to the International Bureau of WIPO, 34, chemin des Colombettes 1211 Geneva 20, Switzerland, Facsimile No.: (41-22) 740.14.35

   For more detailed instructions, see the notes on the accompanying sheet.

2. ☒ The applicant is hereby notified that no international search report will be established and that the declaration under Article 17(2)(a) to that effect is transmitted herewith.

3. ☐ **With regard to the protest** against payment of (an) additional fee(s) under Rule 40.2, the applicant is notified that:

   ☐ the protest together with the decision thereon has been transmitted to the International Bureau together with the applicant's request to forward the texts of both the protest and the decision thereon to the designated Offices.

   ☐ no decision has been made yet on the protest; the applicant will be notified as soon as a decision is made.

4. **Reminders**

   Shortly after **18 months** from the priority date, the international application will be published by the International Bureau. If the applicant wishes to avoid or postpone publication, a notice of withdrawal of the international application, or of the priority claim, must reach the International Bureau as provided in Rules 90 *bis*.1 and 90 *bis*.3, respectively, before the completion of the technical preparations for international publication.

   Within **19 months** from the priority date, but only in respect of some designated Offices, a demand for international preliminary examination must be filed if the applicant wishes to postpone the entry into the national phase **until 30 months** from the priority date (in some Offices even later); otherwise the applicant must, within **20 months** from the priority date, perform the prescribed acts for entry into the national phase before those designated Offices.

   In respect of other designated Offices, the time limit of **30 months** (or later) will apply even if no demand is filed within 19 months.

   See the Annex to Form PCT/IB/301 and, for details about the applicable time limits, Office by Office, see the *PCT Applicant's Guide*, Volume II, National Chapters and the WIPO Internet site.

Name and mailing address of the ISA/US Mail Stop PCT, Attn: ISA/US Commissioner for Patents P.O. Box 1450 Alexandria, Virginia 22313-1450 Facsimile No. (703)305-3230	Authorized officer Carla Myers Valerie Bell-Harris for Telephone No. 703-308-0196

Form PCT/ISA/220 (April 2002)

(*See notes on accompanying sheet*)